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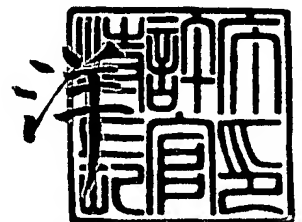
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【プルーフの要否】 要

【書類名】 明細書

【発明の名称】 全長 cDNA

【特許請求の範囲】

【請求項 1】 下記 (a) から (g) のいずれかに記載のポリヌクレオチド。

(a) 配列番号：1～配列番号：1956 のいずれかに記載された塩基配列の蛋白質コード領域を含むポリヌクレオチド。

(b) 配列番号：1957～配列番号：3912 のいずれかに記載のアミノ酸配列からなる蛋白質をコードする塩基配列を含むポリヌクレオチド。

(c) 配列番号：1957～配列番号：3912 から選択されたいずれかの配列番号に記載のアミノ酸配列において、1 若しくは複数のアミノ酸が置換、欠失、挿入、および／または付加したアミノ酸配列からなり、前記選択されたアミノ酸配列からなる蛋白質と機能的に同等な蛋白質をコードする塩基配列を含むポリヌクレオチド。

(d) 配列番号：1～配列番号：1956 から選択されたいずれかの配列番号に記載の塩基配列からなるポリヌクレオチドとハイブリダイズするポリヌクレオチドであって、前記選択された塩基配列によってコードされる蛋白質と機能的に同等な蛋白質をコードする塩基配列を含むポリヌクレオチド。

(e) (a) から (d) に記載のポリヌクレオチドによってコードされる蛋白質の部分アミノ酸配列をコードする塩基配列を含むポリヌクレオチド。

(f) 配列番号：1～配列番号：1956 のいずれかに記載の塩基配列に対して少なくとも 70% の同一性を有する塩基配列を含むポリヌクレオチド。

(g) 配列番号：1～配列番号：1956 のいずれかに記載の塩基配列に対して少なくとも 90% の同一性を有する塩基配列を含むポリヌクレオチド。

【請求項 2】 請求項 1 に記載のポリヌクレオチドのいずれか一つによってコードされる蛋白質、またはその部分ペプチド。

【請求項 3】 請求項 2 に記載されたいずれかの蛋白質、またはペプチドに結合する抗体。

【請求項 4】 請求項 2 に記載されたいずれかの蛋白質、またはペプチドと、請求項 3 に記載の抗体とを接触させ、両者の結合を観察する工程を含む、請求項

2 に記載されたいずれかの蛋白質、またはペプチドの免疫学的測定方法。

【請求項 5】請求項 1 に記載されたポリヌクレオチドのいずれか一つを含むベクター。

【請求項 6】請求項 1 に記載のポリヌクレオチド、または請求項 5 に記載のベクターを保持する形質転換体。

【請求項 7】請求項 1 に記載されたポリヌクレオチドのいずれか一つ、または請求項 5 に記載のベクターを発現可能に保持する形質転換体。

【請求項 8】請求項 7 に記載の形質転換体を培養し、発現産物を回収する工程を含む、請求項 2 に記載されたいずれかの蛋白質またはペプチドの製造方法。

【請求項 9】配列番号：1～配列番号：1956 のいずれかに記載された塩基配列、またはその相補鎖に相補的な塩基配列からなる 15 ヌクレオチド以上の鎖長を持つオリゴヌクレオチド。

【請求項 10】請求項 9 に記載のオリゴヌクレオチドからなる、ポリヌクレオチド合成用プライマー。

【請求項 11】請求項 9 に記載のオリゴヌクレオチドからなる、ポリヌクレオチドの検出用プローブ。

【請求項 12】下記 (a) から (c) のいずれかに記載のポリヌクレオチド。

(a) 請求項 1 に記載のポリヌクレオチドの転写産物と相補的な塩基配列を有するアンチセンスポリヌクレオチド

(b) 請求項 1 に記載のポリヌクレオチドの転写産物を特異的に開裂するリボザイム活性を有するポリヌクレオチド

(c) 宿主細胞における発現時に、RNAi 効果により、請求項 1 に記載のポリヌクレオチドの発現を抑制するポリヌクレオチド

【請求項 13】次の工程を含む、請求項 1 に記載のポリヌクレオチドの検出方法。

a) 標的ポリヌクレオチドと請求項 9 に記載のオリゴヌクレオチドを、ハイブリダイゼーションが可能な条件下でインキュベートする工程、

b) 標的ポリヌクレオチドと請求項 9 に記載のオリゴヌクレオチドのハイブリダ

イゼーションを検出する工程。

【請求項 1 4】 配列番号： 1 ～配列番号： 1 9 5 6 のいずれかに記載された塩基配列および／または配列番号： 1 9 5 7 ～配列番号： 3 9 1 2 のいずれかに記載のアミノ酸配列から選択された少なくとも 1 つの配列情報を含むポリヌクレオチドおよび／または蛋白質データベース。

【発明の詳細な説明】

【 0 0 0 1 】

【発明の属する技術分野】

本発明は、新規な蛋白質をコードするポリヌクレオチド、このポリヌクレオチドによってコードされる蛋白質、及びそれらの新規な用途に関する。

【 0 0 0 2 】

【従来の技術】

現在、世界的なレベルで様々な生物のゲノム配列の解明とその解析が進められている。既に40種類を越える原核微生物、下等真核生物の出芽酵母、多細胞性真核生物である線虫、高等植物であるシロイヌナズナ等で、その全ゲノム配列が決定された。30億塩基対といわれるヒトのゲノムについては、世界的な協力体制のもとでその解析が進められて2001年にドラフト配列が公開された。そして、2003年にはその全構造が明らかになり、公開されようとしている。ゲノム配列を明らかにする目的は、全ての遺伝子の機能や制御、あるいは遺伝子間、蛋白質間、細胞間さらには個体間における相互作用のネットワークとして複雑な生命現象を理解するところにある。種々の生物種のゲノム情報から生命現象を解明していくことは、単に学術分野における研究課題として重要であるのみならず、そこで得られる研究成果をいかに産業上の応用へと発展させていくかという点で、その社会的な意義も大きい。

【 0 0 0 3 】

ところが単にゲノム配列を決定しただけでは、全ての遺伝子の機能を明らかにできるわけではない。例えば酵母では、ゲノム配列から推定された約6,000の遺伝子の約半数しか、その機能を推定できなかった。一方、ヒトには約3～4万種類の遺伝子が存在すると推測されており、さらにオルタナティブスプライシングに

よるバリエーションも考慮に入れると10万種以上のmRNAが存在すると言われている。そこで、ゲノム配列から明らかにされてくる膨大な量の新しい遺伝子の機能を、迅速かつ効率的に解明していくための「ハイスループット遺伝子機能解析システム」の確立が、強く望まれている。

【0 0 0 4】

真核生物のゲノム配列では、多くの場合、一つの遺伝子がイントロンによって複数のエクソンに分断されている。そのため、ゲノム配列情報だけからそこにコードされる蛋白質の構造を正確に予測するには、多くの問題がある。一方、イントロンが除かれたmRNAから作製されるcDNAでは、蛋白質のアミノ酸配列の情報が一つの連続した配列情報として得られるため、容易にその一次構造を明らかにすることが可能である。ヒトのcDNAの研究では、これまでに300万を越えるEST (Expression Sequence Tags) データがパブリックドメインに公開されており、それらはヒトの全遺伝子の80%以上をカバーしているものと推定されている。

これらの情報は、ヒト遺伝子構造の解明やゲノム配列におけるエクソン領域の予測、あるいはその発現プロファイルの推定など、様々な角度から利用されている。ところが、これらのヒトEST情報の多くはcDNAの3' 末端側近傍に集中しているため、特にmRNAの5' 末端近傍の情報が極端に不足している状況にある。また、ヒトcDNAの中で全長でコードされている蛋白質の配列が予測されているmRNAは約1万5千種類程度である。

【0 0 0 5】

完全長cDNAでは、その5' 末端配列からゲノム配列上でのmRNA転写開始点が特定できる上、その配列の中に含まれるmRNAの安定性や翻訳段階での発現制御に関わる因子の解析が可能である。また、翻訳開始点であるATGコドンをも5' 側に含むことから、正しいフレームで蛋白質への翻訳を行うことができる。したがって、適当な遺伝子発現系を適用することで、そのcDNAがコードする蛋白質を大量に生産したり、蛋白質を発現させてその生物学的活性を解析することも可能になる。このように、完全長cDNAの解析からはゲノム配列解析を相補する重要な情報が得られる。また、発現可能な全長cDNAクローンは、その遺伝子の機能の実証的な解析や産業分野での応用への展開において、その重要性はきわめて高い。

【0006】

したがって新規なヒト全長cDNAが単離されれば、それらの遺伝子が関与している種々の疾患に対する医薬品開発に利用され得る。これらの遺伝子がコードする蛋白質はそれ自身に医薬品としての有用性を期待できる。したがって、新規なヒト蛋白質をコードするcDNAの全長を取得することには大きな意義がある。

特にヒト分泌蛋白質、または膜蛋白質には、そのものがティッシュプラスミノーゲンアクチベーター (TPA)のように、医薬品として有用なものや、膜レセプターのように医薬品の標的蛋白質になりうるものが多い。また、シグナル伝達関連蛋白質 (Protein kinase等)、糖蛋白質関連蛋白質、転写関連蛋白質等は疾患との関係が解明されている遺伝子が多い。更に疾患関連蛋白質の遺伝子は、ヒト遺伝子と疾患の関係が解明されている遺伝子が多い遺伝子群である。

したがって、ヒトにおいて分離が進んでいない新規な全長cDNAを提供する意義は大きい。中でも、分泌・膜蛋白質をコードする蛋白質をコードするcDNAは、蛋白質自身に医薬品としての有用性を期待できること、あるいは疾患に関連する遺伝子を多く含む可能性のあることから、未知のcDNAの分離が望まれている。あるいは、疾患との関連性が強いと予測される遺伝子群である、シグナル伝達蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質、そして疾患関連蛋白質をコードする遺伝子も、治療のための標的分子として、またこれらの蛋白質自身に医薬品としての有用性を期待できる。したがって、これらの蛋白質をコードするcDNAの全長を明らかにすることには大きな意義がある。

【0007】

【発明が解決しようとする課題】

本発明は、新規な蛋白質をコードするポリヌクレオチド、該ポリヌクレオチドによってコードされる蛋白質、並びにその用途の提供を課題としている。

【0008】

【課題を解決するための手段】

本発明者らは、オリゴキャップ法[K. Maruyama and S. Sugano, Gene, 138: 171-174 (1994); Y. Suzuki et al., Gene, 200: 149-156 (1997)]を改良した方法(WO 01/04286)で作成した全長率の非常に高いヒトcDNAライブラリーから、全

長cDNAクローンであると予測される、ヒト全長cDNAを効率よくクローニングする方法を開発した。次いで、この方法で取得した全長率の高いcDNAクローンの塩基配列を主に5'側から、また必要に応じ3'側からも決定した。

更に、得られたクローンのうち新規で全長と予測される代表的クローンについて全長塩基配列を決定した。得られた全長塩基配列について、以下に示すデータベースに対してBLASTを用いた相同性検索を行った。本発明の相同性検索は、cDNAの全コード領域を含む全長cDNAの情報に基づいて行われているので、蛋白質のあらゆる部分に対する相同性を解析することができる。したがって本発明においては、相同性検索の信頼性が飛躍的に向上している。

[1] SwissProt (http://www.ebi.ac.uk/ebi_docs/SwissProt_db/swisshome.html)、

[2] GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>)、

[3] nr(重複を除いたGenBankの塩基配列のコーディングシーケンス (CDS) データ、

SwissProt、

PDB(<http://www.rcsb.org/pdb/index.html>)、

PIR(<http://pir.georgetown.edu/pirwww/pirhome.shtml>)、

PRF(<http://www.prf.or.jp/en/>)、を組み合わせで構築されている蛋白質データベース)、および

[4] RefSeq(<http://www.ncbi.nlm.nih.gov/LocusLink/refseq.html>)

【0009】

また得られた5'側の塩基配列をもとに構築した大規模cDNAデータベースを解析して、全長塩基配列を決定したクローンの遺伝子発現プロファイルを解析した。本発明者らは、これらの解析の結果に基づいて、本発明の遺伝子の有用性を明らかにした。

本発明においては、全長塩基配列情報に基づくin silicoでの発現プロファイルの解析によって遺伝子の機能を明らかにしている。発現頻度解析に用いた発現プロファイルは、十分量の断片配列のデータベースに基づいて解析した。この発現プロファイルに、本発明で得られた多くのcDNAクローンの全長塩基配列を照合

することによって、発現頻度解析を行った。このように、量的に十分な解析母体（発現プロファイル）に対して、幅広い遺伝子の全長塩基配列を照合したことによって、信頼性の高い解析が可能となった。すなわち、本発明の全長配列を利用した発現頻度解析の結果は、あるcDNAライブラリーの由来となった組織や細胞の遺伝子発現頻度をより正確に反映していると言えることができる。つまり、本発明のcDNAの全長塩基配列情報によって、信頼性の高い発現頻度解析が可能となったことを意味している。

【0 0 1 0】

本発明における全長cDNAクローンは、[1]オリゴキャップ法による全長率の高いcDNAライブラリーの作成、および[2] 5'末端側の配列をアセンブルし、その結果形成されたクラスターの中でも最も全長らしいもの（5'側に長いものが多い）を選択する、という方法を組み合わせて取得した、全長cDNAクローンである。しかし、本発明が提供するポリヌクレオチドの5'末端および3'末端の配列をもとに設計されたプライマーを利用すれば、必ずしもこのような特殊な方法を用いずとも、容易に全長cDNAの取得が可能となる。なお、発現可能なcDNAを取得するためのプライマー設計は、ポリヌクレオチドの5'末端および3'末端配列を用いることに限定されない。

【0 0 1 1】

すなわち本発明は、次のポリヌクレオチドと、このポリヌクレオチドによってコードされる蛋白質に関する。

〔1〕下記（a）から（g）のいずれかに記載のポリヌクレオチド。

（a）配列番号：1～配列番号：1956のいずれかに記載された塩基配列の蛋白質コード領域を含むポリヌクレオチド。

（b）配列番号：1957～配列番号：3912のいずれかに記載のアミノ酸配列からなる蛋白質をコードする塩基配列を含むポリヌクレオチド。

（c）配列番号：1957～配列番号：3912から選択されたいずれかの配列番号に記載のアミノ酸配列において、1若しくは複数のアミノ酸が置換、欠失、挿入、および／または付加したアミノ酸配列からなり、前記選択されたアミノ酸配列からなる蛋白質と機能的に同等な蛋白質をコードする塩基配列を含むポリ

ヌクレオチド。

(d) 配列番号: 1 ~ 配列番号: 1956 から選択されたいずれかの配列番号に記載の塩基配列からなるポリヌクレオチドとハイブリダイズするポリヌクレオチドであって、前記選択された塩基配列によってコードされる蛋白質と機能的に同等な蛋白質をコードする塩基配列を含むポリヌクレオチド。

(e) (a) から (d) に記載のポリヌクレオチドによってコードされる蛋白質の部分アミノ酸配列をコードする塩基配列を含むポリヌクレオチド。

(f) 配列番号: 1 ~ 配列番号: 1956 のいずれかに記載の塩基配列に対して少なくとも 70% の同一性を有する塩基配列を含むポリヌクレオチド。

(g) 配列番号: 1 ~ 配列番号: 1956 のいずれかに記載の塩基配列に対して少なくとも 90% の同一性を有する塩基配列を含むポリヌクレオチド。

[2] [1] に記載のポリヌクレオチドのいずれか一つによってコードされる蛋白質、またはその部分ペプチド。

[3] [2] に記載されたいずれかの蛋白質、またはペプチドに結合する抗体。

[4] [2] に記載されたいずれかの蛋白質、またはペプチドと、[3] に記載の抗体とを接触させ、両者の結合を観察する工程を含む、[2] に記載されたいずれかの蛋白質、またはペプチドの免疫学的測定方法。

[5] [1] に記載されたポリヌクレオチドのいずれか一つを含むベクター。

[6] [1] に記載のポリヌクレオチド、または [5] に記載のベクターを保持する形質転換体。

[7] [1] に記載されたポリヌクレオチドのいずれか一つ、または [5] に記載のベクターを発現可能に保持する形質転換体。

[8] [7] に記載の形質転換体を培養し、発現産物を回収する工程を含む、[2] に記載されたいずれかの蛋白質またはペプチドの製造方法。

[9] 配列番号: 1 ~ 配列番号: 1956 のいずれかに記載された塩基配列、またはその相補鎖に相補的な塩基配列からなる 15 ヌクレオチド以上の鎖長を持つオリゴヌクレオチド。

[10] [9] に記載のオリゴヌクレオチドからなる、ポリヌクレオチド合成用プライマー。

〔11〕〔9〕に記載のオリゴヌクレオチドからなる、ポリヌクレオチドの検出用プローブ。

〔12〕下記（a）から（c）のいずれかに記載のポリヌクレオチド。

（a）〔1〕に記載のポリヌクレオチドの転写産物と相補的な塩基配列を有するアンチセンスポリヌクレオチド

（b）〔1〕に記載のポリヌクレオチドの転写産物を特異的に開裂するリボザイム活性を有するポリヌクレオチド

（c）宿主細胞における発現時に、RNAi効果により、〔1〕に記載のポリヌクレオチドの発現を抑制するポリヌクレオチド

〔13〕次の工程を含む、〔1〕に記載のポリヌクレオチドの検出方法。

a) 標的ポリヌクレオチドと〔9〕に記載のオリゴヌクレオチドを、ハイブリダイゼーションが可能な条件下でインキュベートする工程、

b) 標的ポリヌクレオチドと〔9〕に記載のオリゴヌクレオチドのハイブリダイゼーションを検出する工程。

〔14〕配列番号：1～配列番号：1956のいずれかに記載された塩基配列および／または配列番号：1957～配列番号：3912のいずれかに記載のアミノ酸配列から選択された少なくとも1つの配列情報を含むポリヌクレオチドおよび／または蛋白質データベース。

【0012】

本発明において、ポリヌクレオチドとはDNAやRNAのようにヌクレオチドが多数重合した分子を意味する。重合するヌクレオチドの数は特に制限されない。ポリヌクレオチドの重合度が比較的低い場合には特にオリゴヌクレオチドとも表現するが、これも本発明のポリヌクレオチドに含まれる。本発明のポリヌクレオチド、またはオリゴヌクレオチドは、天然のものであることもできるし、化学的に合成されたものであることもできる。あるいはまた、鋳型となるDNAをもとにPCRのような酵素的な反応によって合成されたものであっても良い。更に本発明のポリヌクレオチドは、化学的に修飾されたものであっても良い。また本発明には、1本鎖ポリヌクレオチドのみならず、2本鎖ポリヌクレオチドも含まれる。本明細書、特に請求項において、単にポリヌクレオチドと記載するときには、1本鎖ポ

リヌクレオチドのみならず2本鎖ポリヌクレオチドをも指すものとする。2本鎖ポリヌクレオチドを意味するときには、一方の鎖のみについての塩基配列が記載されることになるが、センス鎖の塩基配列に基づいてその相補鎖の塩基配列は必然的に規定される。

【 0 0 1 3 】

本発明によって提供されるcDNAはいずれも全長cDNAである。本発明における全長cDNAとは、そのcDNAの翻訳開始点となるATGコドンを含むことを意味する。天然のmRNAが蛋白質コード領域の上流や下流に本来備えている非翻訳領域の有無は問わない。また本発明の全長cDNAは、望ましくは終止コドンを有する。

【 0 0 1 4 】

【発明の実施の形態】

本発明のすべてのクローン（1956クローン）は新規で、蛋白質の全長をコードするものである。またすべてのクローンは、全長性の高いオリゴキャップ法で取得されたcDNAであり、その5'末端配列をGenBank、UniGene(Human) (<http://www.ncbi.nlm.nih.gov/UniGene>) データベースの"complete cds"表記のあるmRNA配列に対して、BLAST [S. F. Altschul, W. Gish, W. Miller, E. W. Myers & D. J. Lipman, J. Mol. Biol., 215: 403-410 (1990); W. Gish & D. J. States, Nature Genet., 3: 266-272 (1993)]により相同性検索を行って選別された、ヒトmRNAに対して同一でない（すなわち新規である）クローンであり、またアセンブルを行った結果形成されたクラスターのメンバーのうちでより全長性が高いと思われるクローンである。クラスター中で全長性が高いと思われる塩基配列は、5'側に長いものが最も多かった。

【 0 0 1 5 】

本発明の全ての全長cDNAは、5'末端配列と3'末端配列に基づいて設計されたプライマーセット、あるいは5'末端配列に基づいて設計されたプライマーとポリA配列に対応するオリゴdT配列とで構成されるプライマーセットを使用し、PCR (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4) 等の手法を用いることにより合成することができる。表1に、本発明の全長cDNA1956クローンのクローン名とそ

の全長塩基配列を示す配列番号、および全長塩基配列から推定されるCDS部位と翻訳されたアミノ酸を示す配列番号を示す。CDS部位の存在位置については、「[DDBJ/EMBL/GenBank Feature Table Definition] (<http://www.ncbi.nlm.nih.gov/collab/FT/index.html>)」の規則に従って記載した。開始位置番号はメチオニンをコードする塩基である「ATG」の1文字目であり、終了位置番号はストップコドンの3文字目である。これを「..」で挟んで記載した。ただし、終止コドンが現れないクローンについては上記規則に則って「>」を用いて終了位置を記載した。

【 0 0 1 6 】

【表 1】

クローン名	塩基配列 番号	CDS位置	アミノ酸 配列番号
3NB692004045	1	220..>1437	1957
ADIPS2000069	2	48..1538	1958
ADRGL2010315	3	1182..1604	1959
ADRGL2010594	4	203.. 664	1960
AHMSC1000138	5	135.. 455	1961
ASTR02008972	6	455.. 805	1962
ASTR02015162	7	244.. 951	1963
ASTR02016114	8	796..1779	1964
ASTR03000154	9	2154..2807	1965
BEAST2000981	10	149..1357	1966
BLADE2000256	11	461..1687	1967
BLADE2001031	12	27.. 506	1968
BLADE2002310	13	1065..>2616	1969
BLADE2002744	14	82.. 510	1970
BLADE2004849	15	276..1202	1971

BLADE2006043	16	218.. 622	1972
BLADE2007735	17	310.. 723	1973
BLADE2007744	18	1629..>1944	1974
BLADE2007799	19	917.. 2158	1975
BLADE2008809	20	286.. 1575	1976
BRACE1000475	21	2878.. 3471	1977
BRACE2002392	22	76.. 1008	1978
BRACE2003628	23	145.. 1164	1979
BRACE2005991	24	337.. 666	1980
BRACE2010336	25	23.. 1387	1981
BRACE2012528	26	114.. 1289	1982
BRACE2012625	27	84.. 1406	1983
BRACE2012833	28	244.. 651	1984
BRACE2012838	29	127.. 468	1985
BRACE2012936	30	617.. 994	1986
BRACE2012947	31	756.. 1223	1987
BRACE2013009	32	777.. 1487	1988
BRACE2013126	33	334.. 651	1989
BRACE2013132	34	73.. 795	1990
BRACE2016896	35	27.. 1298	1991
BRACE2017359	36	755.. 1228	1992
BRACE2017397	37	99.. 872	1993
BRACE2017580	38	514.. 834	1994
BRACE2017844	39	1674..>2015	1995
BRACE2017872	40	148..>1404	1996
BRACE2017992	41	934.. 1245	1997
BRACE2019348	42	1423.. 2004	1998
BRACE2023633	43	122.. 478	1999
BRACE2023744	44	349.. 771	2000

BRACE2025452	45	55.. 426	2001
BRACE2026404	46	67.. 408	2002
BRACE2027312	47	255.. 848	2003
BRACE2027382	48	1749.. 2090	2004
BRACE2028956	49	133.. 480	2005
BRACE2030039	50	87.. 719	2006
BRACE2032584	51	129.. 485	2007
BRACE2033128	52	296.. 676	2008
BRACE2034434	53	1963.. 2664	2009
BRACE2035120	54	22.. 1938	2010
BRACE2035191	55	207.. 542	2011
BRACE2039362	56	81.. 440	2012
BRACE2039607	57	1850.. 2398	2013
BRACE2042541	58	96.. 1562	2014
BRACE2046976	59	836.. 1345	2015
BRACE2047232	60	1434.. 2363	2016
BRACE2047975	61	299.. 652	2017
BRACE3001403	62	1965.. 2507	2018
BRACE3001973	63	24.. 2702	2019
BRACE3002264	64	72.. 2870	2020
BRACE3002344	65	113.. 3295	2021
BRACE3002541	66	2255.. 2593	2022
BRACE3002756	67	595.. 2700	2023
BRACE3003866	68	2667.. 3542	2024
BRACE3004046	69	2774.. 3277	2025
BRACE3004371	70	467.. 832	2026
BRACE3004767	71	3944.. 4390	2027
BRACE3004887	72	2217.. 2792	2028
BRACE3004981	73	3154.. 3624	2029

BRACE3005870	74	5.. 379	2030
BRACE3005903	75	328..3378	2031
BRACE3006553	76	2589..3344	2032
BRACE3007649	77	4951..5472	2033
BRACE3007869	78	932..1549	2034
BRACE3009075	79	1318..2025	2035
BRACE3009265	80	1886..2374	2036
BRACE3009392	81	2134..3072	2037
BRACE3009416	82	2056..2805	2038
BRACE3009539	83	117.. 449	2039
BRACE3010702	84	1062..1619	2040
BRACE3011447	85	289.. 786	2041
BRACE3011774	86	906..1331	2042
BRACE3013418	87	17..3121	2043
BRACE3013874	88	765..2255	2044
BRACE3013986	89	335.. 661	2045
BRACE3014523	90	318..1532	2046
BRACE3014714	91	1034..2182	2047
BRACE3015090	92	287.. 616	2048
BRACE3015898	93	119.. 448	2049
BRACE3016020	94	62.. 586	2050
BRACE3016167	95	67.. 507	2051
BRACE3016580	96	225.. 578	2052
BRACE3016788	97	1740..2486	2053
BRACE3016810	98	2064..2561	2054
BRACE3016862	99	33.. 335	2055
BRACE3017253	100	86..1342	2056
BRACE3018083	101	1447..2541	2057
BRACE3019570	102	320..3358	2058

BRACE3019611	103	2005..2484	2059
BRACE3019817	104	7.. 345	2060
BRACE3019941	105	1120..3507	2061
BRACE3020356	106	344.. 661	2062
BRACE3020669	107	2192..2650	2063
BRACE3021430	108	243.. 686	2064
BRACE3021517	109	218.. 523	2065
BRACE3021805	110	312..1283	2066
BRACE3022051	111	1042..1515	2067
BRACE3022303	112	2107..3009	2068
BRACE3022312	113	98..1003	2069
BRACE3022340	114	20..2785	2070
BRACE3022847	115	560..1066	2071
BRACE3023604	116	600..>1057	2072
BRACE3024379	117	412.. 717	2073
BRACE3024444	118	129.. 455	2074
BRACE3024497	119	219.. 545	2075
BRACE3024537	120	377.. 724	2076
BRACE3024879	121	142.. 786	2077
BRACE3025627	122	1648..2019	2078
BRACE3025719	123	111..1811	2079
BRACE3026161	124	330.. 722	2080
BRACE3026290	125	211..3225	2081
BRACE3026345	126	2603..3145	2082
BRACE3026456	127	2113..2439	2083
BRACE3026802	128	298..1260	2084
BRACE3026844	129	1231..3081	2085
BRACE3026947	130	1528..3849	2086
BRACE3027256	131	670..1020	2087

BRACE3027931	132	64..1260	2088
BRACE3028360	133	4486..4920	2089
BRACE3028895	134	716..1129	2090
BRACE3028998	135	264.. 785	2091
BRACE3029005	136	394.. 771	2092
BRACE3029021	137	208.. 657	2093
BRACE3029205	138	3800..4531	2094
BRACE3029447	139	1873..2424	2095
BRACE3030538	140	253.. 828	2096
BRACE3031161	141	138.. 494	2097
BRACE3031184	142	57.. 422	2098
BRACE3031185	143	11.. 370	2099
BRACE3031315	144	1220..2563	2100
BRACE3031372	145	1587..2429	2101
BRACE3031579	146	1636..2079	2102
BRACE3031728	147	22..2196	2103
BRACE3031743	148	53.. 805	2104
BRACE3031843	149	115.. 429	2105
BRACE3032385	150	103..2007	2106
BRACE3032537	151	639..1199	2107
BRACE3032538	152	3317..4198	2108
BRACE3032631	153	790..1701	2109
BRACE3032980	154	223.. 618	2110
BRACE3033525	155	1346..1672	2111
BRACE3034183	156	190..1686	2112
BRACE3034389	157	176..1294	2113
BRACE3034964	158	2385..3278	2114
BRACE3034993	159	1533..1838	2115
BRACE3035168	160	829..1149	2116

BRACE3036156	161	3.. 338	2117
BRACE3036271	162	2019..3125	2118
BRACE3036283	163	2599..3186	2119
BRACE3037612	164	2401..2892	2120
BRACE3037637	165	199.. 570	2121
BRACE3037803	166	2507..2884	2122
BRACE3038012	167	2134..2634	2123
BRACE3038030	168	976..1302	2124
BRACE3038570	169	223.. 621	2125
BRACE3038760	170	2145..2906	2126
BRACE3039288	171	876..1511	2127
BRACE3039358	172	385..2664	2128
BRACE3039378	173	479..2254	2129
BRACE3039454	174	351..1073	2130
BRACE3040012	175	145.. 465	2131
BRACE3040239	176	1505..2548	2132
BRACE3040504	177	307.. 738	2133
BRACE3040644	178	1280..3214	2134
BRACE3040863	179	12.. 626	2135
BRACE3041059	180	99..2558	2136
BRACE3041162	181	2041..2604	2137
BRACE3041827	182	3169..3561	2138
BRACE3042046	183	1488..2879	2139
BRACE3042210	184	174.. 533	2140
BRACE3042326	185	216..2366	2141
BRACE3042409	186	238..3258	2142
BRACE3042432	187	2084..2473	2143
BRACE3042594	188	179.. 517	2144
BRACE3043597	189	23.. 460	2145

BRACE3044090	190	1198..1602	2146
BRACE3044172	191	803..3067	2147
BRACE3044247	192	107.. 451	2148
BRACE3044377	193	223.. 900	2149
BRACE3044495	194	893..1510	2150
BRACE3045078	195	90.. 593	2151
BRACE3045145	196	187.. 501	2152
BRACE3045424	197	275.. 619	2153
BRACE3045708	198	219.. 587	2154
BRACE3045981	199	302.. 724	2155
BRACE3046049	200	849..1298	2156
BRACE3046152	201	2241..3440	2157
BRACE3046294	202	189.. 578	2158
BRACE3046466	203	111..2969	2159
BRACE3046491	204	26..2275	2160
BRACE3046609	205	1563..2477	2161
BRACE3046837	206	25.. 558	2162
BRACE3046855	207	3735..4247	2163
BRACE3046966	208	12.. 452	2164
BRACE3047018	209	2886..3425	2165
BRACE3047482	210	43..2313	2166
BRACE3047801	211	17..3757	2167
BRACE3048483	212	2340..2672	2168
BRACE3048565	213	264.. 626	2169
BRACE3048615	214	352.. 729	2170
BRACE3048677	215	238.. 732	2171
BRACE3048756	216	2483..3052	2172
BRACE3048904	217	229.. 759	2173
BRACE3048905	218	1733..2038	2174

BRACE3049186	219	106.. 519	2175
BRACE3049714	220	294..2957	2176
BRACE3050270	221	2725..3291	2177
BRACE3050504	222	287..1306	2178
BRACE3051144	223	176.. 763	2179
BRACE3051621	224	1748..3418	2180
BRACE3051627	225	1216..2235	2181
BRACE3051722	226	816..1190	2182
BRACE3051819	227	3..2801	2183
BRACE3051879	228	193.. 519	2184
BRACE3052321	229	124..1614	2185
BRACE3052410	230	17..2926	2186
BRACE3052486	231	1622..1942	2187
BRACE3052595	232	40.. 780	2188
BRALZ2003119	233	363..1844	2189
BRALZ2007661	234	1159..1746	2190
BRALZ2008930	235	61.. 825	2191
BRALZ2010842	236	173..1048	2192
BRALZ2011337	237	3.. 305	2193
BRALZ2013621	238	214.. 576	2194
BRALZ2013690	239	283.. 603	2195
BRALZ2014054	240	213.. 920	2196
BRAMY2015516	241	747..1292	2197
BRAMY2021098	242	1405..1785	2198
BRAMY2022320	243	320..1975	2199
BRAMY2023939	244	39..>2128	2200
BRAMY2025495	245	552..1031	2201
BRAMY2031516	246	1227..>2798	2202
BRAMY2033895	247	175.. 531	2203

BRAMY2035801	248	1487..1963	2204
BRAMY2036254	249	156.. 548	2205
BRAMY2036266	250	294.. 776	2206
BRAMY2037609	251	107.. 787	2207
BRAMY2039630	252	1281..1703	2208
BRAMY2040915	253	488..2380	2209
BRAMY2041347	254	332..2059	2210
BRAMY2041384	255	682..2211	2211
BRAMY2041507	256	1331..2029	2212
BRAMY2044686	257	1418..1990	2213
BRAMY2046489	258	375.. 698	2214
BRAMY2046537	259	293.. 952	2215
BRAMY3000692	260	1427..1960	2216
BRAMY3001409	261	1952..2428	2217
BRAMY3002329	262	2751..3269	2218
BRAMY3002508	263	1949..2374	2219
BRAMY3002886	264	25..2148	2220
BRAMY3004126	265	1657..2676	2221
BRAMY3004364	266	1056..1466	2222
BRAMY3005184	267	430..3735	2223
BRAMY3005656	268	919..1632	2224
BRAMY3005912	269	3863..4513	2225
BRAMY3007078	270	493..3057	2226
BRAMY3007449	271	229.. 726	2227
BRAMY3007471	272	3.. 344	2228
BRAMY3008436	273	3093..3557	2229
BRAMY3009158	274	116.. 511	2230
BRAMY3009491	275	2262..3581	2231
BRAMY3009556	276	3108..3455	2232

BRAMY3009904	277	286.. 705	2233
BRAMY3010321	278	332..2785	2234
BRAMY3010603	279	311.. 706	2235
BRAMY3010654	280	1357..1947	2236
BRAMY3010902	281	182.. 487	2237
BRAMY3011501	282	185..2437	2238
BRAMY3011581	283	1000..2361	2239
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THYMU3043688	1683	48.. 461	3639
THYMU3043779	1684	159.. 833	3640
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THYMU3043993	1686	87.. 572	3642
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THYMU3047760	1702	2623.. 3039	3658
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TRACH3002188	1723	210.. 584	3679
TRACH3002293	1724	1633.. 2253	3680
TRACH3002752	1725	1018.. 3147	3681
TRACH3002890	1726	197.. 781	3682

TRACH3003037	1727	233..3394	3683
TRACH3003357	1728	597..2234	3684
TRACH3003458	1729	267..2207	3685
TRACH3003872	1730	70.. 543	3686
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TRACH3004596	1735	153.. 536	3691
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TRACH3007689	1747	1626..3743	3703
TRACH3007995	1748	2775..3248	3704
TRACH3008042	1749	543..1694	3705
TRACH3008508	1750	1594..2829	3706
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TRACH3011184	1760	33.. 425	3716
TRACH3011282	1761	100.. 630	3717
TRACH3011313	1762	155..1132	3718
TRACH3011454	1763	285.. 839	3719
TRACH3011503	1764	237..1391	3720
TRACH3011538	1765	185..1324	3721
TRACH3012106	1766	405..2675	3722
TRACH3012460	1767	3.. 605	3723
TRACH3012659	1768	80.. 709	3724
TRACH3012718	1769	2096..2527	3725
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TRACH3012891	1771	236.. 580	3727
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TRACH3015467	1782	283.. 678	3738
TRACH3015951	1783	49..1932	3739
TRACH3016264	1784	734..1672	3740

TRACH3016368	1785	384.. 806	3741
TRACH3016455	1786	2059..2943	3742
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TRACH3017409	1790	22..3924	3746
TRACH3018108	1791	168..1538	3747
TRACH3018191	1792	2795..3268	3748
TRACH3018240	1793	5.. 337	3749
TRACH3018261	1794	29.. 586	3750
TRACH3018519	1795	98.. 406	3751
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TRACH3018606	1797	672..1229	3753
TRACH3018783	1798	273.. 617	3754
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TRACH3018943	1800	113.. 451	3756
TRACH3019058	1801	41..1054	3757
TRACH3019370	1802	206..2761	3758
TRACH3019621	1803	1553..2779	3759
TRACH3019807	1804	3915..4550	3760
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TRACH3020563	1806	2232..3158	3762
TRACH3020605	1807	1391..3862	3763
TRACH3020769	1808	62..>3300	3764
TRACH3020930	1809	40..1773	3765
TRACH3021023	1810	38..1618	3766
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TRACH3021373	1812	1857..4919	3768
TRACH3021544	1813	1471..3357	3769

TRACH3021778	1814	989..2113	3770
TRACH3021834	1815	204.. 860	3771
TRACH3021883	1816	1935..2594	3772
TRACH3022109	1817	14..1000	3773
TRACH3022198	1818	422.. 991	3774
TRACH3022296	1819	45.. 431	3775
TRACH3022732	1820	115.. 426	3776
TRACH3022758	1821	274..2112	3777
TRACH3022960	1822	221..3502	3778
TRACH3023063	1823	300.. 671	3779
TRACH3023203	1824	37.. 429	3780
TRACH3023242	1825	830..1333	3781
TRACH3023373	1826	417..>3334	3782
TRACH3023516	1827	112..1824	3783
TRACH3023752	1828	90.. 998	3784
TRACH3023945	1829	223.. 564	3785
TRACH3023960	1830	1542..3920	3786
TRACH3024020	1831	709..1401	3787
TRACH3024081	1832	463..1197	3788
TRACH3024342	1833	97.. 726	3789
TRACH3024423	1834	964..1926	3790
TRACH3024428	1835	96.. 488	3791
TRACH3024512	1836	97..2523	3792
TRACH3024671	1837	903..2780	3793
TRACH3024823	1838	1468..2226	3794
TRACH3025316	1839	727..1662	3795
TRACH3025346	1840	1687..2352	3796
TRACH3025520	1841	3112..3417	3797
TRACH3026283	1842	45.. 821	3798

TRACH3026299	1843	80..1675	3799
TRACH3026303	1844	155..1705	3800
TRACH3026542	1845	144.. 545	3801
TRACH3026650	1846	56..4174	3802
TRACH3026676	1847	119.. 754	3803
TRACH3026949	1848	410.. 766	3804
TRACH3027229	1849	774..1532	3805
TRACH3027681	1850	64.. 474	3806
TRACH3027701	1851	132..1484	3807
TRACH3028164	1852	63.. 467	3808
TRACH3028180	1853	293..2080	3809
TRACH3028441	1854	81..1685	3810
TRACH3028597	1855	110.. 415	3811
TRACH3028837	1856	1811..4627	3812
TRACH3028855	1857	202..2187	3813
TRACH3029139	1858	186.. 506	3814
TRACH3029329	1859	108..1742	3815
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TRACH3029520	1861	839..1219	3817
TRACH3029592	1862	2928..3299	3818
TRACH3029670	1863	80..1696	3819
TRACH3030176	1864	17..3145	3820
TRACH3030855	1865	2600..3463	3821
TRACH3031316	1866	26.. 463	3822
TRACH3031660	1867	25..1242	3823
TRACH3031678	1868	491..1723	3824
TRACH3032044	1869	2.. 472	3825
TRACH3032150	1870	29..1042	3826
TRACH3032480	1871	97.. 420	3827

TRACH3032570	1872	1515..2471	3828
TRACH3033535	1873	7.. 492	3829
TRACH3034680	1874	17..1813	3830
TRACH3035451	1875	17..>5003	3831
TRACH3036004	1876	996..4160	3832
TRACH3036103	1877	80.. 556	3833
TRACH3036278	1878	40.. 492	3834
TRACH3036750	1879	209..1915	3835
TRACH3036792	1880	110.. 457	3836
TRACH3036897	1881	2016..2777	3837
TRACH3036932	1882	87.. 662	3838
TRACH3037505	1883	81..1694	3839
TRACH3038399	1884	509..3406	3840
TSTOM2000235	1885	17..1378	3841
TSTOM2001571	1886	1784..2608	3842
TSTOM2002611	1887	72.. 641	3843
TSTOM2002682	1888	97.. 480	3844
TUTER1000014	1889	98.. 937	3845
TUTER2001433	1890	80..1579	3846
UTERU2000300	1891	608..1351	3847
UTERU2014998	1892	876..1379	3848
UTERU2016464	1893	662..1540	3849
UTERU2016669	1894	111.. 758	3850
UTERU2020226	1895	1256..1747	3851
UTERU2022955	1896	139.. 543	3852
UTERU2023941	1897	121.. 687	3853
UTERU2024042	1898	192.. 632	3854
UTERU2027369	1899	161.. 697	3855
UTERU2028377	1900	348.. 773	3856

UTERU2029660	1901	1766..2335	3857
UTERU2035926	1902	187.. 552	3858
UTERU2037423	1903	1228..2184	3859
UTERU3000670	1904	122.. 5446	3860
UTERU3001029	1905	1074..3416	3861
UTERU3001394	1906	76.. 651	3862
UTERU3001946	1907	133..2736	3863
UTERU3004635	1908	3..>5144	3864
UTERU3005264	1909	2519..4000	3865
UTERU3005422	1910	51.. 962	3866
UTERU3006538	1911	2549..3055	3867
UTERU3006720	1912	1643..2821	3868
UTERU3007108	1913	343.. 783	3869
UTERU3009775	1914	1679..2092	3870
UTERU3010029	1915	1769..2287	3871
UTERU3010409	1916	2375..2902	3872
UTERU3010604	1917	243.. 761	3873
UTERU3010892	1918	2018..2425	3874
UTERU3010919	1919	125..1669	3875
UTERU3011092	1920	1978..2853	3876
UTERU3011398	1921	4299..4982	3877
UTERU3011558	1922	1239..3335	3878
UTERU3011579	1923	160.. 795	3879
UTERU3011837	1924	836..1627	3880
UTERU3012293	1925	638..2485	3881
UTERU3012414	1926	469..1170	3882
UTERU3012476	1927	66.. 425	3883
UTERU3012599	1928	207.. 632	3884
UTERU3012999	1929	1.. 501	3885

UTERU3013167	1930	2919..3398	3886
UTERU3013302	1931	1461..3221	3887
UTERU3014274	1932	58.. 540	3888
UTERU3014647	1933	199.. 558	3889
UTERU3014906	1934	5.. 625	3890
UTERU3015011	1935	1055..2266	3891
UTERU3015299	1936	470.. 937	3892
UTERU3015647	1937	771..1136	3893
UTERU3015844	1938	1871..2188	3894
UTERU3016070	1939	138..1613	3895
UTERU3016273	1940	135.. 776	3896
UTERU3016274	1941	226..1458	3897
UTERU3016308	1942	220..1974	3898
UTERU3017441	1943	616..3621	3899
UTERU3017626	1944	2588..3340	3900
UTERU3017995	1945	1796..2227	3901
UTERU3018172	1946	2006..2551	3902
UTERU3018255	1947	259.. 741	3903
UTERU3019708	1948	993..2114	3904
UTERU3020090	1949	1828..3153	3905
UTERU3021231	1950	172.. 576	3906
UTERU3021850	1951	665..1906	3907
UTERU3022168	1952	61..3237	3908
UTERU3022588	1953	269..1717	3909
UTERU3022922	1954	66.. 368	3910
UTERU3023141	1955	93.. 947	3911
UTERU3023413	1956	164.. 490	3912

【 0 0 1 7 】

すなわち前記表 1 中の配列番号に示した本発明のポリヌクレオチドの塩基配列に基づいて、当該ポリヌクレオチドを合成するためのプライマーをデザインすることができる。なお全長cDNAの合成を目的とするとき、3'側のプライマーとしてはオリゴdTプライマーを用いることもできる。プライマーの長さは、通常、15bp～100bp、好ましくは15bp～35bpの鎖長を有する。後に述べるLA PCRに用いる場合には、25～35bpの長さとするると良い結果を得ることができる。

【0018】

目的とする塩基配列に基づいて、特異的な増幅を可能とするプライマーを設計する手法は公知である (Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4)。5'側の塩基配列に基づいてプライマーを設計する際には、原則として増幅生成物が翻訳開始点を含むようにする。したがって、たとえば5'側のプライマーを5'側の非翻訳領域(5' UTR)の塩基配列に基づいて設定する場合には、対象となるcDNAに対する特異性を保証できる限り、任意の部分を5'側のプライマーとして選択することができる。

【0019】

全長cDNAを合成する場合には、その増幅対象塩基配列は長いものでは数千bpにも及ぶ。しかしLA PCR(Long and Accurate PCR)等を利用することにより、このような長い領域の合成は可能である。長いDNAの合成には、LA PCRを利用するのが有利である。LA PCRでは、3'→5'エキソヌクレアーゼ活性を持った特殊なDNAポリメラーゼを用いることにより、誤って取りこまれた塩基を除去できる。そのため、長い塩基配列であっても正確に相補鎖合成を進めることができるのである。LA PCRを利用すれば、望ましい条件においては、20 kb以上の増幅が可能とされている。(林健志、実験医学別冊・PCRの最新技術、羊土社、1996)

【0020】

本発明の全長cDNAを合成するための鋳型となるDNAには、様々な方法によって調製したcDNAライブラリーを利用することができる。本発明における全長cDNAクローンは、[1]オリゴキャップ法による全長率の非常に高いcDNAライブラリーの作製、および[2] 5'末端側の配列をアSEMBルし、その結果形成されたクラスタ

一の中でも最も全長らしいクローン（5'側に長いものが多い）を選択する、という方法を組み合わせて取得した、より全長である確率の高いクローンである。

しかし、本発明によって提供される全長塩基配列に基づいてデザインされるプライマーを利用すれば、必ずしもこのような特殊な方法を用いずとも、容易に全長cDNAの取得が可能となる。

【0021】

すなわち、公知の方法によって調製されたcDNAライブラリー、あるいは市販のcDNAライブラリーは、全長mRNAをまったく含まないものではなく、その割合が非常に低い。したがって、通常のクローニング方法では、これらのライブラリーから全長cDNAクローンを直接スクリーニングすることは困難である。しかし、本発明によって新規な全長cDNAの塩基配列が明らかにされた。全長塩基配列が与えられれば、PCRのような酵素的な合成方法を利用して目的とする全長cDNAを合成することが可能である。ただし、より確実に全長cDNAの合成を行うには、たとえばオリゴキャップ法等によって合成された全長率の高いcDNAライブラリーの使用が望ましいことは言うまでもない。

【0022】

本発明の全長cDNAクローンの5'-端を含む塩基配列を利用すれば、ゲノム上のプロモーターを含む転写制御領域を単離することが可能となる。既にヒトゲノムの90%以上をカバーするラフドラフト（精度が少し低いヒトゲノム配列解析）が報告されている（Nature, Vol.409, 814-823, 2001）。さらに、2003年にはヒト全ゲノム配列解析が完了する計画になっている。長いイントロンの存在するヒトゲノムより転写開始点を解析ソフトで解析することは大きな困難がともなう。しかし、本発明の全長cDNAクローンの5'-端を含む塩基配列を用いれば、全長cDNAの5'-端を含む塩基配列からゲノム配列上でのmRNA転写開始点を容易に特定できるため、転写開始点上流配列の中に含まれるプロモーターを含む転写制御に関わるゲノム領域を取得することが容易となる。

【0023】

本発明の全長cDNAによってコードされる蛋白質は、組み換え蛋白質として、また天然の蛋白質として調製することが可能である。組み換え蛋白質は、例えば、

後述するように本発明の蛋白質をコードするDNAを挿入したベクターを適当な宿主細胞に導入し、形質転換体内で発現した蛋白質を精製することにより調製することが可能である。一方、天然の蛋白質は、例えば、後述する本発明の蛋白質に対する抗体を結合したアフィニティーカラムを利用して調製することができる (Current Protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. Jhon Wiley & Sons Section 16.1-16.19)。アフィニティー精製に用いる抗体は、ポリクローナル抗体であってもモノクローナル抗体であってもよい。また、インビトロトランスレーション (例えば、「On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system. Dasso, M. C., Jackson, R. J. (1989) Nucleic Acids Res. 17:3129-3144」参照) などにより本発明の蛋白質を調製することも可能である。

【0024】

前記のようにして明らかにされた本発明による蛋白質の活性に基づいて、本発明の蛋白質と機能的に同等な蛋白質を得ることができる。ある蛋白質が本発明の蛋白質と機能的に同等であるかどうかは、本発明の蛋白質が備える生物学的な活性を指標として、該活性をある蛋白質が有するかどうかを調べることによって確認することができる。

【0025】

これら本発明において同定された蛋白質と機能的に同等な蛋白質は、当業者であれば、例えば、蛋白質中のアミノ酸配列に変異を導入する方法 (例えば、部位特異的変異誘発法 (Current Protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. Jhon Wiley & Sons Section 8.1-8.5)) を利用して調製することができる。また、このような蛋白質は、自然界におけるアミノ酸の変異により生じることもある。本発明には、このように本実施例において同定された蛋白質と同等の機能を有する限り、そのアミノ酸配列 (表1) において1もしくは複数のアミノ酸が置換、欠失、挿入および/または付加された蛋白質も含まれる。

【0026】

蛋白質におけるアミノ酸の変異数や変異部位は、その機能が保持される限り制

限はない。変異数は、典型的には、30%以内、または20%以内、または10%以内であり、好ましくは全アミノ酸の5%以内、または3%以内であり、さらに好ましくは全アミノ酸の2%以内であり、更に好ましくは全アミノ酸の1%以内である。あるいは本発明には複数のアミノ酸として数個のアミノ酸の変異を置換する場合が含まれる。数個とは、たとえば5、更には4または3、あるいは2、更には1のアミノ酸を言う。

置換されるアミノ酸は、蛋白質の機能の保持の観点から、置換前のアミノ酸と似た性質を有するアミノ酸であることが好ましい。例えば、Ala、Val、Leu、Ile、Pro、Met、Phe、Trpは、共に非極性アミノ酸に分類されるため、互いに似た性質を有すると考えられる。また、非荷電性としては、Gly、Ser、Thr、Cys、Tyr、Asn、Glnが挙げられる。また、酸性アミノ酸としては、AspおよびGluが挙げられる。また、塩基性アミノ酸としては、Lys、Arg、Hisが挙げられる。

【0027】

また、本実施例において同定された蛋白質と機能的に同等な蛋白質は、当業者にも周知のハイブリダイゼーション技術あるいは遺伝子増幅技術を利用して単離することも可能である。即ち、当業者であれば、ハイブリダイゼーション技術 (Current Protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. Jhon Wiley & Sons Section 6.3-6.4) を用いて本実施例において同定された蛋白質をコードするDNAの塩基配列 (表1) またはその一部をもとにこれと相同性の高いDNAを単離して、該DNAから機能的に同等な蛋白質を得ることは、通常行いうることである。本発明には、本実施例において同定された蛋白質と同等の機能を有する限り、これら蛋白質をコードするDNAとハイブリダイズするDNAによりコードされる蛋白質も含まれる。機能的に同等な蛋白質を単離する生物としては、例えば、ヒト、マウス、ラット、ウサギ、ブタ、ウシ等の脊椎動物が挙げられるが、これらに制限されない。

【0028】

機能的に同等な蛋白質をコードするDNAを単離するためのハイブリダイゼーションの条件は、洗浄条件として通常「1xSSC、0.1% SDS、37℃」程度であり、より厳しい条件としては「0.5xSSC、0.1% SDS、42℃」程度であり、さらに厳しい

条件としては「0.1xSSC、0.1% SDS、65℃」程度を示すことができる。あるいは、次のような条件を本発明におけるハイブリダイゼーションの条件として示すこともできる。すなわち、ハイブリダイゼーションを「6 x SSC、40 % ホルムアミド、25 °C」、洗浄を「1 x SSC、55 °C」で行う条件を用いることができる。より好ましい条件としては、ハイブリダイゼーションを「6 x SSC、40 % ホルムアミド、37 °C」、洗浄を「0.2 x SSC、55 °C」で行う条件が挙げられる。さらに好ましい条件としては、ハイブリダイゼーションを「6 x SSC、50 % ホルムアミド、37 °C」、洗浄を「0.1 x SSC、62 °C」で行う条件を用いることができる。ハイブリダイゼーションの条件が厳しくなるほどプローブ配列と高い相同性を有するDNAの単離を期待しうる。したがって、ハイブリダイゼーションはストリンジেন্টな条件下で行うことが望ましい。本明細書においてストリンジেন্টな条件としては、洗浄のための条件としてたとえば「0.5xSSC、0.1% SDS、42℃」程度を示すことができる。あるいは、ハイブリダイゼーションを「6 x SSC、40 % ホルムアミド、37 °C」、洗浄を「0.2 x SSC、55 °C」で行う条件をストリンジেন্টな条件として示すこともできる。

【0029】

なお、当業者であれば、SSCの希釈率、ホルムアミド濃度、温度などの諸条件を適宜選択することで、上記の条件と同様のストリンジェンシーのハイブリダイゼーション条件を実現することができる。

ただし、上記SSC、SDSおよび温度の条件の組み合わせは例示であり、当業者であれば、ハイブリダイゼーションのストリンジェンシーを決定する上記若しくは他の要素（例えば、プローブ濃度、プローブの長さ、ハイブリダイゼーション反応時間など）を適宜組み合わせることにより、上記と同様のストリンジェンシーを実現することが可能である。

【0030】

このようなハイブリダイゼーション技術を利用して単離される蛋白質は表1に記載の本発明の蛋白質と比較して、通常、そのアミノ酸配列において高い相同性を有する。本発明は、請求項1（a）に記載の塩基配列に対して高い同一性を有する塩基配列を含むポリヌクレオチドを包含する。また本発明は、請求項1（b

）に記載したポリヌクレオチドがコードするアミノ酸配列に対して高い同一性を有するアミノ酸配列を含む蛋白質、またはペプチドを包含する。高い同一性とは、少なくとも40%以上、好ましくは60%以上、さらに好ましくは70%以上の配列の同一性を指す。あるいはより望ましくは、90%以上、または93%以上、あるいは95%以上、更には97%以上、そして99%以上の同一性を言う。同一性は、BLAST検索アルゴリズムを用いて決定することができる。

【0031】

本発明におけるアミノ酸配列や塩基配列の相同性は、Karlin and Altschul によるアルゴリズムBLAST (Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993)によって決定することができる。このアルゴリズムに基づいて、blastnやblastxと呼ばれるプログラムが開発されている(Altschul et al. J. Mol. Biol. 215:403-410, 1990)。BLASTに基づいてblastnによって塩基配列を解析する場合には、パラメーターはたとえばscore = 100、wordlength = 12とする。また、BLASTに基づいてblastxによってアミノ酸配列を解析する場合には、パラメーターはたとえば score = 50、wordlength = 3とする。BLASTとGapped BLASTプログラムを用いる場合には、各プログラムのデフォルトパラメーターを用いる。これらの解析方法の具体的な手法は公知である(<http://www.ncbi.nlm.nih.gov>)。

【0032】

また、遺伝子増幅技術(PCR) (Current protocols in Molecular Biology ed it. Ausubel et al. (1987) Publish. John Wiley & Sons Section 6.1-6.4)を用いて、本実施例において同定された塩基配列(表1)の一部をもとにプライマーを設計し、これらDNA配列またはその一部と相同性の高いDNA断片を単離して、これをもとに本実施例において同定された蛋白質と機能的に同等な蛋白質を得ることも可能である。

【0033】

本発明はまた、表1に示した配列番号に記載の塩基配列からなるポリヌクレオチド、またはその相補鎖に相補的な塩基配列からなる少なくとも15ヌクレオチドを含むポリヌクレオチドを提供する。ここで「相補鎖」とは、A:T、G:Cの塩基対からなる2本鎖DNAの一方の鎖に対する他方の鎖を指す。また、「相補的」と

は、少なくとも15個の連続したヌクレオチド領域で完全に相補配列である場合に限られず、少なくとも70%、好ましくは少なくとも80%、より好ましくは90%、さらに好ましくは95%以上の塩基配列上の相同性を有すればよい。塩基配列の相同性は、本明細書に記載したアルゴリズムにより決定することができる。

このようなポリヌクレオチドは、本発明の蛋白質をコードするポリヌクレオチドを検出、単離するためのプローブとして、また、本発明のDNAを増幅するためのプライマーとして利用することが可能である。プライマーとして用いる場合には、通常、15bp～100bp、好ましくは15bp～35bpの鎖長を有する。また、プローブとして用いる場合には、本発明のポリヌクレオチドの少なくとも一部若しくは全部の配列を有し、少なくとも15bpの鎖長のDNAが用いられる。プライマーとして用いる場合、3'側の領域は相補的である必要があるが、5'側には制限酵素認識配列やタグなどを付加することができる。

【0034】

また、本発明のポリヌクレオチドには、表1に示した配列番号に記載されたアミノ酸配列からなる本発明の蛋白質の発現を抑制するためのアンチセンスポリヌクレオチドが含まれる。アンチセンスポリヌクレオチドは、アンチセンス効果を引き起こすために、少なくとも15bp以上、たとえば50bp以上、好ましくは100bp以上、さらに好ましくは500bp以上の鎖長を有し、通常、3000bp以内、好ましくは2000bp以内の鎖長を有する。このようなアンチセンスDNAには、本発明の蛋白質の異常（機能異常や発現異常）などに起因した疾患の遺伝子治療への応用も考えられる。該アンチセンスDNAは、例えば、本発明の蛋白質をコードするDNA（例えば、配列番号：1～配列番号：1956に記載の塩基配列）の配列情報を基にホスホロチオエート法（Stein, 1988 Physicochemical properties of phosphorothioate oligodeoxynucleotides. Nucleic Acids Res 16, 3209-21 (1988)）などにより調製することが可能である。

【0035】

その他、本発明のポリヌクレオチドの塩基配列に基づいてデザインすることができる、リボザイム、あるいはRNA interference (RNAi)効果により本発明のポリヌクレオチドの発現を抑制することができるポリヌクレオチドも本発明に含ま

れる。

リボザイムは、本発明のポリヌクレオチドのアンチセンス配列と、触媒作用に必要な触媒ユニットを構成する塩基配列とで構成されるポリヌクレオチドである。リボザイムを構成するアンチセンス配列は、当該リボザイムの触媒ユニットの構造に合わせて、適宜選択することができる。一方リボザイムの触媒ユニットは、公知である。たとえば、ハンマーヘッド型リボザイム(Rossi et al. (1991) *Pharmac. Ther.* 50: 245-254)やヘアピン型のリボザイム(Hampel et al. (1990) *Nucl. Acids Res.* 18: 299-304, and U.S. Pat. No. 5,254,678)が、塩基配列特異的な切断作用を有することが知られている。これらのリボザイムは、アンチセンス配列がハイブリダイズするポリヌクレオチドの特定の位置を、その触媒作用によって切断することができる。

【0036】

例えば、ハンマーヘッド型リボザイムの自己切断ドメインは、G13U14C15という配列のC15の3'側を切断する。ハンマーヘッド型リボザイムの活性にはU14とA9との塩基対形成が重要とされ、C15の代わりにA15またはU15でも切断できることが示されている(Koizumi M, et al: *FEBS Lett* 228: 228, 1988)。基質結合部位が標的部位近傍のRNA配列と相補的なリボザイムを設計すれば、標的RNA中のUC、UUまたはUAという配列を認識する制限酵素的なRNA切断リボザイムを作出することができる(Koizumi M, et al: *FEBS Lett* 239: 285, 1988、小泉誠および大塚栄子: *タンパク質核酸酵素* 35: 2191, 1990、Koizumi M, et al: *Nucl Acids Res* 17: 7059, 1989)。例えば、本発明のDNA(配列番号: 1から配列番号: 1956)中には、標的となり得る部位が複数存在する。アンチセンス配列を選択することにより、本発明のポリヌクレオチドの任意の位置をリボザイムで切断することができる。

【0037】

リボザイムは、好ましくはRNAによって構成される。このようなりボザイムは、化学的に合成することもできるし、あるいは酵素的な反応によって製造することもできる。RNAの化学的な合成方法は公知である。あるいは、リボザイムをコードするDNAをRNAポリメラーゼによって転写することによって、リボザイムを生

成することもできる。転写によってリボザイムを生成するときには、リボザイムをコードするDNAは、RNAポリメラーゼが認識するプロモーターの下流に配置される。RNAポリメラーゼとしては、T7 RNAポリメラーゼやSP6RNAポリメラーゼを用いることができる。更に、リボザイムをコードするDNAを適当なベクターに組み込んで、宿主細胞に導入することによって、宿主細胞中でリボザイムを発現させることもできる。ベクターは当該宿主細胞中での遺伝子の発現を誘導可能なプロモーターを含む。

【0038】

本発明は、本発明のポリヌクレオチドの発現を抑制するsiRNA(small interfering RNA)を提供する。siRNAは、mRNAと同じ塩基配列を含む2本鎖のRNAが、当該mRNAに基づく蛋白質合成を阻害する作用(Fire et al. (1998) Nature 391: 806-811)を利用した、遺伝子発現制御技術である。2本鎖RNAによる遺伝子の発現抑制効果は、RNAi効果と呼ばれている。siRNAによる遺伝子発現制御は、マウスでも有効であったことが知られている(Zamore et al. (2000). Cell 101:25-33; Gur a (2000) Nature 404: 804-808)。つまり、2本鎖RNAの細胞への導入によって、遺伝子選択的に発現を抑制することができる。

【0039】

siRNAの長さは制限されない。細胞に導入された2本鎖のRNAは、細胞内で3'末端から21-23bpからなる断片に酵素的に切断される。2本鎖RNAを切断する酵素は、ダイサー(dicer)と呼ばれている。生成した2本鎖RNAの断片は、同じ配列を持つ標的塩基配列を認識して結合し、当該塩基配列がRNaseIII様のヌクレアーゼ活性によって切断される(Hammond et al. (2000) Nature, 404: 293-298; Zamore et al. (2000). Cell 101: 25-33)。

【0040】

RNAi効果による遺伝子の発現制御のためには、細胞内にsiRNAを導入する。siRNAはリボザイムと同様の方法により、細胞内に導入することができる。すなわち、化学的に合成された2本鎖RNAを細胞内に導入することができる。アンチセンスRNAであれsiRNAであれ、予め合成されたRNAを細胞に導入する場合には、ヌクレアーゼによる分解を防ぐために修飾しておくことができる。たとえば、チオ化さ

れたRNAは、ヌクレアーゼの作用を受けにくい。

【0041】

あるいはsiRNAを細胞内で発現させることもできる。たとえば、センス配列とアンチセンス配列を挿入したベクターを宿主細胞に形質転換し、細胞内で発現させることができる。センス鎖とアンチセンス鎖が連続して配置されていれば、ヘアピンループ構造を持つ2本鎖RNAが発現される。あるいは両者を異なるプロモーターの制御下に発現させて、別々のストランドからなる2本鎖RNAとすることもできる。siRNAの発現のためのプロモーターとしては、U6プロモーターなどが一般に用いられる。

【0042】

本発明のアンチセンスポリヌクレオチド、リボザイム、あるいはsiRNAを構成する塩基配列は、配列番号：1～配列番号：1956に示した塩基配列と完全に同一、あるいは完全に相補的な塩基配列に加え、これらの塩基配列と高い相同性を有する塩基配列であっても良い。アンチセンスポリヌクレオチド、リボザイム、あるいはsiRNAの塩基配列において、高い相同性とは、通常90%以上、好ましくは95%以上、より好ましくは98%以上、更に好ましくは99%以上の相同性を言う。塩基配列の相同性は、たとえば本明細書に記載の方法によって明らかにすることができる。

【0043】

当業者は、発現を抑制すべき遺伝子の塩基配列に基づいて、siRNAをデザインすることができる。一般的なsiRNAのデザインのための方法として、たとえば以下の方法を示すことができる。すなわち、まずターゲット配列としては、次のような領域を避けるのが有利と考えられている。

5'側あるいは3'側の非翻訳領域

スタートコドン付近

これらの領域は、転写調節蛋白質の結合領域であることが多い。また多くのmRNAで保存された塩基配列を含む可能性があるので、目的以外の遺伝子に対して阻害作用を及ぼす場合がある。

したがって、たとえばスタートコドンよりも下流のORFの中にターゲット配列

を設定するのが有利とされている。スタートコドンとターゲット配列との間隔は、たとえば50塩基以上とするのが望ましい。siRNAの塩基配列は、aaから始まり、19-21塩基の連続する塩基配列を含むようにするのが一般的である。またsiRNAの末端には2塩基のオーバーハングが付加される。オーバーハングの塩基配列としては、dTdTやUUなどが用いられる。siRNAを構成する塩基配列のGC含量は、50%前後が好ましい。また一般にその分布は、siRNA全体で均一な方が好ましいとされている。

【0044】

siRNAの作用は、mRNAへの配列特異的なハイブリダイズに基づいている。したがって、できるだけ目的とする遺伝子に特異的な塩基配列をターゲット配列として選択することが、遺伝子に対して特異的な抑制効果を実現する上で重要な条件となる。したがって、ターゲット配列として選択した塩基配列は、相同性検索によって他の遺伝子との相同性が低いことを確認することが望ましい。塩基配列の相同性を決定するためのアルゴリズムは公知である。

【0045】

本発明のsiRNAは、本発明のポリヌクレオチドの発現を抑制する限り、上記のような一般的なデザイン方法によって得ることができる塩基配列に限定されない。たとえば、ターゲット配列が特定の遺伝子に特異的な塩基配列でなくても、相同な塩基配列を有する遺伝子が発現していない細胞においては、目的とする遺伝子に対する特異的な発現抑制作用を期待できる。更に、上記のような一般的なターゲット配列の選択方法によらなくても、RNAi効果を示す2本鎖RNAを得ることは可能である。

【0046】

本発明のDNA、あるいはそのアンチセンス、リボザイム、並びにsiRNAには、例えば、遺伝子治療への応用が考えられる。遺伝子治療の標的となる疾患としては、例えば、癌や各種炎症性疾患が好適であると考えられる。これら分子を遺伝子治療に用いる場合には、例えば、レトロウイルスベクター、アデノウイルスベクター、アデノ随伴ウイルスベクターなどのウイルスベクターやリボソームなどの非ウイルスベクターなどを利用して、ex vivo法やin vivo法などにより患者へ投

与を行えばよい。

【0047】

また本発明は、本発明の蛋白質の部分ペプチドを含む。この部分ペプチドには、例えば、分泌蛋白質においてはシグナルペプチドが除去された蛋白質が含まれる。また、本発明の蛋白質が受容体やリガンドとしての活性を持つものの場合には、その競合阻害剤として機能する、受容体（あるいはリガンド）との結合能を有する部分ペプチドが含まれる。また、抗体調製のための抗原ペプチドが含まれる。部分ペプチドが本発明の蛋白質に特異的であるためには、少なくとも7アミノ酸、好ましくは8アミノ酸以上、より好ましくは9アミノ酸、更に好ましくは10アミノ酸以上のアミノ酸配列からなる。該部分ペプチドは、本発明の蛋白質に対する抗体や本発明の蛋白質の競合阻害剤の調製以外に、例えば、本発明の蛋白質に結合する蛋白質のスクリーニングなどに利用し得る。本発明の部分ペプチドは、例えば、遺伝子工学的手法、公知のペプチド合成法、あるいは本発明の蛋白質を適当なペプチダーゼで切断することによって製造することができる。

【0048】

また、本発明は、本発明のポリヌクレオチドが挿入されたベクターに関する。本発明のベクターは、挿入したDNAを安定に保持するものであれば特に制限されない。例えば宿主に大腸菌を用いるのであれば、クローニング用ベクターとしてはpBluescriptベクター(Stratagene社製)などが好ましい。本発明の蛋白質を生産する目的においてベクターを用いる場合には、特に発現ベクターが有用である。発現ベクターは、試験管内、大腸菌内、培養細胞内、生物個体内で蛋白質を発現するベクターであれば特に制限されない。例えば、試験管内発現であればpBES Tベクター（プロメガ社製）、大腸菌であればpETベクター（Invitrogen社製）、培養細胞であればpME18S-FL3ベクター（GenBank Accession No. AB009864）、生物個体であればpME18Sベクター（Mol Cell Biol. 8:466～472(1988)）などが好ましい。ベクターへの本発明のDNAの挿入は常法により制限酵素サイトを用いたリガーゼ反応により行うことができる（Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 11.4～11.11）。

【0049】

また、蛋白質発現を目的とした発現ベクターの構築にGATEWAYシステム（インビトロジェン株式会社）という技術がある（実験医学 Vol. 18, No. 19（12月号），p2716-2717, 2000）。このシステムはラムダファージのもつ2種類の部位特異的組換え酵素（BPクロナーゼとLRクロナーゼ）とその特異的組換え部位をエントリーベクターと蛋白精製の際に有効なタグが既に挿入されているものも含むデスティネーションベクターにそれぞれ採用し、相同組換え反応を利用することによって発現ベクターを得るものである。

まず、1段階目の組換え反応を用いて目的のDNA断片をエントリーベクターへ挿入し、次にこの目的のDNA断片が挿入されたエントリーベクターとデスティネーションベクター間で2段階目の組換え反応をさせ、迅速かつ高効率で発現ベクターを得ることができる。前述のような制限酵素やリガーゼ反応を用いた定法では、発現ベクターを構築し目的の蛋白質を発現させるまで7～10日間程度の期日が必要となるが、GATEWAYではわずか3～4日間で目的の蛋白質の発現が可能になり、ハイスループットな発現蛋白質の機能解析が実現できる（<http://biotech.nikkeibp.co.jp/netlink/lto/gateway/>）。

【0050】

加えて本発明は、本発明のベクターを保持する形質転換体に関する。本発明のベクターが導入される宿主細胞としては特に制限はなく、目的に応じて種々の宿主細胞が用いられる。蛋白質を高発現させるための真核細胞としては、例えば、COS細胞、CHO細胞などを例示することができる。

宿主細胞へのベクター導入は、例えば、リン酸カルシウム沈殿法、電気パルス穿孔法（Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 9.1-9.9）、リポフェクタミン法（GIBCO-BRL社製）、マイクロインジェクション法などの方法で行うことが可能である。

【0051】

更に表1に示した配列番号に記載の塩基配列からなるポリヌクレオチド、またはその相補鎖に相補的な塩基配列からなる少なくとも15ヌクレオチドを含むポ

リヌクレオチドは、単に全長cDNAの合成のためのプライマーとして利用できるのみならず、全長cDNAによってコードされる本発明の蛋白質の異常を検査・診断するために利用できる。例えば、本発明のポリヌクレオチドをプライマーに用いたポリメラーゼ連鎖反応（ゲノムDNA-PCRやRT-PCR）により本発明の蛋白質をコードするDNAを増幅することができる。また、全長cDNAの5'末端配列からゲノム配列上でのmRNA転写開始点が容易に特定可能なので、PCRやハイブリダイゼーションの手法を用いて5'上流の発現制御領域を容易に取得することができる。取得された遺伝子領域に対して、RFLP解析、SSCP、シーケンシング等の方法により、配列の異常を検査・診断することができる。特に本発明のmRNAの発現が特定の疾患によって変動する場合には、本発明のポリヌクレオチドをプローブやプライマーとして該mRNAの発現量を解析することによって該疾患の検出や診断を行うことができる。

【 0 0 5 2 】

また、本発明は、本発明の蛋白質に結合する抗体に関する。本発明の抗体の形態には特に制限はなく、ポリクローナル抗体やモノクローナル抗体または抗原結合性を有するそれらの一部も含まれる。また、全てのクラスの抗体が含まれる。さらに、本発明の抗体には、ヒト化抗体やキメラ抗体などの特殊抗体も含まれる。

本発明の抗体は、ポリクローナル抗体の場合には、常法に従いアミノ酸配列に相当するオリゴペプチドを合成して家兎に免疫することにより得ることが可能である（Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 11.12～11.13）。一方、モノクローナル抗体は、常法に従い大腸菌で発現し精製した蛋白質を用いてマウスを免疫し、脾臓細胞と骨髓腫細胞を細胞融合させたハイブリドーマ細胞の中から得ることができる（Current protocols in Molecular Biology edit. Ausubel et al. (1987) Publish. John Wiley & Sons. Section 11.4～11.11）。

【 0 0 5 3 】

本発明の蛋白質に結合する抗体は、本発明の蛋白質の精製に加え、例えば、本発明の蛋白質の発現異常や構造異常の検査・診断に利用することも考えられる。

具体的には、例えば組織、血液、または細胞などから蛋白質を抽出し、ウェスタンブロッティング、免疫沈降、ELISA等の方法による本発明の蛋白質の検出を通して、発現や構造の異常の有無を検査・診断することができる。

また、本発明の蛋白質に結合する抗体を、本発明の蛋白質に関連した疾患の治療などの目的に利用することも考えられる。抗体を患者の治療目的で用いる場合には、ヒト抗体、ヒト化抗体、あるいはキメラ抗体が免疫原性の少ない点で好ましい。ヒト抗体は、免疫系をヒトのものと入れ換えたマウス（例えば、「Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice, Mendez, M.J. et al. (1997) Nat. Genet. 15:146-156」参照）に免疫することにより調製することができる。また、ヒト化抗体は、モノクローナル抗体の超可変領域を用いた遺伝子組み換えによって調製することができる (Methods in Enzymology 203, 99-121(1991))。

【0054】

本発明のcDNA（クローン）がコードしているのは、例えば分泌・膜蛋白質、糖蛋白質関連蛋白質、シグナル伝達関連蛋白質、転写関連蛋白質、疾患関連蛋白質、酵素・代謝関連蛋白質、細胞分裂・増殖関連蛋白質、細胞骨格関連蛋白質、核蛋白質・RNA合成関連蛋白質、蛋白質合成・輸送関連蛋白質、細胞防御関連蛋白質、発生・分化関連蛋白質、DNA・RNA結合蛋白質、ATP・GTP結合蛋白質のような機能が予測される蛋白質のアミノ酸配列である。これらの蛋白質としての機能を持つことは、相同性検索の結果から推定することができる。すなわち、本発明の全長cDNAの全長、もしくは部分塩基配列と相同性を示す公知の遺伝子・蛋白質を検索し、その遺伝子とそれがコードしている蛋白質の機能を参照すれば本発明のcDNAがコードしている蛋白質の機能を推定することができる。

【0055】

また、アミノ酸配列中にシグナル配列、膜貫通領域、核移行シグナル、糖鎖付加シグナル、リン酸化部位、及びZinc fingerモチーフ、SH3ドメイン等を見出すことでも本発明のcDNAがコードしている蛋白質の機能を推測できる。特にモチーフ、ドメインなどの構造はいくつかの蛋白質に共通して見出される部分配列構造で、蛋白質の最小限機能構造であり、現在までに機能が明らかとなっているもの

、なっていないもの全て合わせてPfam(<http://www.sanger.ac.uk/Software/Pfam/index.shtml>)のVersion 7. 7 (2 0 0 2 年 1 2 月現在での最新版) においては 4 8 3 2 種類が同定され、データベース化されている。

【 0 0 5 6 】

具体的なモチーフ、ドメイン機能の一例として例えば、免疫反応に関与するT細胞において細胞膜上に発現するT Cell Receptorの細胞内領域に見い出されたITAM (immunoreceptor tyrosine-based activation motif) と呼ばれるモチーフ (Flaswinkel, H et.al. Semin Immunol 1995 Feb;7(1):21-7) はYXXL (チロシンー任意のアミノ酸ー任意のアミノ酸ーロイシン) がタンデムに並んだ構造をとっており、細胞外からの抗原や抗体刺激でこのモチーフの中のチロシン残基がリン酸化酵素ドメインを持った酵素 (LCK) によってリン酸化を受け、そのリン酸化チロシンにZAP70がSH2ドメインを介して結合しシグナルが下流に伝わるということがわかっている (Bu, JY et.al. Proc Natl Acad Sci U S A 1995 May 23;92(11):5106-10, Neumeister, EN et.al. Mol Cell Biol 1995 Jun;15(6):3171-8) 。

【 0 0 5 7 】

これに類似した現象はT細胞だけでなく、肥満細胞でも見い出されており (Chen, T et.al. J Biol Chem 1996 Oct 11;271(41):25308-15) 、アレルギー、アトピー性皮膚炎、喘息などの免疫疾患において、分子レベルで見たときに免疫担当細胞が活性化する最初のプロセスとして理解されている。

【 0 0 5 8 】

上記は一例であるが、単純に記載したこれだけの反応においてもITAM、SH2ドメイン、蛋白質リン酸化酵素ドメインと3つの主要なモチーフ、ドメイン構造が主要な機能を担っており、しかもそれら3つの構造でこのメカニズムが説明できる。よってここで記載した免疫反応だけでなく、さまざまな細胞機能を分子メカニズムで理解するには、共通したモチーフ、ドメイン構造をもつ分子を集めカタログ化すること、そしてその最小構造の機能を解明すること、および未知蛋白質の機能解明にはまず第一にモチーフ、ドメイン構造の検索が非常に重要なことがわかる。また、蛋白質全体の構造はモチーフ、ドメインといった最小限構造の寄せ集めで成り立っており、その結果、タンパク質全体としての機能が発揮される

と考えられている。

【0059】

すなわち、ドメインやモチーフ構造の解析から、その蛋白質が全体として細胞内でどのような働きを担っているかということを分子レベルで極めて正確に予測することが可能である。また、一部アミノ酸配列とGFP蛋白質などとの融合タンパクを作製して、培養細胞等に導入し、例えば細胞膜に局在すれば受容体やイオンチャンネルといった機能を持つ可能性が示唆されたり、核に局在すればDNAに結合したり転写に関与するといった機能予測が可能である。このように蛋白質の局在を調べることで類推できる。

【0060】

本発明で得られた全長cDNAはその全塩基配列、およびそれがコードするアミノ酸配列をもとに上記のような解析を行うことで機能予測が可能であるが、cDNAの配列が全塩基配列でなくても部分的な配列情報(好ましくは300塩基以上)があれば機能予測は可能であることが多い。しかし、部分的な配列情報をもとにした相同性検索からの機能予測は、必ずしも全塩基配列をもとに予測された機能と一致しない場合があり、全塩基配列をもとにした機能予測のほうが好ましいのはいくまでもない。

【0061】

機能予測のより具体的方法として、相同性検索の場合はGenBank、Swiss-Prot、UniGene、nr、RefSeqといった各データベースを対象にBLASTやFASTAなどで相同性検索を行い、ヒットした遺伝子とそれがコードしている蛋白質の機能を参照することで本発明のcDNAがコードしている蛋白質の機能を推定する。また、構造からの予測においては全塩基配列から推定されたアミノ酸配列に対して、シグナル配列、膜貫通領域の予測ならばPSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]やSOSUI [T.Hirokawa et.al. Bioinformatics, 14, 378-379 (1998)] (三井情報開発株式会社販売)、MEMSAT [D.T.Jones, W.R.Taylor & J.M.Thornton, Biochemistry, 33, 3038-3049 (1994)] など、またモチーフやドメインの予測ならばPfamやPROSITE (<http://www.expasy.ch/prosite/>)等に対して検索を行うことによって、クローン中にコードされる蛋白質のより詳細な機能予

測が可能である。

【0062】

このようにして、本発明の全塩基配列が明らかになった全長1956クローンについて、GenBank、Swiss-Prot、nr、RefSeq の各データベースを対象に相同性検索を行った（実施例4および相同性検索結果参照）。また全長塩基配列から推定されたアミノ酸配列に対してPSORT、SOSUIを用いたシグナル配列、および膜貫通領域の検索を行った（実施例5参照）。これらの結果から、アノテーションを基本とした機能予測（Swiss-Protのヒットデータであればキーワードを参照する。nr、RefSeqのヒットデータであればDefinitionやReference情報を参照する）、および推定ORFに対するPSORTを用いたシグナルシーケンス検索、SOSUIを用いた膜貫通領域の検索結果をあわせて、以下14種類の機能カテゴリーへの分類を行った。結果、973クローンについては以下のカテゴリーに属する蛋白質をコードしていることが推定された。

【0063】

分泌・膜蛋白質（551クローン）
糖蛋白関連蛋白質（114クローン）
シグナル伝達関連蛋白質（71クローン）
転写関連蛋白質（106クローン）
疾患関連蛋白質（391クローン）
酵素・代謝関連蛋白質（164クローン）
細胞分裂・増殖関連蛋白質（27クローン）
細胞骨格関連蛋白質（60クローン）
核蛋白質・RNA合成関連蛋白質（40クローン）
蛋白質合成・輸送関連蛋白質（50クローン）
細胞防御関連蛋白質（5クローン）
発生・分化関連蛋白質（16クローン）
DNA・RNA結合蛋白質（119クローン）
ATP・GTP結合蛋白質（68クローン）

【0064】

分泌・膜蛋白質に属すると推定されたクローンは、以下の 5 5 1 クローンであった。

3NB692004045, ADIPS2000069, ADRGL2010315, ASTRO2015162, BLADE2001031, BLADE2002744, BLADE2007744, BRACE2003628, BRACE2012528, BRACE2013126, BRACE2017397, BRACE2017580, BRACE2017992, BRACE2023633, BRACE2030039, BRACE2035191, BRACE3001403, BRACE3001973, BRACE3002264, BRACE3002756, BRACE3004767, BRACE3004981, BRACE3007869, BRACE3009392, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3015898, BRACE3018083, BRACE3021517, BRACE3021805, BRACE3022051, BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024879, BRACE3026345, BRACE3026456, BRACE3026802, BRACE3028360, BRACE3029021, BRACE3030538, BRACE3031372, BRACE3031579, BRACE3031728, BRACE3032385, BRACE3032537, BRACE3032980, BRACE3033525, BRACE3034964, BRACE3034993, BRACE3037637, BRACE3037803, BRACE3038570, BRACE3039358, BRACE3039378, BRACE3040644, BRACE3040863, BRACE3042326, BRACE3042409, BRACE3042432, BRACE3044090, BRACE3046049, BRACE3046466, BRACE3048565, BRACE3050504, BRACE3051144, BRACE3051621, BRACE3052486, BRALZ2010842, BRALZ2011337, BRALZ2013690, BRAMY2015516, BRAMY2021098, BRAMY2025495, BRAMY2037609, BRAMY2041507, BRAMY2044686, BRAMY2046537, BRAMY3002886, BRAMY3004126, BRAMY3007449, BRAMY3009556, BRAMY3009904, BRAMY3010654, BRAMY3010902, BRAMY3015549, BRAMY3016829, BRAMY3018248, BRAWH2000256, BRAWH2010364, BRAWH2011812, BRAWH2011958, BRAWH2012866, BRAWH2014053, BRAWH2016209, BRAWH2016305, BRAWH3001053, BRAWH3001783, BRAWH3001833, BRAWH3003573, BRAWH3005892, BRAWH3008867, BRAWH3010461, BRAWH3010657, BRAWH3011907, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013049, BRAWH3014609, BRAWH3015175, BRAWH3016123, BRAWH3017259, BRAWH3018063, BRAWH3018548, BRAWH3018969, BRAWH3019529, BRAWH3019820, BRAWH3020200, BRAWH3020884, BRAWH3021012, BRAWH3021641, BRAWH3022347, BRAWH3023156, BRAWH3023274, BRAWH3023415, BRAWH3023421, BRAWH3024186, BRAWH3024242, BRAWH3027574, BRAWH3027880, BRAWH3028223, BRAWH3028754, BRAWH3029806, BRAWH3

030810, BRAWH3032298, BRAWH3034114, BRAWH3034134, BRAWH3035914,
BRAWH3036270, BRAWH3038055, BRAWH3038324, BRAWH3040711, BRAWH3040900, BR
AWH3042132, BRAWH3042772, BRAWH3042996, BRAWH3043498, BRAWH3043623, BRAW
H3044151, BRAWH3044676, BRAWH3046196, BRAWH3047063, BRAWH3048374, BRAWH3
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【 0 0 6 5 】

糖蛋白質関連蛋白質に属すると推定されたクローンは、以下の 1 1 4 クローンであった。

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【 0 0 6 6 】

シグナル伝達関連蛋白質に属すると推定されたクローンは、以下の 7 1 クローンであった。

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転写関連蛋白質に属すると推定されたクローンは、以下の 1 0 6 クローンであった。

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【 0 0 6 9 】

このうち、Swiss-Protヒットデータ、及びnr、RefSeqヒットデータが、ヒトの遺伝子と疾患のデータベースであるOnline Mendelian Inheritance in Man (OMIM)に登録されている遺伝子、蛋白質であったクローンは以下の390クローンであった(クローン名の後ろのカッコ内は対象となったOMIM Number)。

ADIPS2000069(146900), ASTRO2015162(606106), ASTRO2016114(603899), ASTRO3000154(601594), BLADE2000256(140750), BRACE1000475(600696), BRACE2012838(605032), BRACE2012947(140580), BRACE2013009(605888), BRACE2016896(601421), BRACE2017397(115437), BRACE2023744(600763), BRACE2027382(606019), BRACE3001403(126141), BRACE3001973(600976), BRACE3002756(603143), BRACE3004767(182790), BRACE3009392(600229), BRACE3013418(182900), BRACE3018083(605268),

BRACE3019941(600595), BRACE3020669(603917), BRACE3025719(605493), BRACE3026345(147470), BRACE3026802(605784), BRACE3028998(603063), BRACE3036283(602052), BRACE3039378(604100), BRACE3040644(603159), BRACE3041059(603486), BRACE3041162(194556), BRACE3042046(311030), BRACE3042432(192321), BRACE3043597(603704), BRACE3044172(601231), BRACE3046152(604950), BRACE3046466(604210;600105), BRACE3046609(606457), BRACE3051621(601313;173900), BRACE3052321(603050),

BRALZ2010842(212138), BRALZ2013621(600712), BRAMY2041384(114070), BRAMY3000692(603971), BRAMY3004126(603071), BRAMY3007078(602410), BRAMY3009491(600286), BRAMY3011501(602869), BRAMY3011581(601243), BRAMY3014027(194542), BRAMY3015086(602879), BRAMY3017920(600365), BRAMY3018248(605464), BRAWH2002333(171891), BRAWH2012866(185605), BRAWH2014053(604581), BRAWH3001638(605003), BRAWH3001783(605514), BRAWH3004335(603244), BRAWH3010602(603216),

BRAWH3011577(601139), BRAWH3011623(164020), BRAWH3017180(601441), BRAWH3017259(603143), BRAWH3018548(193065), BRAWH3019026(602033), BRAWH3021580(179838), BRAWH3023156(137190), BRAWH3023172(603755), BRAWH3023415(604346), BRAWH3024186(179590), BRAWH3029385(602378), BRAWH3029538(600948), BRAWH3031342(603971), BRAWH3032298(601995), BRAWH3032571(603277), BRAWH3033513(604054;261510), BRAWH3034668(603486), BRAWH3034775(605800), BRAWH3034890(606265),

BRAWH3036334(603971), BRAWH3038324(604249), BRAWH3038827(600574), BRAWH3040900(604265), BRAWH3041492(130500), BRAWH3041556(172460), BRAWH3042438(125855), BRAWH3042447(606323), BRAWH3042772(602878), BRAWH3043295(179030), BRAWH3043623(600976), BRAWH3044151(605421), BRAWH3046424(300272), BRAWH3047565(606277), BRAWH3047644(605216), BRAWH3049544(602273), BRCAN2003269(171060;602347), BRCAN2006051(604581), BRCAN2010665(603583), BRCAN2020331(604851),

BRCAN2021325(114855), BRCOC2012386(602277), BRHIP2008756(605819), BRHIP2023735(601670), BRHIP2029529(189972), BRHIP3001076(604673), BRHIP3001481(176889), BRHIP3003984(603722;223900), BRHIP3004215(603294), BRHIP3004725(602075), BRHIP3005037(603526), BRHIP3005307(603197), BRHIP3005673(138385), BRHIP3005801(605704), BRHIP3006449(604275), BRHIP3007609(426000), BRHIP3010289(603130), BRHIP3011567(114207), BRHIP3017146(602878), BRHIP3017855(606406),

BRHIP3021019(176879), BRHIP3023922(156570;250940), BRHIP3025795(603877), BRHIP3027191(601746), BRHIP3027651(604589), BRHIP3028742(602076), BRHIP3029409(604156), BRHIP3030230(602367), BRHIP3032374(603197), BRHIP3035006(604402), BRHIP3036715(142800), BRHIP3037543(602052), BRHIP3039509(601328), BRSSN2004710(600127), BRSTN2006466(138275), BRSTN2008475(605178), BRSTN2011961(176790), BRSTN2012069(130590), BRSTN2016918(137780), BRTHA2019726(147100),

BRTHA2020721(147100), BRTHA2020910(602661), BRTHA2024712(600747), BRTHA2

025869(162280), BRTHA2026071(605297), BRTHA2026290(602306), BRTHA2031917
(118946), BRTHA2033155(601873), BRTHA2033683(111000), BRTHA3003736(13351
0;234050), BRTHA3010135(179590), BRTHA3010212(603971), BRTHA3011187(6058
37), BRTHA3011998(603264), BRTHA3012265(605646), BRTHA3014547(182900), B
RTHA3021708(602654), BRTHA3021971(605609), BRTHA3023403(600597), BRTHA30
26916(601619),

BRTHA3027957(606078), CHONS2001287(146732), CHONS2002829(602981), COLON2
001829(604399), COLON2004911(603937;180100), COLON2005735(111690;111700)
, CTONG2001932(605683), CTONG2010330(606088), CTONG2011801(603971), CTON
G2014206(605609), D90ST2004417(113703), FCBBF3020030(603406), FCBBF30211
91(605119), FCBBF5000384(601737), FEBRA2013570(248600), FEBRA2026582(300
252), FEBRA2028457(164035), FEKID2002637(176875), FELNG2000720(601662),
FELNG2001953(603597),

HCASM2008154(133450), JCMLC1000159(107470;209950), JCMLC2000273(120980),
JCMLC2002095(600738), KIDNE2015987(191845), NIESE2000698(604734), NETRP
2000961(600417), NETRP2003448(179551), NETRP2004017(605344), NETRP200858
2(103195), NT2RI3008179(603808), NT2RI3009480(601804), NT2RI3009524(6042
10;600105), NT2RP8003787(605427), NT2RP8008057(603489), NTONG2003805(601
781), OCBBF2004478(604265), OCBBF2007039(605009), OCBBF2018618(102775),
OCBBF2024589(602462),

OCBBF2030927(603897), OCBBF2036019(601825;256000), OCBBF3001202(140750),
OCBBF3004487(142560), OCBBF3008392(605682), OCBBF3020263(604077), OCBBF
3022166(600848), OCBBF3025475(604148), OCBBF3025503(601653;113650), OCBB
F3025630(604141), OCBBF3026979(602319), PEBLM2005615(600242), PLACE50004
92(602142), PLACE6001933(131550), PLACE6016030(605442), PLACE7000266(188
840), PLACE7001759(600338), PLACE7002303(601542;180500;137600;604229), P
LACE7003985(109684), PLACE7004103(142695),

PLACE7006090(154360), PLACE7006268(603053), PLACE7006498(604394), PLACE7
007379(603105), PLACE7009563(300344), PLACE7009757(601804), PLACE7009936

(600365), PLACE7011559(600831), PLACE7012111(602714), PLACE7014247(601232), PLACE7016526(605490), PUAEN2000594(604679), SKNSH2007306(118990), SMINT2011406(147890), SMINT2011509(606343), SMINT2014721(606090), SPLEN2007689(233700), SPLEN2012571(603430), SPLEN2025012(146900), SPLEN2028417(142995),

SPLEN2033996(603853), SYNOV2003326(602960), SYNOV4009139(603551), TIESE2000609(182465), TESTI2005112(603846), TESTI2007490(601291), TESTI2009739(160745), TESTI2023903(605046), TESTI2030901(600436), TESTI2034913(148060), TESTI2052670(142461), TESTI4001517(148070), TESTI4001679(602850), TESTI4002868(601863;209920), TESTI4003796(603132), TESTI4003944(603971), TESTI4004653(606106), TESTI4005322(603899), TESTI4005653(182465), TESTI4007965(603533),

TESTI4017382(605689), TESTI4017647(603211), TESTI4018436(601754), TESTI4020596(602537), TESTI4021197(602189), TESTI4021569(605464), TESTI4021713(604105), TESTI4023096(604878), TESTI4026080(605575), TESTI4028182(603892), TESTI4031173(190197), TESTI4032128(104776), TESTI4032834(300188), TESTI4032913(106410), TESTI4033177(602038), TESTI4036048(601272), TESTI4039575(600951), TESTI4039904(603899), TESTI4041984(604710), TESTI4046073(300118;309801),

TESTI4047119(606202), TESTI4049786(142600;235700), TESTI4049899(601969), TESTI4051015(602974), TESTI4052775(165250), THYMU3002825(604346), THYMU3008105(194548), THYMU3012402(600686), THYMU3012983(194556), THYMU3013785(604722), THYMU3014173(143010), THYMU3014372(116945), THYMU3014620(605657), THYMU3016518(147100), THYMU3020221(147100), THYMU3020869(602550), THYMU3021586(184756), THYMU3021755(605024), THYMU3022434(601408), THYMU3023400(605180),

THYMU3025118(155735), THYMU3026306(604346), THYMU3026532(600065;116920), THYMU3027671(604143), THYMU3032032(604463), THYMU3032798(601212), THYMU3033649(186780), THYMU3033759(600495), THYMU3037052(300346), THYMU303777

2(147100), THYMU3038158(603033;603034), THYMU3038375(181590), THYMU3040172(186720), THYMU3040746(147110), THYMU3040816(605704), THYMU3040829(602649), THYMU3043200(605596), THYMU3047115(108730), THYMU3047760(604783), TKIDN2011160(605011), TLIVE2007736(604990), TLUNG2000654(148059), TLUNG2001445(146900), TLUNG2001600(147130), TRACH2024730(605611), TRACH3004424(603971), TRACH3005173(151410), TRACH3005191(605333), TRACH3005699(606154), TRACH3006379(148059), TRACH3006800(606154), TRACH3008042(166945), TRACH3009008(601112), TRACH3009701(603330), TRACH3010079(604850), TRACH3010167(601804), TRACH3010342(602943), TRACH3011282(601833), TRACH3011313(113520), TRACH3011503(602862), TRACH3012891(602397), TRACH3015951(604084), TRACH3016455(605286), TRACH3016805(106410), TRACH3018524(176882), TRACH3018907(146900), TRACH3019058(147170), TRACH3019621(191350), TRACH3020769(160776), TRACH3020930(147100), TRACH3021023(147170), TRACH3021373(606030), TRACH3021778(164035), TRACH3021883(603347), TRACH3023373(159350), TRACH3023960(603337), TRACH3024081(605867), TRACH3024671(605942), TRACH3025346(603377;212140), TRACH3026283(601517), TRACH3026299(147170), TRACH3028441(147170), TRACH3028597(604310), TRACH3028837(602127), TRACH3029670(147170), TRACH3030855(173321), TRACH3031660(176912), TRACH3031678(600523), TRACH3032570(602217), TRACH3034680(147170), TRACH3036750(604077), TRACH3037505(147170), TRACH3038399(604032;226980), TUTER2001433(146900), UTERU2024042(602214), UTERU2037423(604077), UTERU3001946(606154), UTERU3004635(103390), UTERU3011398(120240;158810;254090), UTERU3012293(194556), UTERU3012414(604394), UTERU3012999(605567), UTERU3015011(602505), UTERU3015299(601825;256000), UTERU3016308(602127), UTERU3017441(604276), UTERU3017626(603788), UTERU3019708(601430), UTERU3021850(605009), UTERU3022588(123811)

【 0 0 7 0 】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の
1 6 4 クローンであった。

ASTR02008972, BRACE1000475, BRACE2013132, BRACE2016896, BRACE2035120, BR
ACE3017253, BRACE3021805, BRACE3028998, BRACE3031315, BRACE3036283, BRAC
E3041059, BRACE3042409, BRACE3044172, BRACE3046609, BRAMY3009491, BRAMY3
011581, BRAWH2002333, BRAWH2014053, BRAWH3001638, BRAWH3004335,
BRAWH3011331, BRAWH3017180, BRAWH3020928, BRAWH3023415, BRAWH3023421, BR
AWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3029806, BRAWH3032571, BRAW
H3033513, BRAWH3034668, BRAWH3037428, BRAWH3037979, BRAWH3041556, BRAWH3
042438, BRAWH3043295, BRAWH3044151, BRAWH3046424, BRAWH3047692,
BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402, BRCAN2021325, BR
HIP3001481, BRHIP3003126, BRHIP3005307, BRHIP3005673, BRHIP3007195, BRHI
P3007223, BRHIP3011082, BRHIP3011269, BRHIP3021019, BRHIP3023922, BRHIP3
032374, BRHIP3035006, BRHIP3037543, BRHIP3041587, BRSSN2004710,
BRSTN2006466, BRSTN2011961, BRTHA2005448, BRTHA2010672, BRTHA2025869, BR
THA2026311, BRTHA2033155, BRTHA2035743, BRTHA3003736, BRTHA3010135, BRTH
A3010469, BRTHA3023403, CHONS2002829, COLON2004351, CTONG2010330, CTONG2
020582, CTONG3001605, FCBBF3001018, FCBBF3021191, FCBBF5000384,
FEBRA2013570, FEBRA2026582, FEKID2002637, HSYRA2004550, KIDNE2010049, NE
TRP2000961, NT2RI2004818, NT2RP7016508, OCBBF2007039, OCBBF2024589, OCBB
F2036019, OCBBF3004487, OCBBF3005330, OCBBF3009244, PLACE5000492, PLACE6
001933, PLACE7001759, PLACE7003985, PLACE7004103, PLACE7004961,
PLACE7006090, PLACE7006268, PLACE7007379, PLACE7011559, PLACE7012111, PL
ACE7014247, PLACE7016526, SKMUS2008585, SMINT2011509, SMINT2012179, SMIN
T2014721, SPLEN2007689, SYNOV4009139, TBAES2007428, TESTI2005112, TESTI2
007490, TESTI2021654, TESTI2040377, TESTI2049062, TESTI4000621,
TESTI4002799, TESTI4007671, TESTI4020596, TESTI4033177, TESTI4049786, TE
STI4052219, THYMU3002825, THYMU3026306, THYMU3032798, THYMU3034671, THYM

U3036953, THYMU3041428, THYMU3047115, THYMU3047891, TKIDN2011160, TRACH3005173, TRACH3005274, TRACH3009008, TRACH3011313, TRACH3011503, TRACH3012891, TRACH3015136, TRACH3016455, TRACH3018108, TRACH3018261, TRACH3018524, TRACH3019621, TRACH3021544, TRACH3022758, TRACH3023516, TRACH3024020, TRACH3024081, TRACH3027229, TRACH3027701, TRACH3032150, TRACH3038399, TSTOM2001571, TSTOM2002611, UTERU2024042, UTERU3010604, UTERU3010919, UTERU3015299, UTERU3019708, UTERU3021850

【 0 0 7 1 】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 27 クローンであった。

BLADE2000256, BRACE2002392, BRACE3030538, BRACE3036283, BRACE3044495, BRAMY3002886, BRAMY3009556, BRAWH2016209, BRAWH3004350, BRAWH3027574, BRCA N2019907, BRHIP3001076, BRHIP3029409, BRSTN2008475, BRTHA3011265, FEKID2002637, NT2RP8005546, OCBBF3001202, PLACE7011559, SPLEN2033996, TESTI2023903, TESTI4020819, TESTI4049899, THYMU3014372, THYMU3021586, UTERU3010919, UTERU3012999

【 0 0 7 2 】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 60 クローンであった。

BRACE3004767, BRACE3013418, BRACE3051819, BRAMY3005184, BRAMY3015086, BRAMY4000915, BRAMY4001652, BRAWH3001783, BRAWH3015175, BRAWH3018548, BRAWH3019026, BRAWH3021580, BRAWH3021724, BRAWH3027440, BRAWH3027806, BRAWH3029385, BRAWH3040900, BRAWH3041492, BRCAN2020467, BRHIP3003063, BRHIP3003340, BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA3014547, BRTHA3025073, CERVX2000968, JCMLC2000273, NIESE2000698, NT2RI3005923, OCBBF2003518, OCBBF2004478, OCBBF3027969, PLACE7000266, PLACE7004961, SMINT2010753, SPLEN2034934, SYNOV4003174, TESTI2001915, TESTI2009739, TESTI2034913, TESTI4001517, TESTI4004917, TESTI4010902, TESTI4032913, TESTI4051424, THYMU3026532, TLUNG2000654, TRACH3006379, TRACH3016805, TRACH3016953

H3020769, TRACH3022960, TRACH3026650, TRACH3028837, TRACH3029462, TRACH3032570, UTERU3000670, UTERU3001029, UTERU3015011, UTERU3016308

【 0 0 7 3 】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 0 クローンであった。

ASTR03000154, BRACE3014714, BRACE3036283, BRALZ2013621, BRAMY3009556, BRAMY3011501, BRAWH3011623, BRAWH3017180, BRAWH3022651, BRAWH3038252, BRAWH3040695, BRAWH3046424, BRHIP3004215, BRHIP3007223, BRHIP3020046, BRTHA3010530, CTONG2006235, FEBRA2028457, NT2RP7016508, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006268, TESTI2036285, TESTI2037657, TESTI4014932, TESTI4028182, TESTI4032128, TESTI4033177, TESTI4039575, THYMU3012402, THYMU3040829, THYMU3041428, TRACH3002752, TRACH3018108, TRACH3021778, UTERU3004635, UTERU3010409, UTERU3010919, UTERU3013302

【 0 0 7 4 】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 0 クローンであった。

BRACE2016896, BRACE2023744, BRACE3020669, BRACE3030538, BRACE3041059, BRACE3043597, BRAWH2014053, BRAWH3001638, BRAWH3010602, BRAWH3024506, BRAWH3026349, BRAWH3034668, BRAWH3037979, BRAWH3041556, BRAWH3044151, BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2006051, BRCAN2021325, BRHIP3007223, BRSTN2012069, BRTHA2005448, BRTHA2010672, CHONS2002829, CTONG3001605, D90ST2004417, OCBBF2000831, OCBBF2007039, PLACE6019600, PLACE7007379, PLACE7012111, PLACE7016526, TESTI4018436, TESTI4020596, TESTI4032128, TESTI4036048, THYMU3012402, THYMU3033759, THYMU3036953, THYMU3046360, TKIDN2011160, TRACH3016455, TRACH3018519, TRACH3021544, TRACH3025316, TRACH3030855, TRACH3038399, UTERU3014647, UTERU3021850

【 0 0 7 5 】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 クローンであった。

BRACE2012947, BRHIP2029529, BRTHA3003736, THYMU3015571, TRACH3022296

【 0 0 7 6 】

発生、分化関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の
1 6 クローンであった。

ASTR03000154, BRACE3034964, BRAWH3004350, BRAWH3029538, BRAWH3038252, BR
HIP3007424, BRTHA2024712, BRTHA3011265, FEKID2002493, NT2RP8003490, NT2R
P8006452, OCBBF3025503, PLACE7002303, TESTI2026024, TRACH3028180, UTERU3
016070

【 0 0 7 7 】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1
1 9 クローンであった。

ASTR02016114, BEAST2000981, BRACE2012947, BRACE2019348, BRACE3020669, BR
ACE3025719, BRACE3026844, BRACE3031743, BRACE3034183, BRACE3041162, BRAC
E3046152, BRALZ2013621, BRAMY2040915, BRAMY2046537, BRAMY3000692, BRAMY3
007078, BRAMY3011501, BRAMY3011581, BRAMY3014027, BRAMY3018754,
BRAMY4000962, BRAWH3000446, BRAWH3011577, BRAWH3011623, BRAWH3013009, BR
AWH3013264, BRAWH3017477, BRAWH3028796, BRAWH3031342, BRAWH3032571, BRAW
H3034775, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3038827, BRCAN2
020331, BRCOC2012386, BRHIP2027077, BRHIP3004725, BRHIP3028246,
BRSSN2015497, BRTHA2024712, BRTHA3000456, BRTHA3003736, BRTHA3010212, BR
THA3014000, BRTHA3028339, CHONS2000797, CHONS2002829, CTONG2001932, CTON
G2011801, D9OST2003106, FCBBF3020030, FCBBF5000384, FEBRA2028457, HCASM2
008154, NETRP2004017, NT2RI3008179, NT2RI3009480, NT2RP7016508,
NT2RP8003490, NTONG2003805, NTONG2008483, OCBBF2016928, OCBBF3004487, OC
BBF3008392, OCBBF3020263, OCBBF3021361, OCBBF3022166, PLACE7002303, PLAC
E7004103, PLACE7005169, PLACE7009757, PROST2002078, PUAEN2000594, SMINT2
011509, SPLEN2012571, SPLEN2028417, TIESE2000609, TIESE2000904,
TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322, TESTI4005470, TE
STI4005653, TESTI4032128, TESTI4039575, TESTI4039904, TESTI4052775, THYM

U3008105, THYMU3012983, THYMU3014372, THYMU3020869, THYMU3021586, THYMU3026000, THYMU3030072, THYMU3033759, THYMU3037052, THYMU3040829, TLIVE2001616, TRACH3003458, TRACH3004424, TRACH3005191, TRACH3008508, TRACH3010079, TRACH3010167, TRACH3010342, TRACH3015951, TRACH3021778, TRACH3021883, TRACH3022109, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3013302, UTERU3016070, UTERU3022588

【 0 0 7 8 】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 68 クローンであった。

BRACE2013009, BRACE2016896, BRACE3002344, BRACE3014714, BRACE3017253, BRACE3036283, BRACE3051819, BRAMY3011501, BRAMY3018248, BRAWH2014053, BRAWH3015175, BRAWH3024506, BRAWH3029385, BRAWH3032571, BRAWH3037428, BRAWH3041556, BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2003269, BRCAN2006051, BRHIP3007195, BRHIP3027191, BRHIP3041587, BRSTN2012069, BRTHA2020910, BRTHA3003736, HSYRA2004550, KIDNE2010049, NETRP2003448, NT2RP7016508, OCBBF2003518, OCBBF3004487, PLACE6001933, PLACE6019600, PLACE7004961, PLACE7006498, PLACE7011559, PLACE7016526, PUAEN2006639, SMINT2011406, TESTI2009739, TESTI2040377, TESTI4004917, TESTI4013474, TESTI4021569, TESTI4028182, TESTI4049786, TESTI4052219, THYMU3014372, THYMU3032798, THYMU3041428, THYMU3047115, TRACH3005191, TRACH3009061, TRACH3009701, TRACH3012891, TRACH3019370, TRACH3020769, TRACH3022960, TRACH3023960, TRACH3024081, TRACH3038399, TSTOM2001571, UTERU2024042, UTERU3010919, UTERU3012414, UTERU3019708

【 0 0 7 9 】

以下の 1 0 4 クローンについては、上記のいずれのカテゴリーに属するか明らかでないクローンであったが、全長配列に対する相同性検索で何らかの機能が予測されているクローンである。クローン名と相同性検索結果のDefinitionを//で区切り、以下に示した。

BLADE2002310//SH3-domain binding protein 1 [Homo sapiens]

BLADE2007799//Hepatocellular carcinoma-associated antigen 66.
BRACE2017359//Mus musculus suppressor of Ty 6 homolog (S. cerevisiae) (S
upt6h)
BRACE2017872//nuclear receptor-binding SET-domain protein 1 [Mus musculu
s]
BRACE3009416//testis specific ankyrin-like protein 1 [Homo sapiens]
BRACE3016020//SBB131 protein [Homo sapiens]
BRACE3019570//SNAP-25-interacting protein [Rattus norvegicus]
BRACE3022303//Pax transcription activation domain interacting protein [M
us musculus]
BRACE3022340//SNAP-25-interacting protein [Rattus norvegicus]
BRACE3026290//Homo sapiens lethal giant larvae homolog 2 [Homo sapiens]
BRACE3032631//F-box protein FBX13 [Mus musculus].
BRACE3040239//Deltex3 [Mus musculus]
BRACE3047482//tripartite motif-containing 9 [Homo sapiens]
BRACE3049714//NYD-TSPG protein [Homo sapiens]
BRACE3052410//IDN3 protein [Homo sapiens]
BRACE3052595//Nim2 [Rattus norvegicus]
BRALZ2014054//cenexin 2 [Rattus norvegicus].
BRAMY3007471//gene trap locus F3b; transcript expressed during hematopoi
esis 2 [Mus musculus]
BRAMY3010321//MRIP-1 protein [Homo sapiens]
BRAMY3014613//SH3-domain binding protein 1 [Homo sapiens]
BRAMY4001863//Mus musculus enabled homolog (Drosophila) (Enah), mRNA
BRAWH2011796//S-100 protein, alpha chain.
BRAWH3008167//CUB and Sushi multiple domains 1 [Homo sapiens]
BRAWH3009961//Nim2 [Rattus norvegicus]
BRAWH3010726//phosphatidylinositol transfer protein, membrane-associated
; Drosophila retinal degeneration B [Homo sapiens]

BRAWH3015017//axonemal dynein light chain p33.
BRAWH3024231//Tetratricopeptide repeat protein 4.
BRAWH3026938//semaF cytoplasmic domain associated protein 3; semaphorin cytoplasmic domain-associated protein 3A [Mus musculus]
BRAWH3027533//rap2 interacting protein x [Homo sapiens].
BRAWH3030910//Sec23-interacting protein p125 [Homo sapiens]
BRAWH3031710//serologically defined colon cancer antigen 33 [Homo sapiens]
BRAWH3033293//synaptopodin [Homo sapiens]
BRAWH3042568//ventral anterior homeobox containing gene 1 [Mus musculus]
BRAWH3043034//Mus musculus neuregulin 1 (Nrg1)
BRAWH3044122//Munc13-1 [Rattus norvegicus]
BRHIP2026346//lymphocyte specific formin related protein; formin-related gene in leukocytes [Mus musculus]
BRHIP2027563//host cell factor homolog [Homo sapiens]
BRHIP3002114//rTS beta protein [Homo sapiens]
BRHIP3003795//cytochrome P450 retinoid metabolizing protein [Homo sapiens]
BRHIP3006786//peptidylprolyl isomerase (cyclophilin)-like 2; cyclophilin-like protein CyP-60 [Homo sapiens]
BRHIP3017109//Socs-5 [Mus musculus]
BRHIP3019643//Homo sapiens gamma tubulin ring complex protein (76p gene) (76P), mRNA
BRHIP3032148//brain-enriched guanylate kinase-associated [Rattus norvegicus]
BRSTN2006638//synaptotagmin interacting protein 1 [Rattus norvegicus]
BRSTN2016892//BUP protein [Homo sapiens]
BRSTN2016992//DRR1 protein (TU3A protein).
BRSTN2017151//COP9 (constitutive photomorphogenic), subunit 7a (Arabidop

sis); COP9 complex S7a [Mus musculus]
BRTHA2020642//DRR1 protein (TU3A protein).
BRTHA3018409//synaptotagmin-like 4; granuphilin-a; granuphilin-b; granuphilin
hilin
BRTHA3019183//<Ca2+>dependent activator protein for secretion; Ca2+-dependent activator protein for secretion [Mus musculus]
CHONS2001834//tumor endothelial marker 7 precursor [Homo sapiens]
CTONG2009570//rab11 binding protein [Bos taurus].
CTONG2012123//Mus musculus enabled homolog (Drosophila) (Enah), mRNA
CTONG2027591//Mus musculus pecanex homolog (Drosophila) (Pcnx), mRNA.
CTONG3003669//high-glucose-regulated protein 8 [Homo sapiens]
ERLTF2002178//Kelch-like protein X.
HHDPC2008185//jerky [Mus musculus]
NT2RI3001573//F-box protein FBL10 [Mus musculus].
NT2RI3007095//Mus musculus neuregulin 1 (Nrg1), mRNA.
NT2RP8001363//signal peptide, CUB domain, EGF-like 1 [Mus musculus]
NT2RP8001584//alpha integrin binding protein 63 [Homo sapiens]
NT2RP8001604//CUB and Sushi multiple domains 1 [Homo sapiens]
OCBBF3019269//Homo sapiens Dvl-binding protein IDAX (inhibition of the Dvl and Axin complex) (IDAX)
OCBBF3022827//putative Rab5 GDP/GTP exchange factor homologue [Homo sapiens]
OCBBF3023913//Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1C (Ppplrlc)
PLACE6003004//rTS beta protein [Homo sapiens]
PLACE6008315//similar to ALPHA-ACTININ, SARCOMERIC (F-ACTIN CROSS LINKING PROTEIN) (D. melanogaster) [Homo sapiens].
PLACE6010925//NY-REN-50 antigen [Homo sapiens]
PLACE7012127//AAA-ATPase TOB3 [Homo sapiens]

PROST2016566//erythroblast macrophage protein [Mus musculus]
SYNOV2017179//EBP50-PDZ interactor of 64 kD [Homo sapiens]
SYNOV3000345//upregulated by 1,25-dihydroxyvitamin D-3 [Homo sapiens]
TBAES2003917//NG28 protein [Mus musculus]
TESTI2001364//lactate dehydrogenase A -like [Homo sapiens]
TESTI2004601//NYD-TSPG protein [Homo sapiens]
TESTI2009497//GPI-anchored protein p137 (p137GPI).
TESTI4002774//oxysterol binding protein 2 [Mus musculus]
TESTI4003579//FH1/FH2 domains-containing protein (Formin homolog overexpressed in spleen) (FHOS).
TESTI4003703//retinoblastoma-associated protein RAP140 [Homo sapiens]
TESTI4013742//antigen identified by monoclonal antibody 2A8 [Mus musculus]
TESTI4014908//dedicator of cyto-kinesis 2 [Mus musculus]
TESTI4018506//tomosyn [Rattus norvegicus]
TESTI4020342//H326 [Homo sapiens]
TESTI4024294//WW domain binding protein 2 [Mus musculus]
TESTI4039451//B29 protein [Homo sapiens]
TESTI4041482//Rattus norvegicus SEC15 homolog (S. cerevisiae) (Sec15), mRNA
TESTI4043166//lymphocyte specific formin related protein; formin-related gene in leukocytes [Mus musculus].
TESTI4047328//otogelin [Mus musculus]
THYMU3011717//exocyst component protein 70 kDa homolog (S. cerevisiae)
THYMU3016822//erythroblast macrophage protein [Mus musculus]
THYMU3026479//secretory pathway component Sec31B-1 [Homo sapiens]
THYMU3028702//chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; KIAA0159 gene product [Homo sapiens]

THYMU3029719//AAA-ATPase TOB3 [Homo sapiens]
THYMU3038347//tumor stroma and activated macrophage protein DLM-1 [Homo sapiens]
THYMU3038603//WW domain binding protein 2 [Mus musculus]
THYMU3040830//AD-012 protein [Homo sapiens]
THYMU3041603//gamma-tubulin complex protein 2 [Homo sapiens]
TKIDN2003396//Homo sapiens paternally expressed 10 (PEG10), mRNA
TRACH2011057//D-type cyclin-interacting protein 1; MAID protein [Homo sapiens]
TRACH3004412//clusterin-like 1 (retinal); unknown prepropeptide specific to rod photoreceptor [Homo sapiens]
TRACH3012106//erythrocyte protein band 4.1-like 3 [Mus musculus]
UTERU3009775//PAPIN [Rattus norvegicus]
UTERU3010892//adaptor-related protein complex 3, delta 1 subunit; adaptor n, delta [Homo sapiens]
UTERU3017995//p47 [Homo sapiens]

【 0 0 8 0 】

なお、蛋白質の機能が必ずしも上記に示す機能カテゴリーの一つのみに属するわけではないため、いずれで予測された機能カテゴリーにも該当する可能性がある。またこれらの機能カテゴリーで分類されたクローンには、今後の解析により新たな機能が付加される可能性がある。

【 0 0 8 1 】

また、本発明の全塩基配列が明らかになった全長 1 9 5 6 クローンについて、推定されたアミノ酸配列のPfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) に対するドメイン検索の結果（実施例 5 参照）から得られるヒットデータのドメイン、モチーフ名やアクセッション番号を用いて、Pfamのサイト内やInterPro (<http://www.ebi.ac.uk/interpro/>)、PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>)等の各リンク先における各ドメイン、モチーフの詳細な説明や、特にPROSITEにおいては独自の機能カテゴリー分類を参照すること

ができる。このようにして、Pfamでヒットした796クローン中にコードされるタンパク質の機能予測を行い、以下14種類の機能カテゴリーへの分類を行った。結果、624クローンについては以下のカテゴリーに属する蛋白質をコードしていることが推定された。

【0082】

分泌・膜蛋白質（92クローン）
糖蛋白関連蛋白質（81クローン）
シグナル伝達関連蛋白質（125クローン）
転写関連蛋白質（141クローン）
疾患関連蛋白質（4クローン）
酵素・代謝関連蛋白質（264クローン）
細胞分裂・増殖関連蛋白質（13クローン）
細胞骨格関連蛋白質（51クローン）
核蛋白質・RNA合成関連蛋白質（29クローン）
蛋白質合成・輸送関連蛋白質（50クローン）
細胞防御関連蛋白質（4クローン）
発生・分化関連蛋白質（1クローン）
DNA・RNA結合蛋白質（185クローン）
ATP・GTP結合蛋白質（41クローン）

【0083】

分泌・膜蛋白質に属すると推定されたクローンは、以下の92クローンであった。

3NB692004045, BRACE3002264, BRACE3009392, BRACE3013418, BRACE3024879, BRACE3032385, BRACE3039378, BRACE3042432, BRACE3050504, BRACE3051621, BRAMY2046537, BRAMY3004126, BRAWH2000256, BRAWH2011812, BRAWH3023156, BRAWH3025157, BRAWH3027880, BRAWH3036270, BRAWH3037265, BRAWH3042772, BRCAN2003269, BRCAN2022126, BRCOC2006164, BRHIP3002000, BRHIP3005944, BRHIP3008320, BRHIP3011567, BRHIP3014675, BRHIP3016032, BRHIP3017558, BRHIP3025795, BRHIP3033557, BRHIP3039509, BRSTN2010089, BRTHA2031917, BRTHA3

011194, BRTHA3012265, BRTHA3014547, COLON2005735, JCMLC2000273, KIDNE2004531, LYMPB2002236, NT2RP7019682, NT2RP8001363, NT2RP8003787, OCBBF2003518, OCBBF2004478, OCBBF2009536, OCBBF2018618, OCBBF3004487, OCBBF3025475, OCBBF3028001, PEBLM2005615, PLACE6010936, PLACE7004103, PLACE7011559, PLACE7018304, TESTI2018335, TESTI2022323, TESTI2024267, TESTI2036822, TESTI4003602, TESTI4004539, TESTI4005399, TESTI4008305, TESTI4010544, TESTI4014415, TESTI4021569, TESTI4023096, TESTI4026080, TESTI4040559, TESTI4049899, THYMU3015647, THYMU3021404, THYMU3023400, THYMU3026532, THYMU3030752, THYMU3040172, THYMU3044075, TRACH3003357, TRACH3004113, TRACH3004747, TRACH3005699, TRACH3006800, TRACH3009061, TRACH3019370, TRACH3023373, TRACH3031678, TRACH3032150, UTERU3001946, UTERU3016273, UTERU3017626

【 0 0 8 4 】

糖蛋白質関連蛋白質に属すると推定されたクローンは、以下の 8 1 クローンであった。

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3013874, BRACE3017253, BRACE3039358, BRAMY2040915, BRAMY3015549, BRAWH3009961, BRAWH3023415, BRAWH3049544, BRHIP3017558, BRHIP3025795, BRHIP3036371, BRHIP3036715, BRHIP3038735, BRTHA2019726, BRTHA2020400, BRTHA2020721, BRTHA3017791, CERVX2000968, FELNG2000720, JCMLC2000273, KIDNE2004531, NT2RP8008057, OCBBF2000831, OCBBF2004478, OCBBF2030927, PEBLM2005615, PLACE7006090, SPLEN2025012, STOMA2004663, TESTI2021654, TESTI2052670, TESTI4008305, TESTI4022158, TESTI4031173, TESTI4032128, TESTI4037949, TESTI4051424, THYMU3002825, THYMU3014173, THYMU3016518, THYMU3020221, THYMU3025118, THYMU3026306, THYMU3026532, THYMU3037772, THYMU3040746, TLUNG2001445, TLUNG2001600, TRACH3003357, TRACH3004113, TRACH3004412, TRACH3005274, TRACH3005699, TRACH3006800, TRACH3011082, TRACH3011184, TRACH3012659, TRACH3015354, TRACH3018261, TRACH3018907, TRACH3019058, TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023, TRACH3024512, TRACH3026299, TRAC

H3028441, TRACH3029670, TRACH3031316, TRACH3034680, TRACH3036103, TRACH3037505, TUTER2001433, UTERU3001946, UTERU3010409, UTERU3011398, UTERU3015647

【 0 0 8 5 】

シグナル伝達関連蛋白質に属すると推定されたクローンは、以下の 1 2 5 クローンであった。

BLADE2002310, BLADE2008809, BRACE2047975, BRACE3002344, BRACE3003866, BRACE3004767, BRACE3013418, BRACE3015898, BRACE3017253, BRACE3042046, BRACE3044172, BRACE3045424, BRACE3046491, BRACE3051621, BRACE3052321, BRACE3052595, BRAMY3005184, BRAMY3009491, BRAMY3010321, BRAMY3014613, BRAMY3015547, BRAMY3017920, BRAWH2012866, BRAWH3009961, BRAWH3017180, BRAWH3018063, BRAWH3019026, BRAWH3022431, BRAWH3024186, BRAWH3026349, BRAWH3027574, BRAWH3027806, BRAWH3029385, BRAWH3031342, BRAWH3032340, BRAWH3035914, BRAWH3037428, BRAWH3044122, BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCOC2001355, BRHIP3003306, BRHIP3006294, BRHIP3006786, BRHIP3011460, BRHIP3017109, BRHIP3021019, BRHIP3028570, BRHIP3037543, BRHIP3041587, BRTHA2026290, BRTHA2027250, BRTHA3014547, BRTHA3020771, BRTHA3021708, BRTHA3023403, BRTHA3026916, CTONG2009570, ERLTF2002369, FEKID2001001, FEKID2002637, FELNG2001953, KIDNE2010049, LYMPB2002344, N1ESE2000698, NETRP2003448, NT2RI2004818, NTONG2008483, OCBBF3006986, OCBBF3021086, OCBBF3021502, OCBBF3023175, PLACE5000492, PLACE6000055, PLACE6019600, PLACE7009936, PLACE7014247, PLACE7016526, PUAEN2006639, SKMUS2008585, SKMUS2009557, SMINT2017964, SPLEN2007689, SYNOV2017179, SYNOV4009575, TESTI4002774, TESTI4004695, TESTI4010902, TESTI4012960, TESTI4013474, TESTI4020342, TESTI4020596, TESTI4021197, TESTI4022158, TESTI4028042, TESTI4029731, TESTI4033177, TESTI4036048, TESTI4046073, TESTI4047808, TESTI4049786, TESTI4051865, THYMU3013785, THYMU3025683, THYMU3032798, TRACH2024730, TRACH3003037, TRACH3003357, TRACH3005173, TRACH3011538, TRACH3018519, TRACH3020605, TRACH3024020, TRACH3030176, TRACH3

031660, TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042,
UTERU3001029, UTERU3006720, UTERU3010919, UTERU3021231, UTERU3022168

【 0 0 8 6 】

転写関連蛋白質に属すると推定されたクローンは、以下の 1 4 1 クローンであ
った。

ASTRO2016114, BEAST2000981, BRACE2019348, BRACE3025719, BRACE3026844, BR
ACE3026947, BRACE3029021, BRACE3034183, BRACE3040239, BRACE3041162, BRAC
E3047482, BRAMY2041347, BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3
014027, BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209,
BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3013009, BRAWH3013264, BR
AWH3015175, BRAWH3015610, BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAW
H3027533, BRAWH3027880, BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3
032571, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3042787,
BRAWH3044122, BRAWH3046424, BRCAN2021452, BRCOC2012386, BRHIP2027077, BR
HIP2029663, BRHIP3005037, BRHIP3007609, BRHIP3017256, BRHIP3019824, BRHI
P3027651, BRHIP3028246, BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA3
000456, BRTHA3003225, BRTHA3010212, BRTHA3014000, BRTHA3028339,
CHONS2000797, CTONG2006235, CTONG2011801, FCBBF3020030, FEBRA2002260, HC
ASM2008154, KIDNE2018268, NETRP2003103, NETRP2004017, NT2RI3009480, NTON
G2003805, NTONG2008483, OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3
008392, OCBBF3019269, OCBBF3020263, OCBBF3022827, OCBBF3025503,
OCBBF3026361, PLACE7005169, PLACE7007973, PLACE7009757, PLACE7018512, SM
INT2014721, SPLEN2012571, SPLEN2036608, TIESE2000904, TESTI2036822, TEST
I2040377, TESTI4000370, TESTI4000621, TESTI4001679, TESTI4002799, TESTI4
003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4024494,
TESTI4028182, TESTI4032913, TESTI4039904, TESTI4051054, TESTI4052775, TH
YMU2008207, THYMU2038199, THYMU3008105, THYMU3012983, THYMU3014372, THYM
U3021586, THYMU3022434, THYMU3026000, THYMU3030072, THYMU3034671, THYMU3
037617, THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616,

TLUNG2000654, TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113, TRACH3004412, TRACH3004424, TRACH3005274, TRACH3010079, TRACH3010167, TRACH3015951, TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3015011, UTERU3016070, UTERU3018172, UTERU3022588

【 0 0 8 7 】

疾患関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 クローンであった。

BRAWH3041928, BRHIP3000859, BRTHA3018409, THYMU3025642

【 0 0 8 8 】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 2 6 4 クローンであった。

BRACE1000475, BRACE2003628, BRACE2012528, BRACE2013132, BRACE2016896, BRACE2035120, BRACE2042541, BRACE2047975, BRACE3002344, BRACE3009392, BRACE3013418, BRACE3015898, BRACE3017253, BRACE3019941, BRACE3024444, BRACE3031315, BRACE3031372, BRACE3032537, BRACE3033525, BRACE3034183, BRACE3034964, BRACE3039288, BRACE3039454, BRACE3041059, BRACE3042409, BRACE3044172, BRACE3046491, BRACE3049714, BRACE3050270, BRACE3051819, BRACE3052410, BRACE3052595, BRAMY3007078, BRAMY3009491, BRAMY3011581, BRAMY3014613, BRAMY4000915, BRAWH2000256, BRAWH2002333, BRAWH2012866, BRAWH2014053, BRAWH2016785, BRAWH3009961, BRAWH3010657, BRAWH3013264, BRAWH3015175, BRAWH3017180, BRAWH3017259, BRAWH3019026, BRAWH3021724, BRAWH3022431, BRAWH3023415, BRAWH3024186, BRAWH3028796, BRAWH3029385, BRAWH3029806, BRAWH3032571, BRAWH3033513, BRAWH3034668, BRAWH3034743, BRAWH3037979, BRAWH3041556, BRAWH3043295, BRAWH3044122, BRAWH3044985, BRAWH3046424, BRAWH3047692, BRAWH3048724, BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402, BRCAN2021325, BRCOC2001355, BRCOC2006164, BRHIP2029663, BRHIP3001481, BRHIP3002000, BRHIP3002114, BRHIP3002141, BRHIP3003063, BRHIP3003126, BRHIP3003795, BRHIP3004725, BRHIP3005307, BR

HIP3005673, BRHIP3007195, BRHIP3007223, BRHIP3011082, BRHIP3012289, BRHI
P3016032, BRHIP3019643, BRHIP3021019, BRHIP3032374, BRHIP3033557, BRHIP3
035006, BRHIP3037543, BRHIP3038030, BRHIP3041587, BRSSN2004710,
BRSSN2011843, BRSTN2011961, BRSTN2016918, BRTHA2001304, BRTHA2005448, BR
THA2026290, BRTHA2026311, BRTHA2027250, BRTHA2030036, BRTHA2033683, BRTH
A2035743, BRTHA2036295, BRTHA2037247, BRTHA3003736, BRTHA3010135, BRTHA3
014547, BRTHA3021786, BRTHA3023403, BRTHA3026916, CHONS2002829,
COLON2004351, CTONG2010330, CTONG2020582, CTONG2026987, FCBBF3001018, FC
BBF3021191, FEBRA2013570, FEBRA2026582, FEHRT2002708, FEKID2002637, HHDP
C2008185, HSYRA2004550, KIDNE2004531, KIDNE2010049, LYMPB2002236, NT2RI2
004818, NT2RI3001967, NT2RP7016508, NT2RP8003490, NT2RP8003787,
NT2RP8005546, OCBBF2000831, OCBBF2007039, OCBBF2024589, OCBBF3001616, OC
BBF3004487, OCBBF3021086, OCBBF3023175, OCBBF3025503, OCBBF3026088, OCBB
F3026361, PLACE5000492, PLACE6003004, PLACE7003985, PLACE7004103, PLACE7
004961, PLACE7006090, PLACE7007379, PLACE7008136, PLACE7012111,
PLACE7014247, PLACE7016526, SKMUS2008585, SKMUS2009557, SMINT2011406, SM
INT2011509, SYNOV2017179, SYNOV4003174, SYNOV4009139, TIESE2000609, TIES
E2002665, TESTI2001364, TESTI2005112, TESTI2007490, TESTI2018335, TESTI2
021112, TESTI2021654, TESTI2030901, TESTI2037877, TESTI2049062,
TESTI4000621, TESTI4002774, TESTI4002799, TESTI4003404, TESTI4003565, TE
STI4003602, TESTI4003703, TESTI4005399, TESTI4007671, TESTI4010544, TEST
I4010721, TESTI4012960, TESTI4017854, TESTI4020342, TESTI4020596, TESTI4
020819, TESTI4021129, TESTI4021197, TESTI4023096, TESTI4024494,
TESTI4026080, TESTI4028182, TESTI4031066, TESTI4033177, TESTI4040598, TE
STI4041482, TESTI4046073, TESTI4047808, TESTI4049786, TESTI4051424, TEST
I4051865, TESTI4052219, THYMU3000390, THYMU3002825, THYMU3014372, THYMU3
023400, THYMU3025683, THYMU3026306, THYMU3026479, THYMU3031878,
THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428, THYMU3047115, TH
YMU3047891, TRACH2022113, TRACH2024730, TRACH3003037, TRACH3005274, TRAC

H3006800, TRACH3009008, TRACH3009061, TRACH3011313, TRACH3016455, TRACH3017409, TRACH3018108, TRACH3018261, TRACH3019621, TRACH3021544, TRACH3023516, TRACH3024020, TRACH3024081, TRACH3024342, TRACH3024512, TRACH3025316, TRACH3026303, TRACH3026650, TRACH3027229, TRACH3027701, TRACH3029329, TRACH3032150, TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042, UTERU3001946, UTERU3010604, UTERU3010919, UTERU3015299, UTERU3017441, UTERU3019708, UTERU3020090, UTERU3022168

【 0 0 8 9 】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 3 クローンであった。

BRACE3022303, BRAWH3017260, BRHIP2008756, BRHIP3028570, BRSTN2006638, NT2RI2004818, PLACE7009563, PLACE7016526, SMINT2014721, THYMU3025642, THYMU3033626, TRACH3029329, UTERU3010919

【 0 0 9 0 】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 1 クローンであった。

BRACE2046976, BRACE3013874, BRACE3047482, BRACE3051819, BRAMY3015549, BRAWH3015175, BRAWH3018548, BRAWH3021580, BRAWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3032298, BRAWH3049544, BRHIP3003340, BRHIP3012736, BRHIP3036936, BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA2031917, BRTHA3011361, BRTHA3025073, CTONG2008989, HSYRA2007338, LYMPB2002458, OCBBF3008835, OCBBF3027969, PEBLM2006298, PLACE7000266, PLACE7004103, PLACE7004961, SMINT2011406, SYNOV4003174, TESTI2006543, TESTI2034913, TESTI4001517, TESTI4005653, TESTI4008305, TESTI4041049, TESTI4051424, TESTI4051865, THYMU3020221, THYMU3038158, TLUNG2000654, TRACH3002890, TRACH3006379, TRACH3012460, TRACH3018524, TRACH3020769, TRACH3028837, UTERU3011837

【 0 0 9 1 】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンは

、以下の 2 9 クローンであった。

BRACE2016896, BRACE3032537, BRACE3034183, BRACE3039288, BRAWH3013264, BRAWH3032571, BRCOC2006164, BRHIP3004725, BRSSN2011843, BRTHA2026290, BRTHA3003736, BRTHA3014547, NT2RP7016508, NT2RP8005546, OCBBF3004487, OCBBF3021086, OCBBF3026361, PLACE5000492, TESTI4000621, TESTI4002799, TESTI4010721, TESTI4012960, THYMU3014372, THYMU3033626, THYMU3041428, TRACH3017409, TRACH3029462, UTERU3010919, UTERU3019708

【 0 0 9 2 】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 0 クローンであった。

BRACE3033525, BRACE3041059, BRAMY4001652, BRAWH3010657, BRAWH3013264, BRAWH3034668, BRAWH3036247, BRAWH3037428, BRAWH3037979, BRCAN2000923, BRCAN2002892, BRCAN2006051, BRCAN2021325, BRCAN2021718, BRHIP2029663, BRHIP3002000, BRHIP3003126, BRHIP3007223, BRHIP3011082, BRSTN2010089, BRTHA2036295, BRTHA3012265, CHONS2002829, D9OST2004417, HHDPC2008185, NE TRP2003448, OCBBF2007039, OCBBF3021086, PLACE6003004, PLACE6010925, PLACE7006498, PLACE7007379, PLACE7012111, PLACE7016526, TESTI2023903, TESTI2036285, TESTI4003602, TESTI4012960, TESTI4014415, TESTI4030864, TESTI4051865, THYMU3036953, THYMU3047891, TRACH3004113, TRACH3006800, TRACH3009061, TRACH3021544, TRACH3026650, UTERU3001946, UTERU3012414

【 0 0 9 3 】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 クローンであった。

BRHIP3027191, SYNOV4009575, TESTI2023903, TRACH3029462

【 0 0 9 4 】

発生、分化関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 クローンであった。

CHONS2000797

【 0 0 9 5 】

DNA・RNA結合蛋白質のカテゴリに属すると推定されたクローンは、以下の 185 クローンであった。

ASTRO2016114, BEAST2000981, BRACE2012625, BRACE2016896, BRACE2019348, BRACE3019941, BRACE3025719, BRACE3026844, BRACE3026947, BRACE3029021, BRACE3031743, BRACE3032537, BRACE3034183, BRACE3039288, BRACE3040239, BRACE3041162, BRACE3047482, BRACE3050270, BRALZ2013621, BRAMY2041347, BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027, BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209, BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3011623, BRAWH3013009, BRAWH3013264, BRAWH3015175, BRAWH3015610, BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAWH3027533, BRAWH3027607, BRAWH3027880, BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3032571, BRAWH3035403, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3038055, BRAWH3042787, BRAWH3044122, BRCAN2020331, BRCAN2021452, BRCOC2006164, BRCOC2012386, BRHIP2027077, BRHIP2029663, BRHIP3002141, BRHIP3004725, BRHIP3005037, BRHIP3007609, BRHIP3017256, BRHIP3019824, BRHIP3027651, BRHIP3028246, BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA2026290, BRTHA2037247, BRTHA3000456, BRTHA3003225, BRTHA3003736, BRTHA3010212, BRTHA3014000, BRTHA3014547, BRTHA3028339, CHONS2000797, CTONG2003517, CTONG2006235, CTONG2011801, CTONG2026987, D9OST2003106, FCBBF3020030, FEBRA2002260, FEBRA2028457, FEHRT2002708, HCASM2008154, KIDNE2018268, NETRP2003103, NETRP2004017, NT2RI3009480, NT2RP7016508, NT2RP8005546, NTONG2003805, NTONG2008483, OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3001616, OCBBF3004487, OCBBF3008392, OCBBF3019269, OCBBF3020263, OCBBF3021086, OCBBF3021361, OCBBF3022827, OCBBF3025503, OCBBF3026361, PLACE5000492, PLACE7004103, PLACE7005169, PLACE7007973, PLACE7008136, PLACE7009757, PLACE7018512, PROST2002078, SMINT2011509, SMINT2014721, SPLEN2012571, SPLEN2036608, T1ESE2000609, T1ESE2000904, TESTI2036822, TESTI2040377, TESTI4000370, TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4

012960, TESTI4024494, TESTI4028182, TESTI4032913, TESTI4039904,
TESTI4051054, TESTI4052775, THYMU2008207, THYMU2038199, THYMU3008105, THYMU3012983, THYMU3014372, THYMU3021586, THYMU3022434, THYMU3023400, THYMU3026000, THYMU3030072, THYMU3037617, THYMU3040829, THYMU3041428, THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616, TLUNG2000654,
TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113, TRACH3004412, TRACH3004424, TRACH3005274, TRACH3010079, TRACH3010167, TRACH3015951, TRACH3017409, TRACH3021778, TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3015011, UTERU3016070, UTERU3019708, UTERU3020090, UTERU3022168, UTERU3022588, UTERU3023141

【 0 0 9 6 】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 41 クローンであった。

BRACE3042409, BRAWH2002333, BRAWH2014053, BRAWH3015175, BRAWH3029385, BRAWH3029806, BRAWH3034743, BRAWH3037428, BRAWH3047692, BRCAN2000923, BRCA N2002892, BRCAN2022126, BRCOC2001355, BRCOC2006164, BRHIP3007195, BRSSN2004710, BRTHA2026290, BRTHA2033683, BRTHA3026916, CTONG2020582, HSYRA2004550, NETRP2003448, PLACE6019600, PLACE7004961, PLACE7006498, PLACE7016526, SMINT2011406, TESTI4010544, TESTI4014415, TESTI4028182, TESTI4029731, TESTI4040559, TESTI4041482, TESTI4052219, THYMU3013785, THYMU3047115, TRACH2024730, TRACH3024081, TRACH3029329, TRACH3031660, UTERU3012414

【 0 0 9 7 】

以下の 172 クローンについては、Pfamでヒットデータ（実施例 5 参照）があったものの、上記のいずれのカテゴリーに属するか明らかでないクローンであった。今後同様のドメイン、モチーフを持つタンパク質のデータの蓄積と共に機能がより詳細に解明され、上記のカテゴリーに分類できる可能性がある。

BLADE2001031, BRACE2010336, BRACE2013009, BRACE2017872, BRACE2023744, BRACE2034434, BRACE3001973, BRACE3002756, BRACE3005903, BRACE3014523, BRAC

E3019570, BRACE3022340, BRACE3026345, BRACE3036283, BRACE3040644, BRACE3043597, BRACE3046466, BRACE3048615, BRALZ2010842, BRAMY2031516, BRAMY2041384, BRAMY3002886, BRAMY3011501, BRAMY3015086, BRAMY3018754, BRAMY4000962, BRAWH2011796, BRAWH2016223, BRAWH3001783, BRAWH3003573, BRAWH3008167, BRAWH3011331, BRAWH3011577, BRAWH3014609, BRAWH3021574, BRAWH3022347, BRAWH3022719, BRAWH3024231, BRAWH3026938, BRAWH3027440, BRAWH3030772, BRAWH3030910, BRAWH3033448, BRAWH3034775, BRAWH3038252, BRAWH3038324, BRAWH3038827, BRAWH3042438, BRAWH3042568, BRAWH3044151, BRAWH3045118, BRAWH3048374, BRCAN2010665, BRCAN2019907, BRCAN2020234, BRCAN2025093, BRCOC2006639, BRHIP2013958, BRHIP2026346, BRHIP2027563, BRHIP3001878, BRHIP3004710, BRHIP3005142, BRHIP3005231, BRHIP3006449, BRHIP3007424, BRHIP3009753, BRHIP3010289, BRHIP3020733, BRHIP3029409, BRHIP3030230, BRHIP3033734, BRSSN2015497, BRTHA2038345, BRTHA3011187, BRTHA3021971, BRTHA3026161, BRTHA3027171, BRTHA3027638, CHONS2001287, CHONS2001834, DFNES2011221, ERLTF2002178, FCBBF3012443, FCBBF3024911, FCBBF5000384, FEBRA2000805, FEBRA2023498, FEKID2002493, HCHON2009766, JCMLC2002751, KIDNE2015987, NT2RI3001573, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP7020343, NT2RP8000633, NT2RP8001604, NT2RP8006452, NT2RP8007920, NT2RP8009119, OCBBF3001202, OCBBF3005330, OCBBF3023913, OCBBF3026979, PEBLM2001803, PLACE6001933, PLACE7002303, PUAEN2000594, PUAEN2000684, SMINT2010753, SPLEN2022785, SPLEN2028417, SYNOV2003326, TBAES2003917, TBAES2007428, TESOP2002005, TESTI2005564, TESTI2009739, TESTI2011020, TESTI2018867, TESTI2049041, TESTI4001569, TESTI4002141, TESTI4002868, TESTI4004031, TESTI4007965, TESTI4011926, TESTI4013742, TESTI4024294, TESTI4035898, TESTI4039451, TESTI4041984, TESTI4043166, TESTI4046873, TESTI4047328, TESTI4047569, TESTI4051015, TESTI4052598, THYMU3003007, THYMU3012402, THYMU3015042, THYMU3015571, THYMU3017761, THYMU3019476, THYMU3021755, THYMU3033649, THYMU3040126, THYMU3046360, TKIDN2011051, TKIDN2011160, TLIVE2007736, TRACH3007689, TRACH3012106, TRACH3

015346, TRACH3016805, TRACH3018606, TRACH3022296, TRACH3022758,
TRACH3023203, TRACH3028855, TRACH3030855, TRACH3032570, UTERU2016669, UT
ERU3001394, UTERU3009775, UTERU3011558, UTERU3011579, UTERU3017995, UTER
U3018255, UTERU3021850

【 0 0 9 8 】

なお、モチーフやドメインの機能が必ずしも上記に示す機能カテゴリーの一つのみに属するわけではないため、いずれで予測された機能カテゴリーにも該当する可能性がある。またこれら以外にPfamでヒットデータがなかった残りのクローンについても、今後タンパク質のデータの蓄積と共に新たなドメイン、モチーフが見い出された場合、再びクローンの推定アミノ酸配列を新しいデータベースに対して解析することで新たな機能を有したドメイン、モチーフが発見され、カテゴリー分類できる可能性がある。

【 0 0 9 9 】

これらクローンにコードされる蛋白質は、いずれも全長アミノ酸配列を備えることから、適当な発現系を適用して組み換え体として発現させたり、細胞にインジェクションすることにより、あるいは、そのタンパクを特異的に認識する抗体を作製し、用いることで、その生物学的活性、及び細胞増殖・分化といった細胞状態変化への作用を解析することが可能である。

【 0 1 0 0 】

各蛋白質は、それぞれ次に示すような手法にもとづいて、それぞれの蛋白質の生物学的活性の解析が可能である。

分泌蛋白質、膜蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Ion Channels』(R.H. Ashley編、1995)、

『Growth Factors』(I. McKay, I. Leigh編、1993)、『Extracellular Matrix』(M.A. Haralson, J.R. Hassell編、1995)

糖蛋白質関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Glycobiology』(M. Fukuda, A. Kobata編、1993)、

「Method in Molecular Biology」(Humana Press社)シリーズの『Glycoprotein Analysis in Biomedicine』(Elizabeth F.Hounsell編、1993)、

シグナル伝達関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Signal Transduction』(G.Milligan編、1992)、

『Protein Phosphorylation』(D.G.Hardie編、1993)、または「Method in Molecular Biology」(Humana Press社)シリーズの『Signal Transduction Protocols』(David A. Kendall, Stephen J.Hill編、1995)、

転写関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Gene Transcription』(B.D.Hames, S.J.Higgins編、1993)、

『Transcription Factors』(D.S.Latchman編、1993)、

酵素・代謝関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Enzyme Assays』(ROBERT EISENTHAL and MICHAEL J. DANSON編、1992)、

細胞分裂・増殖関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Cell Growth, Differentiation and Senescence』(GEORGE STUDZINSKI編、2000)、

細胞骨格関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Cytoskeleton: Signaling and Cell Regulation』(KERMIT L. CARRAWAY and CAROLIE A. CAROTHERS CARRAWAY編、2000)、

「Method in Molecular Biology」(Humana Press社)シリーズの『Cytoskeleton Methods and Protocols』(Gavin, Ray H. 編、2000)、

核蛋白質・RNA合成関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Nuclear Receptors』(DIDIER PICARD編、1999)、

『RNA Processing』(STEPHEN J. HIGGINS and B. DAVID HAMES編、1994)、

蛋白質合成・輸送関連蛋白質：

「The Practical Approach Series」(IRL PRESS社)の『Membrane Transport』(STEPHEN A. BALDWIN編、2000)、

「Method in Molecular Biology」(Humana Press社)シリーズの『Protein Synthesis Methods and Protocols』(Martin, Robin編、1998)、

細胞防御関連蛋白質：

「Method in Molecular Biology」(Humana Press社)シリーズの『DNA Repair Protocols』(Henderson, Daryl S.、1999)、

『Chaperonin Protocols』(Schneider, Christine編、2000)、

発生・分化関連蛋白質：

「Method in Molecular Biology」(Humana Press社)シリーズの『Developmental Biology Protocols』(ROBERT EISENTHAL and MICHAEL J. DANSON編、1992)、

DNA・RNA結合蛋白質：

「Method in Molecular Biology」(Humana Press社)シリーズの『DNA-Protein Interactions Principles and Protocols』(Kneale, G. Geoff編、1994)、

『RNA-Protein Interaction Protocols』(Haynes, Susan R.編、1999)、

ATP・GTP結合蛋白質：

「Method in Molecular Biology」(Humana Press社)シリーズの『Signal Transduction Protocols』(David A. Kendall, Stephen J. Hill編、1995)

これら以外の手法については、Methods in Enzymology(Academic Press)を参照して蛋白質の活性を解析することができる。

【 0 1 0 1 】

なお、上述したカテゴリー分類において、分泌・膜蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中に growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue 等、分泌・膜蛋白質と推定される記載があった、もしくはPSORTとSOSUIによる推定ORFの解析の結果、シグナルシーケンスや膜貫通領域があった、またPfamによるドメイン、モチーフ検索の結果、受容体、イオンチャンネル、ホルモン、成

長因子などと推測されるような例えば 7 transmembrane receptor, Pancreatic hormone peptides, Ion transport protein, Fibroblast growth factor等のドメイン、モチーフがあったクローンである。

【 0 1 0 2 】

糖蛋白質関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中に glycoprotein 等、糖蛋白質関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、糖タンパク質、糖転移酵素などGlycobiologyに関わると推測されるような例えばImmunoglobulin domain, Glycosyl transferases group 1等のドメイン、モチーフがあったクローンである。

【 0 1 0 3 】

シグナル伝達関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中に serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain等、シグナル伝達関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、タンパク質リン酸化酵素、脱リン酸化酵素、SH2ドメイン、Small Gタンパク質などと推測されるような例えばEukaryotic protein kinase domain, Protein phosphatase 2C, Ras family等のドメイン、モチーフがあったクローンである。

【 0 1 0 4 】

転写関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中に transcription regulation, zinc finger, homeobox 等、転写関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、転写因子や転写調節に関わるタンパク質などと推測されるような例えばbZIP transcription factor, Zinc finger, C2H2 type等のドメイン、モチーフがあったクローンである。

【 0 1 0 5 】

疾患関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中に disease mutation, syndrome 等、疾患関連蛋白質と推定される記載があった、あるいは全長塩基配列に対するSwiss-Prot、nr、RefS

eqヒットデータが、後述するヒトの遺伝子と疾患のデータベースであるOnline Mendelian Inheritance in Man (OMIM) (<http://www.ncbi.nlm.nih.gov/0mim/>)に登録されている遺伝子や蛋白質であった、また、Pfamによるドメイン、モチーフ検索の結果、特定の疾患で発現が見られるようなタンパク質や、疾患で発現が上昇したり減少したりすると推測されるような例えばWilm's tumour protein, von Hippel-Lindau disease tumor suppressor protein等のドメイン、モチーフがあったクローンである。

【0106】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にmetabolism, oxidoreductase, E.C.No. (Enzyme commission number)等、酵素・代謝関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、転移酵素、合成酵素、加水分解酵素などと推測されるような例えばAldehyde dehydrogenase family, Chitin synthase, Glucose-6-phosphate dehydrogenase等のドメイン、モチーフがあったクローンである。

【0107】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis等、細胞分裂・増殖関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、サイクリン、細胞増殖制御タンパク質などと推測されるような例えばCyclin, Cell division protein等のドメイン、モチーフがあったクローンである。

【0108】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にstructural protein, cytoskeleton, actin-binding, microtubules等、細胞骨格関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、アクチン、キネシン、フィブロネクチンなどと推測されるような例えばActin, Fibronectin type I domain, Kinesin motor domain等のドメイン、モチーフがあったクローンである。

【 0 1 0 9 】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にnuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation等、核蛋白質・RNA合成関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、スプライシング因子、RNA合成酵素、ヘリカーゼなどと推測されるような例えばHepatitis C virus RNA dependent RNA polymerase, DEAD/DEAH box helicase等のドメイン、モチーフがあったクローンである。

【 0 1 1 0 】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にtranslation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle等、蛋白質合成・輸送関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、翻訳関連タンパク質、ユビキチン関連タンパク質、Ribosomal proteinなどと推測されるような例えばTranslation initiation factor SUI1, Ubiquitin family, Ribosomal protein L16等のドメイン、モチーフがあったクローンである。

【 0 1 1 1 】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にheat shock, DNA repair, DNA damage等、細胞防御関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、分子シャペロン、DNA修復タンパク質などと推測されるような例えばHsp90 protein, DNA mismatch repair protein等のドメイン、モチーフがあったクローンである。

【 0 1 1 2 】

発生・分化関連蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にdevelopmental protein等、発生・分化関連蛋白質と推定される記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、器官形成関連タンパク質などと推測されるような例えばFloricaula / Lea

fy protein等のドメイン、モチーフがあったクローンである。

【0113】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にDNA-binding, RNA-binding等と記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、転写因子、DNAリガーゼをはじめとしたDNA・RNA関連酵素類、Zinc-finger関連タンパク質などと推測されるような例えばTranscription factor WhiB, B-box zinc finger, tRNA synthetases class I (C)等のドメイン、モチーフがあったクローンである。

【0114】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンとは、相同性検索の結果、ヒットデータ中にATP-binding, GTP-binding等と記載があった、あるいはPfamによるドメイン、モチーフ検索の結果、ATPase等をはじめとしたATP・GTP関連酵素類、Gタンパク質などと推測されるような例えばE1-E2 ATPase, Ras family等のドメイン、モチーフがあったクローンである。

【0115】

疾患関連蛋白質については、前述したように機能ごとの解析が可能であるほか、疾患関連蛋白質を発現して得られた特異認識抗体を用いて、特定の疾患と蛋白質の発現量や活性との相関を知ることができる。あるいは、ヒトの遺伝子と疾患のデータベースであるOMIMを利用し、解析が可能である。なおOMIMには常に新しい情報が付加されている。したがって当業者は、特定の疾患と本発明の遺伝子との新たな関係を最新のデータベースから見出すことができる。疾患関連蛋白質は、診断マーカー、発現・活性の増減を制御する薬剤、あるいは遺伝子治療のターゲットになるなど医薬品の開発等に有用である。

【0116】

また、分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質をはじめ、上記の14種類のカテゴリーの蛋白質に限らず、種々の機能をもつ蛋白質についても、OMIMを利用してキーワードで検索すると、各キーワードにおいて、多くの疾患に関連した結果が得られた（分泌、膜蛋白質について、OMIMで検索した結果を一例として以下に示す）。あるいは、例えば転写

関連蛋白質やシグナル伝達関連蛋白質については、疾患との関連がそれぞれ、藤井・田村・諸橋・影山・佐竹編の実験医学増刊「転写因子研究1999」Vol.17, No.3, (1999)や、遺伝子医学Vol.3, No.2(1999)で報告されている。例えば、がんを例に挙げると、裳華房生命科学シリーズ「がんの生物学」(松原聡著、1992)にあるように、がんには分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質ばかりでなく、酵素・代謝関連蛋白質、細胞骨格関連蛋白質、細胞分裂・増殖関連蛋白質といった多くの蛋白質が関与することが示されている。このように、疾患関連蛋白質ばかりでなく、分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質等も疾患に関与することが多く、医療産業上のターゲットとして、有用なことがわかる。

【0117】

一例として、分泌、膜蛋白質について、OMIMで検索した結果を以下に示す。OMIM検索に用いたキーワードには、

- (1) secretion protein
- (2) membrane protein
- (3) channel
- (4) extracellular matrix

を用いた。

【0118】

検索結果には、OMIM登録番号記号のみを記載した。なお、番号は検索結果表示時に最初に現れる50件のみ記した。この番号をもとにOMIMで疾患と遺伝子や蛋白質との関係を示すデータを見ることができる。また、OMIMデータは日々更新されている。

1) Secretion protein (分泌蛋白質)

このキーワードで検索された疾患と関連のある遺伝子は436登録されており、そのうちの50遺伝子は以下のOMIM番号をもつ。

*604667、*104760、*176860、*139320、*118910、*151675、*107400、*604029、
#200100、*177061、*600946、*601693、*139250、*176880、*600998、*603850、
*605083、*147572、*179513、*606055、*604028、*125950、*157147、*246700、

*602926、*600560、*602421、*603215、185860、*600174、*179512、*109270、*179511、*179510、*179509、*601146、*604710、*177020、*138120、*170280、*600626、*164160、*168470、*154545、*603831、*601652、*104311、*601489、*603062、*102720

【 0 1 1 9 】

2) Membrane protein (膜蛋白質)

このキーワードで検索された疾患と関連のある遺伝子は 1 8 7 3 登録されており、そのうちの 5 0 遺伝子は以下のOMIM番号をもつ。

*130500、*605704、*305360、*153330、*109270、*173610、*170995、*120920、*170993、*309060、*104776、*602333、*605703、*602690、*605943、*159430、*600897、*606867、*133090、*601178、*602413、*602003、*604405、*605940、*603237、*109280、*606958、*600378、*606959、*602173、*107776、*602334、*125305、*602335、*309845、*601134、*605731、*606795、*185881、*607178、*603177、*154045、*603214、*603718、*606909、*600594、*603241、*606629、*603657、*600182

【 0 1 2 0 】

3) Channel (膜蛋白質のメンバー)

このキーワードで検索された疾患と関連のある遺伝子は 4 4 9 登録されており、そのうちの 5 0 遺伝子は以下のOMIM番号をもつ。

*176266、*600724、*605427、*182390、*123825、*114208、*114206、*114205、*176267、*600053、*601784、*603749、*182392、*600937、*603415、*114204、*114209、*114207、*607370、*604528、*604527、*601011、*600760、*192500、*118425、*600228、*600359、*176261、*602235、*600761、*182389、*300008、*600877、*605692、*300338、*602232、*603537、*182391、*176263、*602343、*601328、*605874、*604385、*603939、*602208、*601534、*601958、*603220、*600504、*607368

【 0 1 2 1 】

4) Extracellular matrix

このキーワードで検索された疾患と関連のある遺伝子は 2 6 7 登録されており、

そのうちの 5 0 遺伝子は以下のOMIM番号をもつ。

*605912、*602201、*603479、*604633、*601418、*601548、*115437、*154870、
*120361、*602285、*600754、*602262、*134797、*602261、*603320、*603321、
*604871、*604629、*601807、#154700、*128239、*600310、*605470、*185250、
*178990、*603767、*120360、*185261、*116935、*607056、*253700、*190180、
*600985、*188826、*193300、*276901、*308700、*120150、*602109、*120324、
*600514、#177170、#247100、#116920、#200610、*605127、*601313、*601652、
*120180、*154790

また、これらと同様に、前述のカテゴリー分類のところに示した各種のキーワード等もOMIMの検索に用いることによって疾患との関連をみることができる。

【 0 1 2 2 】

また、本発明のcDNAの塩基配列を用いれば、そのcDNAの塩基配列を有する遺伝子の発現頻度を解析することができる。更にこうして解析された発現頻度情報に基づいて、当該遺伝子の機能を予測することができる。

【 0 1 2 3 】

疾患に関連した遺伝子を調べる方法として病態組織と正常組織において遺伝子発現量の違いを調べる発現頻度解析がある。発現頻度解析には、ノーザンブロットティング法やRT-PCR法、およびDNAマクロアレイやDNAマイクロアレイを用いた発現頻度解析法がある(実験医学 Vol.17, No.8, 980-1056 (1999)、村松・那波監修 細胞工学別冊「DNAマイクロアレイと最新PCR法」(秀潤社, 2000))。更に、こういった解析方法以外に、発現している遺伝子の塩基配列をコンピューターを利用した解析で比較することによっても発現頻度を解析することができる。例えば、BODYMAPと呼ばれるデータベースは、様々な組織・細胞のcDNAライブラリーから、無作為に遺伝子クローンを抽出し、3'末端領域の塩基配列の相同性情報をもとにして、相同性のあるものはまとめてクラスターとすることによって、クラスター単位で遺伝子を分類して、各クラスターに含有されるクローンの個数を比較することによって遺伝子の発現頻度情報を得ている (<http://bodymap.ims.u-tokyo.ac.jp/>)。

【 0 1 2 4 】

このような解析手法により、病態組織と正常組織において遺伝子発現量の違いを調べた結果から発現量の違いが明らかな遺伝子は、その疾患に関連した遺伝子といえる。また、病態組織でなくとも、病態に関連した特異的な現象を再現させた培養細胞と正常細胞において遺伝子発現量の違いを調べた結果から発現量の違いが明らかな遺伝子は、その疾患に関連した遺伝子といえる。

【 0 1 2 5 】

全塩基配列が明らかになった 1 9 5 6 クローンについて、以下のデータベースを用いて、特定の病態や機能に関連する遺伝子を選択した（実施例 8. 「in silicoにおける発現頻度解析」参照）。本発明の解析に用いたデータベースは、1, 4 0 2, 0 7 0 個のクローンの塩基配列をデータベース化したものであり、解析母数としては十分なデータベースである。このデータベースを構成している配列情報は、実施例 1 に示した様々な組織や細胞由来の cDNA ライブラリーから cDNA クローンを無作為に選択して、その 5' 末端領域の配列を決定することによって得た。

【 0 1 2 6 】

次にこのデータベースにある各クローンの塩基配列を、塩基配列の相同性検索プログラムによって相同な配列同士をカテゴライズし（クラスター化）、各クラスターに属するクローン数を各ライブラリー毎に集計し規格化することによって、ある遺伝子の cDNA ライブラリー内での存在比を解析した。この解析によって、cDNA ライブラリーのソースとなっている組織や細胞における、ある遺伝子の発現頻度情報を得た。

【 0 1 2 7 】

次に本発明の cDNA の塩基配列を持つ遺伝子の、組織や細胞間での発現を解析するために、大量の cDNA クローンを解析した組織や細胞由来のライブラリーを組織・細胞間での発現量の比較の対象にした。すなわち 6 0 0 個以上の cDNA クローンの塩基配列を解析した組織や細胞について、先に規格化した数値を組織間や細胞間で比較し、遺伝子の発現頻度の変化を解析した。この解析によって以下に続く病態や機能に関連する遺伝子であることが示された。なお、以降に示される表 2 ～表 2 4 中の各数値は、相対的な発現頻度を示し、数値が大きいほど発現量が多

いことを示す。

【 0 1 2 8 】

骨粗鬆症に関連する遺伝子

骨粗鬆症とは、骨の成分が全体として減少し、骨折しやすくなった病態であるが、その発症には骨を産生する骨芽細胞と、骨を吸収する破骨細胞の働きのバランス、すなわち骨代謝が関与する。したがって単球／マクロファージ系の前駆細胞から分化する破骨細胞（Molecular Medicine 38. 642-648. (2001)）の増加に関連する遺伝子は、骨代謝に関連した骨粗鬆症に関する遺伝子である。

【 0 1 2 9 】

単球／マクロファージ系の前駆細胞（糖タンパク質CD34を発現している細胞：CD34+細胞）での発現頻度と比較して、CD34+細胞を破骨細胞分化因子（Molecular Medicine 38. 642-648. (2001)）で処理した細胞で増加または減少する遺伝子を、塩基配列情報にしたがって解析し、探索した。CD34+細胞のRNAから作製したライブラリー（CD34C）、CD34+細胞を破骨細胞分化因子で処理した細胞のRNAから作製したライブラリー（D30ST、D60STまたはD90ST）のcDNAを解析して比較した結果（表2）、両者で発現変化のある遺伝子は以下の12クローンであった。BRAWH3018063, BRHIP3020046, BRSSN2013696, BRSTN2012069, BRTHA2027229, D90ST2003106, D90ST2003989, D90ST2004417, OCBBF2016928, TESTI4005653, TESTI4013474, THYMU3032798

これらのクローンは骨粗鬆症に関する遺伝子である。

【 0 1 3 0 】

神経細胞分化関連遺伝子

神経細胞の分化に関する遺伝子は、神経疾患の治療に有用な遺伝子である。神経系の細胞を分化誘導して発現変化する遺伝子は、神経疾患に関すると考えられている。

神経系の培養細胞NT2を分化誘導（レチノイン酸(RA)刺激またはRA刺激後さらに増殖阻害剤処理）して発現変化する遺伝子を探索した。未分化なNT2細胞由来のライブラリー（NT2RM）と分化誘導処理した細胞のライブラリー（NT2RP, NT2RIまたはNT2NE）のcDNAを解析して比較した結果（表3）、両者で発現変化のある

遺伝子は以下の 1 0 2 クローンであった。

BLADE2004849, BRACE2003628, BRACE2012528, BRAMY2023939, BRAMY2031516, BRAMY4002628, BRAWH3010461, BRAWH3017259, BRAWH3018063, BRAWH3022651, BRAWH3024186, BRCAN2019653, BRCAN2022126, BRCOC2012386, BRHIP3002000, BRHIP3007223, BRHIP3021019, BRSTN2011961, BRSTN2012069, BRTHA2033155, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3021971, CHONS2002829, CTONG2006235, FCBBF3012443, FEBRA2026582, LIVER2008465, NT2NE2011107, NT2NE2016041, NT2RI2004818, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI2023671, NT2RI2028537, NT2RI3001573, NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3007095, NT2RI3008179, NT2RI3009480, NT2RI3009524, NT2RP7003439, NT2RP7007387, NT2RP7014178, NT2RP7014778, NT2RP7016508, NT2RP7017139, NT2RP7019682, NT2RP7020343, NT2RP8000633, NT2RP8001363, NT2RP8001407, NT2RP8001584, NT2RP8001604, NT2RP8001605, NT2RP8003490, NT2RP8003657, NT2RP8003787, NT2RP8005546, NT2RP8006452, NT2RP8006521, NT2RP8007416, NT2RP8007503, NT2RP8007920, NT2RP8008057, NT2RP8009119, NT2RP8009248, NTONG2008483, OCBBF2003518, OCBBF3001333, OCBBF3004908, PLACE7004103, PROST2017910, SMINT2009292, SPLEN2012571, TIESE2000904, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4005653, TESTI4007965, TESTI4012960, TESTI4018436, THYMU3001776, THYMU3002887, THYMU3029795, THYMU3041428, THYMU3047115, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3009008, TRACH3016805, TRACH3016885, TRACH3026303, UTERU2016669

これらの遺伝子は神経疾患に関する遺伝子である。

【 0 1 3 1 】

アルツハイマー病関連遺伝子

アルツハイマー病とは記憶力が低下し、進行すれば生活が困難となり介護が必要となる脳神経系の疾患であり、進行すれば脳そのものが萎縮する。その発症の要因はストレスなどの環境因子、高血圧やコレステロール血症などの血管因子も関わりがあるといわれているが、未だ不明である。したがって、正常脳組織とア

ルツハイマーの病態組織を比較した時、発現に差のある遺伝子はアルツハイマー病に関連する遺伝子であり、病態の発症メカニズムの解明や、遺伝子診断に有用であると考えられる。アルツハイマー患者の脳皮質由来のライブラリー (BRALZ、BRASW) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 4)、両者で発現変化のある遺伝子は以下の 2 9 8 クローンであった。

ASTR02016114, BRACE2002392, BRACE2012528, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRALZ2003119, BRALZ2007661, BRALZ2008930, BRALZ2010842, BRALZ2011337, BRALZ2013621, BRALZ2013690, BRALZ2014054, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3

022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651,
BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BR
AWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAW
H3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3
027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616,
BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BR
AWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAW
H3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3
031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340,
BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BR
AWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAW
H3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3
035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334,
BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BR
AWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCA
N2010665, BRCAN2019653, BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2
015153, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3003063,
BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409, BRHIP3008320, BR
HIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3021019, BRHIP3028246, BRHI
P3028570, BRSTN2010089, BRSTN2012069, BRSTN2016992, BRTHA2033155, BRTHA3
003736, BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194,
BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, CT
ONG2006235, CTONG2009033, CTONG2020582, D9OST2003106, DFNES2001829, KIDN
E2010049, MESAN2017133, NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3
009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483,
OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PL
ACE7006240, PROST2007444, PROST2017910, TBAES2007428, TESTI2005112, TEST
I2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4
004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4013474,

TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3041428, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3013167

これらの遺伝子はアルツハイマー病に関する遺伝子である。

【 0 1 3 2 】

パーキンソン病関連遺伝子

パーキンソン病とは脳内の黒質で作られるドーパミンという神経伝達物質が十分量作られなくなり、その結果、手が震え、筋肉の動きが固くなって身体の動きが鈍くなる等の運動障害を引き起こす脳神経系の疾患である。脳の神経細胞は通常、歳を取るにつれて少しずつ減少するが、パーキンソン病では黒質の神経細胞が普通よりも早く著しく減少する。よって脳組織全体と黒質とを比較した時、発現に差のある遺伝子は黒質特異的な変動をするパーキンソン病に関連する遺伝子であり、発症メカニズムの解明や遺伝子診断に有用であると考えられる。黒質由来のライブラリー (BRSSN) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 5)、両者で発現変化のある遺伝子は以下の 305 クローンであった。

ASTRO2016114, BRACE2012528, BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3025719, BRACE3026802, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446,

BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BR

CAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP2029643, BRHIP3001573, BRHIP3002000, BRHIP3003063, BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSSN2004303, BRSSN2004710, BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198, BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016992, BRSTN2017104, BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, CTONG2006235, CTONG2009033, CTONG2011801, CTONG2020582, D9OST2003106, DFNES2001829, KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292, T1ESE2000904, TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3022198, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3013167

これらの遺伝子はパーキンソン病に関する遺伝子である。

【 0 1 3 3 】

短期記憶・痴呆症に関連する遺伝子

脳組織の中で海馬とは記憶を扱う非常に重要な部位であり、得た情報の情報の要・不要を判断して、他の脳部位に記憶を蓄えさせる、記憶固定の働きがある。

H3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2019953, BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177, BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125, BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735, BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563, BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626, BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338, BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878, BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141, BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931, BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340, BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710, BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037, BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3

005673, BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294,
BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172, BRHIP3007195, BR
HIP3007223, BRHIP3007291, BRHIP3007409, BRHIP3007424, BRHIP3007609, BRHI
P3007960, BRHIP3008082, BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3
009753, BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269,
BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185, BRHIP3012289, BR
HIP3012357, BRHIP3012736, BRHIP3012997, BRHIP3013078, BRHIP3013588, BRHI
P3013698, BRHIP3014675, BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3
017109, BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855,
BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880, BRHIP3019956, BR
HIP3020046, BRHIP3020155, BRHIP3020733, BRHIP3021019, BRHIP3021499, BRHI
P3021987, BRHIP3022656, BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3
025795, BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160,
BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246, BRHIP3028570, BR
HIP3028742, BRSTN2010089, BRSTN2012069, BRSTN2016992, BRTHA2001953, BRTH
A2008502, BRTHA2031517, BRTHA2033155, BRTHA2035743, BRTHA3003417, BRTHA3
003736, BRTHA3005988, BRTHA3007662, BRTHA3010135, BRTHA3010212,
BRTHA3011194, BRTHA3011265, BRTHA3012265, BRTHA3017791, BRTHA3020771, BR
THA3021971, BRTHA3023403, CHONS2002829, CTONG2006235, CTONG2009033, CTON
G2020582, D90ST2003106, DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2
017133, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923,
NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OC
BBF2000831, OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLAC
E7004103, PLACE7006240, PROST2007444, SMINT2012179, SYNOV4004210, TBAES2
007428, TESTI2005112, TESTI2005564, TESTI2021654, TESTI4001569,
TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TE
STI4003944, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TEST
I4014908, TESTI4022158, TESTI4029297, THYMU3000776, THYMU3002887, THYMU3
003007, THYMU3003350, THYMU3007308, THYMU3008105, THYMU3021586,

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これらの遺伝子は記憶および痴呆症に関する遺伝子である。

【 0 1 3 4 】

平衡感覚・運動機能に関する遺伝子

小脳は平衡感覚と筋肉運動、運動学習の中枢である。この領域は運動の調節に関与していると考えられており、小脳が動作することによって無意識的にスムーズな運動をすることが可能になる。また、運動だけでなく読み書きなどより高次の運動の慣れにも小脳が関与していることも最近の研究で解明されつつある。脳組織全体と小脳とを比較した時、発現に差のある遺伝子は平衡感覚や運動機能に関与する遺伝子であり、脳が制御する運動機能の分子メカニズム解明に有用であると考えられる。小脳由来のライブラリー (BRACE) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 7)、両者で発現変化のある遺伝子は以下の 5 0 2 クローンであった。

ASTRO2016114, BRACE1000475, BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956, BRACE2030039, BRACE2032584, BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973, BRACE3002344, BR

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LIVER2008465, MESAN2017133, NOVAR2000783, NT2RI2009233, NT2RI2015533, NT
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PROST2007444, TBAES2007428, TESTI2005112, TESTI2018867, TESTI2021654, TE
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これらの遺伝子は平衡感覚および運動機能に関する遺伝子である。

【 0 1 3 5 】

感覚器からの情報伝達に関与する遺伝子

視床は、大脳と結びつきの強い神経細胞が集まった部分であり、脊髄などから伝わってきた感覚情報を大脳の関係部分に伝えたり、大脳の運動の指令を調節する。例えば視覚では映像を大きさ、形、色に分け、聴覚では音声を音量、耳障りの良し悪しで分け、大脳皮質の感覚野に送る。脳組織全体と視床とを比較した時、発現に差のある遺伝子は感覚器からの情報伝達に関与する遺伝子であり、脳が制御する情報伝達の分子メカニズム解明に有用であると考えられる。視床由来のライブラリー (BRTHA) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 8)、両者で発現変化のある遺伝子は以下の 4 4 0 クローンであった。

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE2002392, BRACE2012528, BRACE2019348, BRACE3004371, BRACE3004767, BRACE3019941, BRACE3022312, BRACE3022340, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3036156, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAMY3009556, BRAMY3010654, BRAMY4001863, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892,

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009858, BRTHA3010135, BRTHA3010212, BRTHA3010469, BRTHA3010530,
BRTHA3010540, BRTHA3010717, BRTHA3011187, BRTHA3011194, BRTHA3011229, BR
THA3011265, BRTHA3011306, BRTHA3011361, BRTHA3011510, BRTHA3011892, BRTH
A3011998, BRTHA3012265, BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3
014105, BRTHA3014507, BRTHA3014547, BRTHA3014835, BRTHA3014854,
BRTHA3014920, BRTHA3016616, BRTHA3017791, BRTHA3018409, BRTHA3018623, BR
THA3019183, BRTHA3020369, BRTHA3020771, BRTHA3021569, BRTHA3021708, BRTH
A3021786, BRTHA3021971, BRTHA3022641, BRTHA3023403, BRTHA3023590, BRTHA3
023929, BRTHA3024600, BRTHA3025073, BRTHA3026161, BRTHA3026180,
BRTHA3026556, BRTHA3026916, BRTHA3027171, BRTHA3027318, BRTHA3027638, BR
THA3027820, BRTHA3027879, BRTHA3027957, BRTHA3028339, BRTHA3028505, CHON

S2002829, CTONG2006235, CTONG2009033, CTONG2011801, CTONG2020582, D90ST2
003106, DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133,
NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT
2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518, OCBB
F2009536, OCBBF2018618, OCBBF3001333, OCBBF3004487, OCBBF3008835, PLACE6
003004, PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292,
TBAES2007428, TESTI2005112, TESTI2021654, TESTI2039342, TESTI4002072, TE
STI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TESTI4004210, TEST
I4004695, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4007965, TESTI4
010979, TESTI4013474, TESTI4014908, TESTI4022158, TESTI4029297,
TESTI4032913, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, TH
YMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYM
U3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3
003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625,
TRACH3007689, TRACH3008508, TRACH3008632, TRACH3009008, TRACH3010079, TR
ACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRAC
H3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3
010409, UTERU3012414, UTERU3013167, UTERU3017995, UTERU3018172

これらの遺伝子は感覚器からの情報伝達に関する遺伝子である。

【 0 1 3 6 】

情動反応に関する遺伝子

扁桃は脳の感情中枢である。扁桃を通過した情報は感情反応、例えばパニック
や恐怖反応などを引き起こす。刺激が扁桃で情動評価されて強い恐怖を生じたと
き、扁桃は脳の各部に警戒信号を出す。その結果、手の平の発汗、心悸亢進、血
圧上昇、アドレナリンの急激分泌等の反応が起きる。いわば扁桃体は身体に警戒
信号を送り、その結果として体を警戒態勢に入らせる一種の防衛本能を司ってい
る組織とも言える。脳組織全体と扁桃とを比較した時、発現に差のある遺伝子は
情動反応に関与する遺伝子であり、感情反応や恐怖反応、パニックなどの分子メ
カニズム解明に有用であると考えられる。扁桃由来のライブラリー (BRAMY) と

、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 9)、両者で発現変化のある遺伝子は以下の 3 5 7 クローンであった。

ASTR02016114, BRACE2002392, BRACE2012528, BRACE2017397, BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031315, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2015516, BRAMY2021098, BRAMY2022320, BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895, BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609, BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384, BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537, BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508, BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184, BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449, BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491, BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603, BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234, BRAMY4001652, BRAMY4001863, BRAMY4001913, BRAMY4002575, BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3

018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026,
BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BR
AWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAW
H3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3
022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900,
BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BR
AWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAW
H3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3
027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806,
BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BR
AWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAW
H3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3
031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117,
BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BR
AWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAW
H3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3
036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265,
BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BR
AWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2022126, BRCA
N2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3
002000, BRHIP3002691, BRHIP3003063, BRHIP3003984, BRHIP3004215,
BRHIP3004774, BRHIP3005673, BRHIP3007223, BRHIP3007409, BRHIP3008320, BR
HIP3012736, BRHIP3014675, BRHIP3017146, BRHIP3017855, BRHIP3018784, BRHI
P3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSTN2010089, BRSTN2
012069, BRSTN2016992, BRTHA2026071, BRTHA2033155, BRTHA3003736,
BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BR
THA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, BRTHA3026916, CHON
S2002829, CTONG2006235, CTONG2009033, CTONG2020582, D90ST2003106, DFNES2
001829, KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2010795,

NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2000831, OCBBF2003518, OCBBF2018618, OCBBF2030927, OCBBF3001333, OCBBF3004487, OCBBF3009244, PLACE6008315, PLACE6010936, PLACE7004103, PLACE7006240, PROST2007444, SPLEN2012571, SYNOV4004210, SYNOV4009575, TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158, TESTI4029297, TESTI4032913, TESTI4043223, TESTI4046073, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3008105, THYMU3019476, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3013167

これらの遺伝子は情動反応に関する遺伝子である。

【 0 1 3 7 】

癌関連遺伝子

癌の組織では、正常組織とは異なる遺伝子のセットが発現して組織・細胞の癌化に寄与していると考えられている。したがって、正常組織とは異なる発現をする遺伝子は癌関連遺伝子である。正常な組織と比較して癌組織で発現変化する遺伝子を探索した。

乳がん由来のライブラリー (TBAES) と、正常な乳房由来のライブラリー (BEAST) のcDNAを解析して比較した結果 (表 1 0)、両者で発現変化のある遺伝子は以下の 1 0 クローンであった。

BRSTN2011961, BRSTN2012069, TBAES2003917, TBAES2005361, TBAES2007428, TBAES2007548, TBAES2007862, TESTI2005564, TESTI4017854, TRACH3016805

【0138】

子宮頸癌由来のライブラリー (TCERX) と、正常な子宮頸管由来のライブラリー (CERVX) のcDNAを解析して比較した結果 (表 11)、両者で発現変化のある遺伝子は以下の 6 クローンであった。

BRACE2017397, BRHIP2027077, BRSTN2011961, BRSTN2012069, CERVX2000812, CERVX2000968

【0139】

結腸がん由来のライブラリー (TCOLN) と、正常な結腸由来のライブラリー (COLON) のcDNAを解析して比較した結果 (表 12)、両者で発現変化のある遺伝子は以下の 10 クローンであった。

BRSTN2011961, BRSTN2012069, COLON2001829, COLON2001866, COLON2004351, COLON2004911, COLON2005623, COLON2005735, OCBBF3001333, SMINT2017964

【0140】

食道がん由来のライブラリー (TESOP) と、正常な食道由来のライブラリー (N ESOP) のcDNAを解析して比較した結果 (表 13)、両者で発現変化のある遺伝子は以下の 14 クローンであった。

BRAMY3004364, BRAWH3027533, BRHIP3007223, BRSTN2011961, BRSTN2012069, CTONG2011801, CTONG3002518, SMINT2009292, TESOP2002005, TESOP2003308, TESOP2004110, TESOP2008556, UTERU3015011, UTERU3017995

【0141】

腎臓がん由来のライブラリー (TKIDN) と、正常な腎臓由来のライブラリー (KIDNE) のcDNAを解析して比較した結果 (表 14)、両者で発現変化のある遺伝子は以下の 43 クローンであった。

BRACE2002392, BRACE2012528, BRACE3004371, BRAMY2039630, BRAMY3004364, BRAMY3008436, BRAWH2004078, BRAWH3012662, BRAWH3021574, BRAWH3022651, BRAWH3037428, BRCAN2019953, BRCAN2022126, BRHIP3002000, BRHIP3002691, BRHIP3012997, BRHIP3020046, BRSTN2012069, BRSTN2016992, BRTHA3010212, CTONG2006235, KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RI2015533, NT2RP7007387, OCBB

F3004487, PLACE6008315, SYNOV4004210, TESTI2005112, THYMU3001776, THYMU3002887, THYMU3029795, THYMU3032867, TKIDN2000319, TKIDN2003396, TKIDN2010602, TKIDN2011051, TKIDN2011160

【 0 1 4 2 】

肝臓がん由来のライブラリー (TLIVE) と、正常な肝臓由来のライブラリー (LIVER) のcDNAを解析して比較した結果 (表 1 5)、両者で発現変化のある遺伝子は以下の 1 4 クローンであった。

BRAWH3022651, BRCAN2020412, BRSTN2012069, BRTHA3003736, CTONG2006235, LIVER2008465, TESTI4013474, THYMU3002887, THYMU3038158, TLIVE2000142, TLIVE2001616, TLIVE2007736, TLIVE2008797, TRACH3027229

【 0 1 4 3 】

肺がん由来のライブラリー (TLUNG) と、正常な肺由来のライブラリー (HLUNG) のcDNAを解析して比較した結果 (表 1 6)、両者で発現変化のある遺伝子は以下の 1 7 クローンであった。

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069, HLUNG2012600, ME SAN2009156, NTONG2008483, PROST2007444, TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297, THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428, TRACH3022198

【 0 1 4 4 】

卵巣がん由来のライブラリー (TOVER) と、正常な卵巣由来のライブラリー (NOVER) のcDNAを解析して比較した結果 (表 1 7)、両者で発現変化のある遺伝子は以下の 3 クローンであった。

BRSTN2012069, NOVAR2000783, THYMU3002887

【 0 1 4 5 】

胃がん由来のライブラリー (TSTOM) と、正常な胃由来のライブラリー (STOMA) のcDNAを解析して比較した結果 (表 1 8)、両者で発現変化のある遺伝子は以下の 9 クローンであった。

BRSTN2012069, CHONS2002829, STOMA2003894, STOMA2004663, THYMU3001776, TSTOM2000235, TSTOM2001571, TSTOM2002611, TSTOM2002682

【 0 1 4 6 】

子宮がん由来のライブラリー (TUTER) と、正常な子宮由来のライブラリー (UTERU) のcDNAを解析して比較した結果 (表 1 9)、両者で発現変化のある遺伝子は以下の 1 2 8 クローンであった。

BRACE2012528, BRACE2017397, BRACE3004371, BRACE3036283, BRACE3040863, BRAMY2031516, BRAMY3005184, BRAWH2004078, BRAWH3004350, BRAWH3022651, BRAWH3024186, BRAWH3029806, BRAWH3031342, BRCAN2022126, BRHIP3001076, BRHIP3002000, BRHIP3002141, BRHIP3005307, BRHIP3007223, BRHIP3017855, BRHIP3020046, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016892, BRTHA3003736, BRTHA3011265, BRTHA3023403, BRTHA3027879, CHONS2002829, CTONG2001932, CTONG2003517, CTONG2006235, CTONG2011801, CTONG3002518, DFNES2001829, KIDNE2010049, LIVER2008465, NT2RI3005923, OCBBF3001333, OCBBF3004487, PLACE6008315, PLACE7006240, PROST2007444, SPLEN2012571, SYNNOV4000598, SYNNOV4009575, TIESE2000904, TESTI4002072, TESTI4002195, TESTI4002774, TESTI4002799, TESTI4003703, TESTI4003944, TESTI4005399, TESTI4005653, TESTI4024245, TESTI4029297, THYMU3002887, THYMU3021586, THYMU3026350, THYMU3032798, THYMU3034616, THYMU3034671, TRACH3003872, TRACH3005699, TRACH3006800, TRACH3008632, TRACH3009008, TUTER1000014, TUTER2001433, UTERU2000300, UTERU2014998, UTERU2016464, UTERU2016669, UTERU2020226, UTERU2022955, UTERU2023941, UTERU2024042, UTERU2027369, UTERU2028377, UTERU2029660, UTERU2035926, UTERU2037423, UTERU3000670, UTERU3001029, UTERU3001394, UTERU3001946, UTERU3004635, UTERU3005264, UTERU3005422, UTERU3006538, UTERU3006720, UTERU3007108, UTERU3009775, UTERU3010029, UTERU3010409, UTERU3010604, UTERU3010892, UTERU3010919, UTERU3011092, UTERU3011398, UTERU3011558, UTERU3011579, UTERU3011837, UTERU3012293, UTERU3012414, UTERU3012476, UTERU3012599, UTERU3012999, UTERU3013167, UTERU3013302, UTERU3014274, UTERU3014647, UTERU3014906, UTERU3015011, UTERU3015299, UTERU3015647, UTERU3015844, UTERU3016070, UTERU3016273, UTERU3016274, UTERU3016308, UTERU3017441, UTERU3017626, UT

ERU3017995, UTERU3018172, UTERU3018255

【 0 1 4 7 】

舌がん由来のライブラリー (CTONG) と、正常な舌由来のライブラリー (NTONG) のcDNAを解析して比較した結果 (表 2 0)、両者で発現変化のある遺伝子は以下の 6 7 クローンであった。

BRACE2012528, BRAMY4001863, BRAWH3021574, BRAWH3022651, BRAWH3024186, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3007223, BRHIP3012997, BRHIP3020046, BRSSN2013696, BRSTN2011961, BRSTN2012069, BRTHA2027229, BRTHA2033155, BRTHA3011194, BRTHA3022641, CTONG2001932, CTONG2003517, CTONG2006235, CTONG2008989, CTONG2009033, CTONG2009570, CTONG2010330, CTONG2011801, CTONG2012123, CTONG2014206, CTONG2014959, CTONG2020582, CTONG2026987, CTONG2027150, CTONG2027591, CTONG2027783, CTONG2027959, CTONG3001605, CTONG3002518, CTONG3002588, CTONG3003669, CTONG3008223, NT2RI2009233, NTONG2002278, NTONG2003805, NTONG2004829, NTONG2008483, NTONG2009468, OCBBF3004487, PLACE6008315, PLACE7004103, SKNMC2003639, SPLEN2012571, SPLEN2019092, SYN0V4009575, T1ESE2000904, TESTI2005564, TESTI2018867, TESTI4002799, TESTI4005653, TESTI4032913, THYMU3021586, THYMU3047115, TRACH3006717, TRACH3007625, TRACH3016805, TRACH3036932, TRACH3038399, UTERU2000300

これらの遺伝子は、癌に関する遺伝子である。

【 0 1 4 8 】

また、発生や分化に関連する遺伝子を調べる方法として、発生・分化途中の組織・細胞と、成体の組織細胞において遺伝子発現量の違いを調べる発現頻度解析がある。組織の発生・分化に関する遺伝子は、その組織の構築と機能発現に関する遺伝子であり、傷害のある組織を任意に再生せしめる再生医学に利用可能な有用な遺伝子である。

【 0 1 4 9 】

先に記した1,402,070個のクローンの塩基配列のデータベースを基にして得た遺伝子発現頻度情報を用いて、発生・分化途中の組織・細胞と成体の組織・細胞

とを比較して遺伝子発現頻度に変化のある遺伝子を解析した。

【 0 1 5 0 】

胎児の脳由来のライブラリー (FCBBF, FEBRAまたはOCBBF) と成体の脳由来のライブラリー (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTNまたはBRTHA) のcDNAを解析し、胎児と成体で比較した結果 (表 2 1) 、両者で発現変化のある遺伝子は以下の 9 1 6 クローンであった。

ASTR02008972, ASTR02016114, BLADE2004849, BRACE1000475, BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956, BRACE2030039, BRACE2032584, BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973, BRACE3002344, BRACE3002541, BRACE3002756, BRACE3003866, BRACE3004046, BRACE3004371, BRACE3004767, BRACE3004887, BRACE3004981, BRACE3005870, BRACE3005903, BRACE3006553, BRACE3007649, BRACE3007869, BRACE3009075, BRACE3009265, BRACE3009392, BRACE3009416, BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774, BRACE3013418, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3014714, BRACE3015090, BRACE3015898, BRACE3016020, BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810, BRACE3016862, BRACE3017253, BRACE3018083, BRACE3019570, BRACE3019611, BRACE3019817, BRACE3019941, BRACE3020356, BRACE3020669, BRACE3021430, BRACE3021517, BRACE3021805, BRACE3022051, BRACE3022303, BRACE3022312, BRACE3022340, BRACE3022847, BRACE3023604, BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024537, BRACE3024879, BRACE3025627, BRACE3025719, BRACE3026161, BRACE3026290, BRACE3026345, BRACE3026456, BRACE3026802, BRACE3026844, BRACE3026947, BRACE3027256, BRACE3027931, BRACE3028360, BRACE3

028895, BRACE3028998, BRACE3029005, BRACE3029021, BRACE3029205,
BRACE3029447, BRACE3030538, BRACE3031161, BRACE3031184, BRACE3031185, BR
ACE3031315, BRACE3031372, BRACE3031579, BRACE3031728, BRACE3031743, BRAC
E3031843, BRACE3032385, BRACE3032537, BRACE3032538, BRACE3032631, BRACE3
032980, BRACE3033525, BRACE3034183, BRACE3034389, BRACE3034964,
BRACE3034993, BRACE3035168, BRACE3036156, BRACE3036271, BRACE3036283, BR
ACE3037612, BRACE3037637, BRACE3037803, BRACE3038012, BRACE3038030, BRAC
E3038570, BRACE3038760, BRACE3039288, BRACE3039358, BRACE3039378, BRACE3
039454, BRACE3040012, BRACE3040239, BRACE3040504, BRACE3040644,
BRACE3040863, BRACE3041059, BRACE3041162, BRACE3041827, BRACE3042046, BR
ACE3042210, BRACE3042326, BRACE3042409, BRACE3042432, BRACE3042594, BRAC
E3043597, BRACE3044090, BRACE3044172, BRACE3044247, BRACE3044377, BRACE3
044495, BRACE3045078, BRACE3045145, BRACE3045424, BRACE3045708,
BRACE3045981, BRACE3046049, BRACE3046152, BRACE3046294, BRACE3046466, BR
ACE3046491, BRACE3046609, BRACE3046837, BRACE3046855, BRACE3046966, BRAC
E3047018, BRACE3047482, BRACE3047801, BRALZ2003119, BRALZ2007661, BRALZ2
008930, BRALZ2010842, BRALZ2011337, BRALZ2013621, BRALZ2013690,
BRALZ2014054, BRAMY2015516, BRAMY2021098, BRAMY2022320, BRAMY2023939, BR
AMY2025495, BRAMY2031516, BRAMY2033895, BRAMY2035801, BRAMY2036254, BRAM
Y2036266, BRAMY2037609, BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2
041384, BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537,
BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508, BRAMY3002886, BR
AMY3004126, BRAMY3004364, BRAMY3005184, BRAMY3005656, BRAMY3005912, BRAM
Y3007078, BRAMY3007449, BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3
009491, BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603,
BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234, BRAMY4001652, BR
AMY4001863, BRAMY4001913, BRAMY4002575, BRAMY4002628, BRAWH2000256, BRAW
H2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2
011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955,

BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BR

AWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2000923, BRCAN2002662, BRCAN2002892, BRCAN2003269, BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2007525, BRCAN2008701, BRCAN2009168, BRCAN2010547, BRCAN2010581, BRCAN2010665, BRCAN2015402, BRCAN2015757, BRCAN2018269, BRCAN2018667, BRCAN2019653, BRCAN2019907, BRCAN2019953, BRCAN2020234, BRCAN2020331, BRCAN2020412, BRCAN2020467, BRCAN2020880, BRCAN2021325, BRCAN2021452, BRCAN2021718, BRCAN2022126, BRCAN2025093, BRCAN2027593, BRCAN2028702, BRCOC2001355, BRCOC2002777, BRCOC2006164, BRCOC2006639, BRCOC2006942, BRCOC2009638, BRCOC2010115, BRCOC2012386, BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177, BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125, BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735, BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563, BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626, BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338, BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878, BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141, BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931, BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340, BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710, BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037, BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673, BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294, BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172, BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409, BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082, BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753, BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269, BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185, BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997, BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675, BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109, BRHIP3017146, BRHIP3017256, BRHIP

P3017558, BRHIP3017855, BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880, BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733, BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656, BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795, BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160, BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246, BRHIP3028570, BRHIP3028742, BRSSN2004303, BRSSN2004710, BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198, BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2000312, BRSTN2006466, BRSTN2006638, BRSTN2008475, BRSTN2009247, BRSTN2010089, BRSTN2010416, BRSTN2011688, BRSTN2011961, BRSTN2012069, BRSTN2016892, BRSTN2016918, BRSTN2016992, BRSTN2017104, BRSTN2017151, BRSTN2018712, BRTHA2000969, BRTHA2001304, BRTHA2001953, BRTHA2002091, BRTHA2003759, BRTHA2005448, BRTHA2006720, BRTHA2008502, BRTHA2008598, BRTHA2010672, BRTHA2012189, BRTHA2014647, BRTHA2018304, BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566, BRTHA2020642, BRTHA2020695, BRTHA2020721, BRTHA2020781, BRTHA2020910, BRTHA2021212, BRTHA2021440, BRTHA2021450, BRTHA2022074, BRTHA2022914, BRTHA2022968, BRTHA2023402, BRTHA2023437, BRTHA2024177, BRTHA2024354, BRTHA2024712, BRTHA2025869, BRTHA2026071, BRTHA2026290, BRTHA2026311, BRTHA2027227, BRTHA2027229, BRTHA2027250, BRTHA2028297, BRTHA2029969, BRTHA2030036, BRTHA2030213, BRTHA2031517, BRTHA2031917, BRTHA2032763, BRTHA2033122, BRTHA2033155, BRTHA2033320, BRTHA2033469, BRTHA2033683, BRTHA2034281, BRTHA2034576, BRTHA2035743, BRTHA2036055, BRTHA2036295, BRTHA2037247, BRTHA2038279, BRTHA2038345, BRTHA2038353, BRTHA3000456, BRTHA3002411, BRTHA3003225, BRTHA3003417, BRTHA3003736, BRTHA3005988, BRTHA3006593, BRTHA3007469, BRTHA3007662, BRTHA3009858, BRTHA3010135, BRTHA3010212, BRTHA3010469, BRTHA3010530, BRTHA3010540, BRTHA3010717, BRTHA3011187, BRTHA3011194, BRTHA3011229, BRTHA3011265, BRTHA3011306, BRTHA3011361, BRTHA3011510, BRTHA3011892, BRTHA3011998, BRTHA3012265, BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3014105, BRTHA3014507, BRTHA3

014547, BRTHA3014835, BRTHA3014854, BRTHA3014920, BRTHA3016616,
BRTHA3017791, BRTHA3018409, BRTHA3018623, BRTHA3019183, BRTHA3020369, BR
THA3020771, BRTHA3021569, BRTHA3021708, BRTHA3021786, BRTHA3021971, BRTH
A3022641, BRTHA3023403, BRTHA3023590, BRTHA3023929, BRTHA3024600, BRTHA3
025073, BRTHA3026161, BRTHA3026180, BRTHA3026556, BRTHA3026916,
BRTHA3027171, BRTHA3027318, BRTHA3027638, BRTHA3027820, BRTHA3027879, BR
THA3027957, BRTHA3028339, BRTHA3028505, CHONS2002829, CTONG2001932, CTON
G2006235, CTONG2009033, CTONG2011801, CTONG2020582, CTONG2027959, D90ST2
003106, DFNES2001829, FCBBF3001018, FCBBF3002188, FCBBF3005160,
FCBBF3012443, FCBBF3020030, FCBBF3021191, FCBBF3024911, FCBBF5000384, FE
BRA2000805, FEBRA2002260, FEBRA2012625, FEBRA2013069, FEBRA2013570, FEBR
A2017736, FEBRA2017811, FEBRA2023498, FEBRA2026582, FEBRA2026977, FEBRA2
028222, FEBRA2028457, JCMLC2000273, KIDNE2010049, KIDNE2017153,
LIVER2008465, MESAN2017133, NOVAR2000783, NT2NE2011107, NT2RI2009233, NT
2RI2010795, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2R
P8001604, NT2RP8001605, NT2RP8007920, NT2RP8009119, NTONG2008483, NTONG2
009468, OCBBF2000831, OCBBF2003518, OCBBF2004478, OCBBF2007039,
OCBBF2009536, OCBBF2014745, OCBBF2016928, OCBBF2018229, OCBBF2018618, OC
BBF2019761, OCBBF2024589, OCBBF2024779, OCBBF2025631, OCBBF2030927, OCBB
F2036019, OCBBF3000743, OCBBF3000830, OCBBF3001076, OCBBF3001202, OCBBF3
001333, OCBBF3001616, OCBBF3003745, OCBBF3004487, OCBBF3004908,
OCBBF3005330, OCBBF3005843, OCBBF3006986, OCBBF3007078, OCBBF3007704, OC
BBF3008392, OCBBF3008835, OCBBF3009244, PLACE5000492, PLACE6003004, PLAC
E6008315, PLACE6010936, PLACE7004103, PLACE7006240, PROST2007444, PROST2
017910, SMINT2009292, SMINT2012179, SPLEN2012571, SYNOV4004210,
SYNOV4009575, TIESE2000609, TIESE2000904, TBAES2007428, TESTI2005112, TE
STI2005564, TESTI2009497, TESTI2018867, TESTI2021654, TESTI2039342, TEST
I4001569, TESTI4002072, TESTI4002195, TESTI4002774, TESTI4002799, TESTI4
003602, TESTI4003703, TESTI4003944, TESTI4004210, TESTI4004695,

TESTI4005013, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4007965, TESTI4010979, TESTI4012960, TESTI4013474, TESTI4014908, TESTI4020596, TESTI4022158, TESTI4029297, TESTI4032913, TESTI4035770, TESTI4043223, TESTI4046073, THYMU3000776, THYMU3002887, THYMU3003007, THYMU3003350, THYMU3007308, THYMU3008105, THYMU3019476, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3033626, THYMU3034671, THYMU3037827, THYMU3038214, THYMU3041428, THYMU3044075, TKIDN2000319, TLIVE2007736, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3007995, TRACH3008508, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3021544, TRACH3022109, TRACH3022198, TRACH3024342, TRACH3024671, TRACH3025316, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, TSTOM2000235, UTERU2000300, UTERU2027369, UTERU3000670, UTERU3005422, UTERU3010409, UTERU3012414, UTERU3013167, UTERU3015011, UTERU3016273, UTERU3017995, UTERU3018172

【 0 1 5 1 】

胎児の心臓由来のライブラリー (FEHRT) 成体の心臓由来のライブラリー (HEART) のcDNAを解析し、胎児と成体で比較した結果 (表 2 2)、両者で発現変化のある遺伝子は以下の 1 0 クローンであった。

BRACE2012528, BRACE3004371, BRCAN2003814, BRSTN2011961, BRSTN2012069, BRSTN2016992, HEART2002531, NTONG2008483, PROST2002078, TIESE2000609

【 0 1 5 2 】

胎児の腎臓由来のライブラリー (FEKID) 成体の腎臓由来のライブラリー (KIDNE) のcDNAを解析し、胎児と成体で比較した結果 (表 2 3)、両者で発現変化のある遺伝子は以下の 2 1 クローンであった。

BRACE3004371, BRAMY2039630, BRAMY3004364, BRAWH2004078, BRHIP3002000, BRSTN2011961, BRSTN2012069, BRTHA2027229, KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RP7

007387, TESTI2005112, TESTI4002799, THYMU3001776, THYMU3029795,
THYMU3032867

【 0 1 5 3 】

胎児の肺由来のライブラリー (FELNG) 成体の肺由来のライブラリー (HLUNG) のcDNAを解析し、胎児と成体で比較した結果 (表 2 4)、両者で発現変化のある遺伝子は以下の 1 8 クローンであった。

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069, HLUNG2012600, ME
SAN2009156, NTONG2008483, PROST2007444, TESTI4003703, TESTI4005653, TEST
I4013474, TESTI4029297, THYMU3001776, THYMU3033626, THYMU3034671, THYMU3
041428, THYMU3044188, TRACH3022198

これらの遺伝子は組織・細胞の再生に関する遺伝子である

【 0 1 5 4 】

本発明のcDNAがコードしている蛋白質が、例えば、細胞の増殖・分化などの細胞状態を制御する因子である場合には、以下のようにして医薬品開発を行うことができる。ある種の細胞に、本発明によって提供される蛋白質や抗体を細胞内にマイクロインジェクションすることによって、細胞の増殖・分化などの細胞状態変化や、細胞内の特定の遺伝子の活性化または抑制を指標に低分子化合物等をスクリーニングすることができる。このスクリーニングは、例えば、以下のように行うことができる。

【 0 1 5 5 】

まず、本発明の蛋白質を発現させ組換え蛋白質の精製品を取得する。次いで、その精製蛋白質を、各種細胞株または初代培養細胞の細胞内にマイクロインジェクションして、増殖・分化などの細胞の変化を調べる。または、ある特定の細胞状態変化に作用することが知られている遺伝子の誘導をmRNA量、蛋白質量で検出する。あるいは、ある特定の細胞状態変化に影響を与えることが知られている遺伝子産物 (蛋白質) の働きにより変化した細胞内の物質 (低分子化合物など) 量で検出する。そのときに培養液等に活性をスクリーニングしたい物質 (低分子でも高分子でも可能) を添加しておくことにより、細胞状態の変化に及ぼす影響を指標にスクリーニングできる。

【0156】

マイクロインジェクションしなくとも、本発明で取得した遺伝子を導入した形質転換細胞株を用いてのスクリーニングが可能である。本発明で取得した遺伝子産物が特定の細胞状態変化に作用することが明らかになった場合には、該遺伝子産物の変化を指標にスクリーニングできる。このようなスクリーニングにより、本発明による蛋白質が細胞状態、機能を制御するのを活性化または抑制する物質が開発されれば、医薬品への応用が考えられる。

【0157】

また、本発明のcDNAがコードしている蛋白質が、例えば、分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質、疾患関連蛋白質については、それぞれの蛋白質を用いた機能の解析に基づいて、例えば以下のようにして医薬品開発を行うことができる。

【0158】

膜蛋白質の場合、細胞上に発現して受容体やリガンドとして機能する蛋白質である可能性が高い。したがって、本発明によって提供される膜蛋白質を、公知の、あるいは新規なリガンドや受容体との結合活性に基づいてスクリーニングすれば、新たなリガンド-受容体の関係を見出すことができる。スクリーニングは公知の方法に従って行うことができる。

たとえば次のようにして本発明の蛋白質に対するリガンドをスクリーニングすることができる。すなわち（a）本発明の蛋白質またはその部分ペプチド、またはそれらを発現する細胞に被検試料を接触させる工程、および（b）該蛋白質、該ペプチドまたは該細胞に結合する被検試料を選択する工程、とによって特定の蛋白質に結合するリガンドのスクリーニングが可能となる。

【0159】

一方、例えば、以下のようにして本発明の蛋白質の受容体を発現する細胞をスクリーニングすることもできる。すなわち、（a）本発明の蛋白質またはその部分ペプチドに被検細胞試料を接触させる工程、および（b）該蛋白質またはその部分ペプチドに結合する細胞を選択する工程、とによって特定の蛋白質に結合する受容体のスクリーニングが可能である。

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明の蛋白質を発現させ組換え蛋白質の精製品を取得する。次いで、その精製蛋白質を標識し、各種細胞株または初代培養細胞に対して結合アッセイを行い、これにより受容体を発現している細胞を選定する（本庶・新井・谷口・村松編 新生化学実験講座 7 増殖分化因子とその受容体 p203-236（1991）東京化学同人）。標識としては、 ^{125}I などのRI標識のほか、酵素（アルカリホスファターゼ等）標識も可能である。

また、本発明の蛋白質を標識せずに用いて、本発明の蛋白質と受容体を発現している細胞とを結合させた後に、本発明の蛋白質に対する抗体を標識して用いて検出することも考えられる。上記スクリーニングにより得られた本発明の蛋白質の受容体を発現する細胞は、後述するように該受容体のアゴニストやアンタゴニストのスクリーニングに用いることが可能である。

【0160】

上記のスクリーニングにより、本発明の蛋白質が結合するリガンドや、本発明の蛋白質の受容体やその受容体を発現する細胞が得られれば、それらリガンドや受容体と結合する化合物のスクリーニングが可能となる。またそれらの結合活性を指標に、両者の結合を阻害する化合物（例えば、受容体アゴニストやアンタゴニスト）のスクリーニングが可能となる。

このスクリーニング方法は、本発明の蛋白質が受容体である場合は、（a）被検試料の存在下で、本発明の蛋白質または本発明の蛋白質を発現する細胞とリガンドとを接触させる工程、（b）該蛋白質または該蛋白質を発現する細胞とリガンドとの結合活性を検出する工程、および（c）被検試料非存在下において検出した場合と比較して該結合活性を低下させる化合物を選択する工程、を含む。また本発明の蛋白質がリガンドである場合には、（a）被検試料の存在下で、本発明の蛋白質を該蛋白質の受容体または該受容体を発現する細胞に接触させる工程、（b）該蛋白質とその受容体または該受容体を発現する細胞との結合活性を検出する工程、および（c）被検試料非存在下において検出した場合と比較して、該結合活性を低下させる化合物を選択する工程、を含む。

スクリーニングに用いる被検試料としては、例えば、細胞抽出液、遺伝子ライ

ブラリーの発現産物、合成低分子化合物、合成ペプチド、天然化合物などが挙げられるが、これらに制限されない。また、本発明の蛋白質との結合活性を指標とした上記のスクリーニングにより単離された化合物を被検試料として用いることも可能である。

【0161】

このスクリーニングにより単離される化合物は、本発明の蛋白質自体または本発明の蛋白質に対する受容体のアゴニストやアンタゴニストの候補となる。本発明の受容体とリガンドとの結合活性の低下によるリン酸化などの細胞内シグナルの変化をもとに、得られた化合物が本発明の蛋白質の受容体のアゴニストであるかアンタゴニストであるかを判定することができる。また、スクリーニングによって得られる化合物は、生体内において、本発明の蛋白質と相互作用する分子（受容体も含む）との該相互作用を阻害する化合物の候補ともなる。本発明の蛋白質、または本発明の蛋白質に結合する受容体、またはリガンド、更にはこれらの化合物は、本発明の蛋白質が関連する疾患の予防薬や治療薬への応用、または本発明の蛋白質が関連する疾患の検査薬への応用などが考えられる。

【0162】

分泌蛋白質の場合、細胞の増殖・分化などの細胞状態を制御する因子の可能性はある。新たな細胞状態を制御する因子は、ある種の細胞に、本発明によって提供される分泌蛋白質を加えることによって、細胞の増殖・分化などの細胞の状態変化や、細胞内の特定の遺伝子の活性化を指標にスクリーニングすることにより見出すことができる。

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明の蛋白質を発現させ組換え蛋白質の精製品を取得する。次いで、その精製蛋白質を、各種細胞株または初代培養細胞に添加して、増殖・分化などの細胞の変化を調べる。または、ある特定の細胞状態の変化に影響を与えることが知られている遺伝子の誘導をmRNA量、蛋白質量で検出する。あるいはある特定の細胞状態変化に影響を与えることが知られている遺伝子産物（蛋白質）の働きにより変化した細胞内の物質（低分子化合物など）量で検出する。

【0163】

このようなスクリーニングにより、本発明による蛋白質が細胞状態、機能を制御するとなれば、本発明の蛋白質は、関連した疾患に対して、そのまま、あるいは一部適した状態に改変して、医薬品や検査薬への応用が考えられる。

また、先に膜タンパクについて記述したように、本発明によって提供される分泌蛋白質を用いて、公知の、あるいは新規なリガンドや受容体との結合活性に基づいてスクリーニングすれば、新たなリガンド-受容体の関係を見出すことができ、同様の方法でアゴニスト、アンタゴニストの判定が可能となる。こうして得られる化合物は、生体内において、本発明の蛋白質と相互作用する分子(受容体も含む)との該相互作用を阻害する化合物の候補ともなる。これら化合物は、本発明の蛋白質が関連する疾患の予防薬や治療薬、あるいは検査薬への応用が考えられる。

【0164】

シグナル伝達関連蛋白質、転写関連蛋白質の場合は、細胞内外の刺激に反応して、ある蛋白質や遺伝子に作用する因子の可能性がある。新たな蛋白質、遺伝子に作用する因子は、ある種の細胞に、本発明によって提供される蛋白質を発現させることによって、細胞内の特定の遺伝子や蛋白質の活性化を指標にスクリーニングすることにより見出すことができる。

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明の蛋白質を発現した形質転換細胞株を取得する。次いで、その形質転換細胞株と、もとの未形質転換細胞株とにおいて、ある特定の遺伝子の変化をmRNA量、蛋白質量で検出する。あるいは、ある特定の遺伝子産物(蛋白質)の働きにより変化した細胞内の物質(低分子化合物など)量で検出する。さらには、ある特定の遺伝子の発現調節領域とマーカー遺伝子(ルシフェラーゼ、 β -ガラクトシダーゼ等)の融合遺伝子を導入した細胞に、本発明によって提供される蛋白質を同時に発現させることによって、特定の遺伝子の発現の変化を、マーカー遺伝子産物(蛋白質)由来の活性で判定する。

【0165】

このようなスクリーニングにより、影響を受けた蛋白質や遺伝子が疾患に関連していた場合、本発明による蛋白質を利用し、直接的に、または、間接的に、そ

の発現や活性調節を行う化合物や遺伝子のスクリーニングが可能となる。

例えば、まず、本発明の蛋白質を発現させ組換え蛋白質の精製品を取得する。次に影響を受けた蛋白質や遺伝子を精製し、その結合を調べる。または、予め阻害剤の候補となる化合物を加えておいた後、それら結合の変化を調べる。あるいは、例えば他遺伝子の発現調節を行う本発明の蛋白質をコードする遺伝子の5'上流転写調節領域を取得し、マーカー遺伝子と融合した遺伝子を導入した細胞に、化合物などを添加して、当該遺伝子の発現を制御する因子を見いだす。

【0166】

このようなスクリーニングによって得られた化合物は、本発明による蛋白質が関連した疾患に対して医薬品への応用が考えられる。スクリーニングによって得られた制御因子が蛋白質であっても、同様に、その蛋白質の発現・活性に本来ない影響を与える化合物があれば、その化合物は、本発明による蛋白質が関連した疾患に対して医薬品への応用が考えられる。

分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質、疾患関連蛋白質のいずれの場合でも、本発明による蛋白質が酵素としての活性を有するとなれば、本発明によって提供される蛋白質に化合物を適当な条件下で添加し、化合物の変化を指標にスクリーニングすれば可能である。また、この活性を指標に本発明による蛋白質の活性を阻害する化合物のスクリーニングも可能である。

【0167】

このスクリーニングは、例えば、以下のように行うことが可能である。まず、本発明の蛋白質を発現させ組換え蛋白質の精製品を取得する。次いで、その精製蛋白質に、化合物を添加して、化合物量および反応生成物量を調べる。または、予め阻害剤の候補となる化合物を加えておいた後、精製蛋白質と反応する化合物(基質)を加えて、その基質量および反応生成物量の変化を調べる。

このようなスクリーニングにより、得られた化合物は、本発明の蛋白質が関連した疾患に対して、医薬品への応用が考えられる。また本発明の蛋白質が生体において正常に機能しているかどうかを調べるなどの検査への応用が考えられる。

【0168】

本発明の分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質が、新たな疾患関連蛋白質であるかは、上記に挙げた以外に、本発明による蛋白質を発現して得られた特異認識抗体を用いて、特定の疾患と蛋白質の発現量や活性との相関を知ることができる。あるいは、「Method in Molecular Biology」(Humana Press社)シリーズの『Molecular Diagnosis of Genetic Diseases』(Rob Elles編、1996)を参考に解析が可能である。

疾患関連蛋白質は、前述のようなスクリーニングの対象となり、その発現・活性を制御する薬剤の開発に有用である。また、関連した疾患の診断マーカー、あるいは遺伝子治療のターゲットになるなど医療産業上、有用である。

【0169】

以上により単離された化合物を医薬品として用いる場合には、単離された化合物自体を直接患者に投与する以外に、公知の製剤学的方法により製剤化して投与を行うことも可能である。例えば、薬理学上許容される担体もしくは媒体、具体的には、滅菌水や生理食塩水、植物油、乳化剤、懸濁剤などと適宜組み合わせて製剤化して投与することが考えられる。患者への投与は、例えば、動脈内注射、静脈内注射、皮下注射など当業者に公知の方法により行いうる。投与量は、患者の体重や年齢、投与方法などにより変動するが、当業者であれば適当な投与量を適宜選択することが可能である。また、該化合物がDNAによりコードされうるものであれば、該DNAを遺伝子治療用ベクターに組み込み、遺伝子治療を行うことも考えられる。投与量、投与方法は、患者の体重や年齢、症状などにより変動するが、当業者であれば適宜選択することが可能である。

【0170】

更に本発明は、表1に記載された塩基配列および／またはアミノ酸配列から選択された少なくとも1つを含む全長cDNAおよび／または蛋白質データベースに関する。データベースとは、塩基配列情報を検索可能な機械可読式の情報として蓄積した情報の集合を意味する。本発明のデータベースは、本発明によって提供されるcDNAの塩基配列の少なくとも一つを含む。本発明のデータベースは、本発明によって提供されるcDNAのみから構成されていても良いし、公知の全長cDNAやEST等の塩基配列情報をも含むものであることができる。本発明のデータベースに

は、塩基配列情報のみならず、本発明によって明らかにされた遺伝子の機能情報や、その全長cDNAを保持したクローンの名称などの付随した情報を合わせて記録したり、あるいはリンクさせておくことができる。

【0171】

本発明のデータベースは、遺伝子断片の情報に基づく、遺伝子全長の取得に有用である。本発明に基づくデータベースは、いずれも全長cDNAの塩基配列情報からなっている。したがって、ディファレンシャルディスプレイ法や、サブトラクション法によって得られた遺伝子断片の塩基配列を、このデータベースの情報に照合すれば、断片の塩基配列に基づいて遺伝子の全長塩基配列を明らかにすることができる。

しかも本発明のデータベースを構成する全長cDNAの配列情報は、全長であることのみならず、遺伝子の発現頻度情報や、公知の遺伝子や蛋白質との相同性検索結果を伴っていることから、遺伝子断片の機能解析を飛躍的に迅速化する。更に本発明のデータベースは、ヒトの遺伝子に関する情報を蓄積しているものであることから、他の種から単離された遺伝子の塩基配列情報に基づくヒトのホモログの単離に有用である。

【0172】

現在では、ディファレンシャルディスプレイ法や、サブトラクション法によって、さまざまな遺伝子断片情報を得ることができる。一般にこれらの遺伝子断片は、その全長を取得するためのツールとして用いられる。遺伝子断片が公知の遺伝子のものであれば、公知のデータベースとの照合によって、その全長を明らかにすることは容易である。しかし、公知の遺伝子データベースに一致する塩基配列を見出せない場合には、全長cDNAのクローニングを行わなければならない。これらの断片情報に基づいて全長塩基配列を取得する工程は、しばしば困難を伴う。遺伝子の全長を取得しない限り、その遺伝子がコードする蛋白質のアミノ酸配列は明らかにできない。したがって、本発明のデータベースは、公知の遺伝子のデータベースでは解明することのできない、遺伝子断片に対応する全長cDNAの特定に貢献する。

なお本明細書において引用された全ての先行技術文献は、参照として本明細書

に組み入れられる。

【 0 1 7 3 】

【実施例】

実施例 1. オリゴキャップ法による cDNA ライブラリーの作製

(1) mRNA 抽出と購入

ヒト組織（下記に示す）より、文献（J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989）記載の方法により全 RNA として mRNA を抽出した。また、ヒト培養細胞やヒト初代培養細胞（下記に示す）をカタログ記載の方法で培養後、文献（J. Sambrook, E. F. Fritsch & T. Maniatis, Molecular Cloning Second edition, Cold Spring harbor Laboratory Press, 1989）記載の方法により全 RNA として mRNA を抽出した。

【 0 1 7 4 】

以下にライブラリー名とその由来の関係を、「ライブラリー名：由来」の順に示した。サブトラクションしたものについては、サブトラクトライブラリーの作り方も示した。

<ヒト組織より mRNA 抽出>

NTONG：正常舌 (Tongue)；

CTONG：舌癌 (Tongue, Cancer)；

FCBBF：胎児脳 (Brain, Fetal)；

OCBBF：胎児脳 (Brain, Fetal)；

PLACE：胎盤 (Placenta)；

SYNOV：滑膜組織 (Synovial membrane tissue from rheumatoid arthritis)；

CORDB：臍帯血 (Cord blood)。

【 0 1 7 5 】

<培養細胞より mRNA 抽出>

BNGH4：H4 細胞 (ATCC #HTB-148)；

IMR32：IMR32 細胞 (ATCC #CCL-127)；

SKNMC：SK-N-MC 細胞 (ATCC #HTB-10)；

3NB69：NB69細胞(RCB #RCB0480)；
BGGI1：GI1細胞(RCB #RCB0763)；
NB9N4：NB9細胞(RCB #RCB0477)；
SKNSH：SK-N-SH細胞(RCB #RCB0426)；
AHMSC：HMSC細胞((間葉細胞, Human mesenchymal cell)；
CHONS：軟骨細胞(Chondrocyte)；
ERLTF：TF-1細胞((赤白血病細胞, erythroleukemia)；
HELAC：HeLa細胞；
JCMLC：白血病患者細胞(Leukemia, myelogenous)；
MESTC：間葉系幹細胞((Mesenchyme stem cell)；
NIESE：間葉系幹細胞(Mesenchymal stem cell)；
NCRRM：胎生期癌細胞(Embryonal carcinoma)；
NCRRP：胎生期癌細胞(Embryonal carcinoma)をレチノイン酸(RA)処理誘導；
T1ESE：間葉系幹細胞(Mesenchymal stem cell) をトリコスタチンと5アザシチジン処理誘導；
NT2RM：NT2細胞(STARATAGENE #204101)；
NT2RP：NT2細胞をレチノイン酸(RA)処理誘導5週間；
NT2RI：NT2細胞をRA処理誘導5週間後、生育阻害剤処理2週間；
NT2NE：NT2細胞をRA処理と生育阻害剤処理により神経分化後、神経を濃縮回収(NT2 Neuron)；
NTISM：NT2細胞(STARATAGENE #204101)をRA処理誘導5週間後、生育阻害剤処理を2週間したmRNAから作製したcDNAライブラリーから、未分化NT2細胞のmRNAと重複するcDNAをSubtract Kit (Invitrogen #K4320-01)を用いてサブトラクトしたライブラリー(NT2RI-NT2RM)。

RCBは、理化学研究所ジーンバンク・細胞開発銀行より分譲をうけたものであり、ATCCは、American Type Culture Collectionより分譲をうけたものである。

【 0 1 7 6 】

<初代培養細胞よりmRNA抽出>

ASTRO：正常神経膠星状細胞(Normal Human Astrocyte) NHA5732, 宝酒造 #CC256

5 ;

DFNES : 新生児正常皮膚繊維芽細胞 (Normal Human Dermal Fibroblasts (Neonatal Skin); NHDF-Neo) NHDF2564, 宝酒造 #CC2509 ;

MESAN : 正常メサングウム細胞 (Normal human mesangial cells) NHMC56046-2, 宝酒造 #CC2559 ;

NHNPC : 正常神経前駆細胞 (Normal human neural progenitor cells) NHNP5958, 宝酒造 #CC2599 ;

PEBLM : 正常末梢血単核細胞 (Human peripheral blood mononuclear cells) HPBM C5939, 宝酒造 #CC2702 ;

HSYRA : 滑膜細胞HS-RA (Human synoviocytes from rheumatoid arthritis), 東洋紡 #T404K-05 ;

PUAEN : 正常肺動脈内皮細胞 (Human pulmonary artery endothelial cells), 東洋紡 #T302K-05 ;

UMVEN : 正常臍帯静脈内皮細胞 (Human umbilical vein endothelial cells) HUVEC, 東洋紡 #T200K-05 ;

HCASM : 正常冠動脈平滑筋細胞HCASM (Human coronary artery smooth muscle cells), 東洋紡 #T305K-05 ;

HCHON : 正常軟骨細胞HC (Human Chondrocytes), 東洋紡 #T402K-05 ;

HHDPC : 正常頭髮毛乳頭細胞HDPC (Human dermal papilla cells), 東洋紡 #THPCK-001 ;

CD34C : CD34+細胞 (AllCells, LLC #CB14435M) ;

D30ST : CD34+細胞を破骨細胞分化因子 (ODF) 処理誘導3日間 ;

D60ST : CD34+細胞をODF処理誘導6日間 ;

D90ST : CD34+細胞をODF処理誘導9日間 ;

ACTVT : 活性化T細胞 (Activated T-cell) ;

LYMPB : リンパ芽球 (Lymphoblast, EB virus transferred B cell) ;

NETRP : 好中球 (Neutrophil)。

【 0 1 7 7 】

次いで、以下に示すヒト組織より全RNAとして抽出されたmRNAを購入した。以

下にライブラリー名とその由来の関係を、「ライブラリー名：由来」の順に示した。サブトラクションしたものについては、サブトラクトライブラリーの作り方も示した。

<ヒト組織よりのmRNAを全RNAで購入>

ADRGL：副腎(Adrenal gland), CLONTECH #64016-1 ;
BRACE：小脳(Brain, cerebellum), CLONTECH #64035-1 ;
BRAWH：全脳(Brain, whole), CLONTECH #64020-1 ;
FEBRA：胎児脳(Brain, Fetal), CLONTECH #64019-1 ;
FELIV：胎児肝臓(Liver, Fetal), CLONTECH #64018-1 ;
HEART：心臓(Heart), CLONTECH #64025-1 ;
HLUNG：肺(Lung), CLONTECH #64023-1 ;
KIDNE：腎臓(Kidney), CLONTECH #64030-1 ;
LIVER：肝臓(Liver), CLONTECH #64022-1 ;
MAMGL：乳腺(Mammary Gland), CLONTECH #64037-1 ;
PANCR：膵臓(Pancreas), CLONTECH #64031-1 ;
PROST：前立腺(Prostate), CLONTECH #64038-1 ;
SALGL：唾液腺(Salivary Gland), CLONTECH #64026-1 ;
SKMUS：骨格筋(Skeletal Muscle), CLONTECH #64033-1 ;
SMINT：小腸(Small Intestine), CLONTECH #64039-1 ;
SPLEN：脾臓(Spleen), CLONTECH #64034-1 ;
STOMA：胃(Stomach), CLONTECH #64090-1 ;
TBAES：乳癌(Breast, Tumor), CLONTECH #64015-1 ;
TCERX：子宮頸管癌(Cervix, Tumor), CLONTECH #64010-1 ;
TCOLN：結腸癌(Colon, Tumor), CLONTECH #64014-1 ;
TESTI：精巣(Testis), CLONTECH #64027-1 ;
THYMU：胸腺(Thymus), CLONTECH #64028-1 ;
TLUNG：肺癌(Lung, Tumor), CLONTECH #64013-1 ;
TOVAR：卵巣癌(Ovary, Tumor), CLONTECH #64011-1 ;
TRACH：気管(Trachea), CLONTECH #64091-1 ;

TUTER：子宮癌(Uterus, Tumor), CLONTECH #64008-1；
UTERU：子宮(Uterus), CLONTECH #64029-1；
ADIPS：脂肪組織(Adipose), Invitrogen #D6005-01；
BLADE：膀胱(Bladder), Invitrogen #D6020-01；
BRALZ：アルツハイマー患者大脳皮質(Brain, cortex, Alzheimer), Invitrogen #D6830-01；
CERVX：子宮頸管(Cervix), Invitrogen #D6047-01；
COLON：結腸(Colon), Invitrogen #D6050-0；
NESOP：食道(Esophagus), Invitrogen #D6060-01；
PERIC：心膜(Pericardium), Invitrogen #D6105-01；
RECTM：直腸(Rectum), Invitrogen #D6110-01；
TESOP：食道癌(Esophageal, Tumor), Invitrogen #D6860-01；
TKIDN：腎臓癌(Kidney, Tumor), Invitrogen #D6870-01；
TLIVE：肝臓癌(Liver, Tumor), Invitrogen #D6880-01；
TSTOM：胃癌(Stomach, Tumor), Invitrogen #D6920-01；
BEAST：成人乳房(Adult Breast), STARATAGENE #735044；
FEHRT：胎児心臓(Heart, Fetal), STARATAGENE #738012；
FEKID：胎児腎臓(Kidney, Fetal), STARATAGENE #738014；
FELNG：胎児肺(Lung, Fetal), STARATAGENE #738020；
NOVAR：成人卵巣(Adult Ovary), STARATAGENE #735260；
BRASW：アルツハイマー患者大脳皮質組織 [BRALZ：アルツハイマー患者大脳皮質 (Brain, cortex, Alzheimer), Invitrogen #D6830-01] のmRNAから作製したcDNA ライブラリーから、全脳組織 [BRAWH：全脳(Brain, whole), CLONTECH #64020-1] のmRNAと重複するcDNAをSubtract Kit (Invitrogen #K4320-01)を用いてサブトラクトしたライブラリー (BRALZ-BRAWH)。

【 0 1 7 8 】

さらに、次に示すヒト組織よりポリA(+) RNAとして抽出・精製されたmRNAを購入した。各組織由来のポリA(+) RNAに、ポリA(-)RNAを混ぜたRNAからcDNAライブラリーを作製した。ポリA(-)RNAは、全脳(Brain, whole), CLONTECH #64020-1の

全RNAからポリA(+)RNAをオリゴdTセルロースで除くことにより調製した。以下にライブラリー名とその由来の関係を、「ライブラリー名：由来」の順に示した。

<ヒト組織よりのmRNAをポリA(+) RNAで購入>

BRAMY：扁桃(Brain, amygdala), CLONTECH #6574-1；

BRCAN：尾状核(Brain, caudate nucleus), CLONTECH #6575-1；

BRCOC：脳梁(Brain, corpus callosum), CLONTECH #6577-1；

BRHIP：海馬(Brain, hippocampus), CLONTECH #6578-1；

BRSSN：黒質(Brain, substantia nigra), CLONTECH #6580-1；

BRSTN：視床下核(Brain, subthalamic nucleus), CLONTECH #6581-1；

BRTHA：視床(Brain, thalamus), CLONTECH #6582-1。

【 0 1 7 9 】

(2) cDNAライブラリーの作製

それぞれのRNAよりオリゴキャップ法[M. Maruyama and S. Sugano, Gene, 138 : 171-174 (1994)]を改良した方法(WO 01/04286)によりcDNAライブラリーを作製した。Oligo-cap linker (agcaucgagu cgcccuuguu ggccuacugg/配列番号：3 9 1 3) およびOligo dT primer (gcggtgaag acggcctatg tggccttttt tttttttttt tt/配列番号：3 9 1 4) を用いて、WO 01/04286に記載したようにBAP (Bacterial Alkaline Phosphatase) 処理、TAP (Tobacco Acid Pyrophosphatase) 処理、RNAライゲーション、第一鎖cDNAの合成とRNAの除去を行った。次いで、5' (ag catcgagt cggccttggt g/配列番号：3 9 1 5) と3' (gcggtgaag acggcctatg t/配列番号：3 9 1 6) のPCRプライマーを用いPCR (polymerase chain reaction) により2本鎖cDNAに変換し、SfiIで切断した。次いで、通常は2kb以上（場合によっては3kb以上）に分画したcDNA断片をDraIIIで切断したベクターpME18SFL3 (図 1) (GenBank AB009864, Expression vector) にcDNAの方向性を決めてクローニングし、cDNAライブラリーを作製した。

【 0 1 8 0 】

全長cDNA配列解析に用いたcDNAライブラリー名とその由来の関係を以下に示した。『』内にライブラリー名を、その後の()内にライブラリーソースのタイプと由来などを/で区切って記載した。

- 『3NB69』 (培養細胞／NB69細胞 (RCB #RCB0480))
- 『ADIPS』 (組織／脂肪組織 (Adipose) (Invitrogen #D6005-01))
- 『ADRGL』 (組織／副腎 (Adrenal gland) (CLONTECH #64016-1))
- 『AHMSC』 (培養細胞／HMSC細胞 (間葉細胞； Human mesenchymal cell))
- 『ASTRO』 (初代培養細胞／正常神経膠星状細胞 (Normal Human Astrocyte) NHA5
732 (宝酒造 #CC2565))
- 『BEAST』 (組織／成人乳房 (Adult Breast) (STARATAGENE #735044))
- 『BLADE』 (組織／膀胱 (Bladder) (Invitrogen #D6020-01))
- 『BRACE』 (組織／小脳 (Brain, cerebellum) (CLONTECH #64035-1))
- 『BRALZ』 (組織／アルツハイマー患者大脳皮質 (Brain, cortex, Alzheimer)
(Invitrogen #D6830-01))
- 『BRAMY』 (組織／扁桃 (Brain, amygdala) (CLONTECH #6574-1))
- 『BRAWH』 (組織／全脳 (Brain, whole) (CLONTECH #64020-1))
- 『BRCAN』 (組織／尾状核 (Brain, caudate nucleus) (CLONTECH #6575-1))
- 『BRCOC』 (組織／脳梁 (Brain, corpus callosum) (CLONTECH #6577-1))
- 『BRHIP』 (組織／海馬 (Brain, hippocampus) (CLONTECH #6578-1))
- 『BRSSN』 (組織／黒質 (Brain, substantia nigra) (CLONTECH #6580-1))
- 『BRSTN』 (組織／視床下核 (Brain, subthalamic nucleus) (CLONTECH #6581-
1))
- 『BRTHA』 (組織／視床 (Brain, thalamus) (CLONTECH #6582-1))
- 『CERVX』 (組織／子宮頸管 (Cervix) (Invitrogen #D6047-01))
- 『CHONS』 (培養細胞／軟骨細胞 (Chondrocyte))
- 『COLON』 (組織／結腸 (Colon) (Invitrogen #D6050-0))
- 『CTONG』 (組織／舌癌 (Tongue, Cancer))
- 『D90ST』 (初代培養細胞／CD34+細胞 (ODF誘導9日))
- 『DFNES』 (初代培養細胞／新生児正常皮膚繊維芽細胞 (Normal Human Dermal F
ibroblasts (Neonatal Skin); NHDF-Neo) NHDF2564 (宝酒造 #CC2509))
- 『ERLTF』 (培養細胞／TF-1細胞 (赤白血病細胞； erythroleukemia))
- 『FCBBF』 (組織／胎児脳 (Brain, Fetal))

- 『FEBRA』 (組織／胎児脳(Brain, Fetal) (CLONTECH #64019-1))
- 『FEHRT』 (組織／胎児心臓 (Heart, Fetal) (STARATAGENE #738012))
- 『FEKID』 (組織／胎児腎臓 (Kidney; Fetal))
- 『FELNG』 (組織／胎児肺 (Lung, Fetal) (STARATAGENE #738020))
- 『HCASM』 (初代培養細胞／正常冠動脈平滑筋細胞HCASMC(Human coronary artery smooth muscle cells) (東洋紡 #T305K-05))
- 『HCHON』 (初代培養細胞／正常軟骨細胞HC(Human Chondrocytes) (東洋紡 #T402K-05))
- 『HEART』 (組織／心臓 (Heart) (CLONTECH #64025-1))
- 『HHDPC』 (初代培養細胞／正常頭髮毛乳頭細胞HDPC(Human dermal papilla cells) (東洋紡 #THPCK-001))
- 『HLUNG』 (組織／肺 (Lung) (CLONTECH #64023-1))
- 『HSYRA』 (初代培養細胞／滑膜細胞HS-RA(Human synoviocytes from rheumatoid arthritis)(東洋紡 #T404K-05))
- 『JCMLC』 (培養細胞／白血病細胞 (Leukemia, myelogenous))
- 『KIDNE』 (組織／腎臓 (Kidney) (CLONTECH #64030-1))
- 『LIVER』 (組織／肝臓 (Liver) (CLONTECH #64022-1))
- 『LYMPB』 (初代培養細胞／リンパ芽球(Lymphoblast, EB virus transferred B cell))
- 『MESAN』 (初代培養細胞／正常メサングウム細胞(Normal human mesangial cells) NHMC56046-2 (宝酒造 #CC2559))
- 『MESTC』 (培養細胞／間葉系幹細胞 (Mesenchyme stem cell))
- 『N1ESE』 (培養細胞／間葉系幹細胞(Mesenchymal stem cell))
- 『NETRP』 (初代培養細胞／好中球 (Neutrophil))
- 『NOVAR』 (組織／成人卵巣 (Adult Ovary) (STARATAGENE #735260))
- 『NT2NE』 (培養細胞／NT2細胞 神経分化後濃縮回収 (NT2 Neuron))
- 『NT2RI』 (培養細胞／NT2細胞 RA誘導5週間後生育阻害剤処理2週間)
- 『NT2RP』 (培養細胞／NT2細胞 RA誘導5週間)
- 『NTONG』 (組織／正常舌 (Tongue))

- 『OCBBF』 (組織／胎児脳 (Brain, Fetal))
- 『PEBLM』 (初代培養細胞／正常末梢血単核細胞 (Human peripheral blood mononuclear cells) HPBMC5939 (宝酒造 #CC2702))
- 『PERIC』 (組織／心膜 (Pericardium) (Invitrogen #D6105-01))
- 『PLACE』 (組織／胎盤 (Placenta))
- 『PROST』 (組織／前立腺 (Prostate) (CLONTECH #64038-1))
- 『PUAEN』 (初代培養細胞／正常肺動脈内皮細胞 (Human pulmonary artery endothelial cells) (東洋紡 #T302K-05))
- 『RECTM』 (組織／直腸 (Rectum) (Invitrogen #D6110-01))
- 『SKMUS』 (組織／骨格筋 (Skeletal Muscle) (CLONTECH #64033-1))
- 『SKNMC』 (培養細胞／SK-N-MC細胞 (ATCC #HTB-10))
- 『SKNSH』 (培養細胞／SK-N-SH細胞 (RCB #RCB0426))
- 『SMINT』 (組織／小腸 (Small Intestine) (CLONTECH #64039-1))
- 『SPLEN』 (組織／脾臓 (Spleen) (CLONTECH #64034-1))
- 『STOMA』 (組織／胃 (Stomach) (CLONTECH #64090-1))
- 『SYNOV』 (組織／滑膜組織 (Synovial membrane tissue from rheumatoid arthritis))
- 『TIESE』 (培養細胞／間葉系幹細胞 (Mesenchymal stem cell) (トリコスタチンと 5 アザシチジン処理))
- 『TBAES』 (組織／乳癌 (Breast, Tumor) (CLONTECH #64015-1))
- 『TESOP』 (組織／食道癌 (Esophageal, Tumor) (Invitrogen #D6860-01))
- 『TESTI』 (組織／精巣 (Testis) (CLONTECH #64027-1))
- 『THYMU』 (組織／胸腺 (Thymus) (CLONTECH #64028-1))
- 『TKIDN』 (組織／腎臓癌 (Kidney, Tumor) (Invitrogen #D6870-01))
- 『TLIVE』 (組織／肝臓癌 (Liver, Tumor) (Invitrogen #D6880-01))
- 『TLUNG』 (組織／肺癌 (Lung; Tumor))
- 『TRACH』 (組織／気管 (Trachea) (CLONTECH #64091-1))
- 『TSTOM』 (組織／胃癌 (Stomach, Tumor) (Invitrogen #D6920-01))
- 『TUTER』 (組織／子宮癌 (Uterus, Tumor) (CLONTECH #64008-1))

『UTERU』（組織／子宮（Uterus）（CLONTECH #64029-1））

【 0 1 8 1 】

オリゴキャップ法を改良した方法で作製した高全長率cDNAライブラリー（既知 mRNA のタンパク質コード領域を指標にして算出した各cDNAライブラリーの5' 端の全長率は平均 9 0 %）は、真核細胞での発現が可能な発現ベクターpME18SFL3を用いて作製した。pME18SFL3にはクローニング部位の上流にSR α プロモーターとSV40 small tイントロンが組み込まれており、またその下流にはSV40ポリA 付加シグナル配列が挿入されている。pME18SFL3のクローン化部位は非対称性のDraII I サイトとなっており、cDNA断片の末端にはこれと相補的なSfiI部位を付加しているため、クローン化したcDNA断片はSR α プロモーターの下流に一方向性に挿入される。したがって、全長cDNAを含むクローンでは、得られたプラスミドをそのままCOS細胞などに導入することにより、一過的に遺伝子を発現させることが可能である。すなわち、非常に容易に、遺伝子産物である蛋白質として、あるいはそれらの生物学的活性として実験的に解析することが可能となっている。

【 0 1 8 2 】

（3）オリゴキャップ法で作製したcDNAライブラリーからのクローンの5'-末端の全長性の評価

これらより得たクローンのプラスミドDNAについて、cDNAの5' 端（一部のクローンについては3' 端も）の塩基配列をDNAシーケンシング試薬（BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems社製）を用い、マニュアルに従ってシーケンシング反応後、DNAシーケンサー（ABI PRISM 3700, PE Biosystems社製）でDNA塩基配列を解析した。得られたデータをデータベース化した。

【 0 1 8 3 】

オリゴキャップ法を改良した方法で作製したヒトcDNAライブラリーの約111万クローンの5'-末端の全長率を次の方法で求めた。公共データベース中のヒト既知mRNAと5'-末端配列が一致する全クローンについて、公共データベース中の既知mRNA配列より長く5'-末端が伸びている場合、または5'-末端は短いが翻訳開始コドンは有している場合を「全長」と判断し、翻訳開始コドンを含んでいない場

合を「非全長」と判断した。これをもとに5'-末端の全長率〔全長クローン数／（全長クローン数＋非全長クローン数）〕を計算した。この結果、5'-末端の全長率は、90%であった。この結果より、オリゴキャップ法で取得したヒトcDNAライブラリーからのクローンの5'-端配列の全長率が非常に高いことが分かった。

【0 1 8 4】

実施例 2. cDNAクローン末端配列解析と全長塩基配列解析クローンの選択

各cDNAライブラリーより得たクローンのプラスミドDNAについて、cDNAの5'末端の塩基配列をDNAシーケンシング試薬（Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction KitまたはBigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems社製）を用い、マニュアルに従ってシーケンシング反応後、DNAシーケンサー（ABI PRISM 3700, PE Biosystems社製）で解析した。得られたデータについてはデータベース化を行った。

【0 1 8 5】

解析されたcDNAクローンの5'末端配列については、GenBank、UniGeneのcomplete cdsの表記があるデータを対象にしたBLASTによる相同性検索を行い、ヒトのmRNA配列に同一なものは除いた。次にクラスタリングを行い、相同性90%以上かつコンセンサス配列が50塩基対以上の場合、同一グループと見なし、グループを形成させた。グループ内の、より5'-側に長いクローンを選択し、選択されたクローンについては必要に応じ3'末端配列を5'末端配列と同様の方法で解析取得した。取得された末端配列のデータを解析し、5'末端と3'末端の配列でコンティグを作るクローンは除いた。更に再度前記と同様にBLASTによる相同性検索によりヒトのmRNA配列（特許化または特許出願された配列を含む）に同一なものは除いた。こうして選択したクローンより全長塩基配列解析を行うクローンを得た。

【0 1 8 6】

実施例 3. 全長塩基配列解析

全長塩基配列解析に選抜されたクローンについて各々全長cDNAの塩基配列を決定した。塩基配列は、主にカスタム合成DNAプライマーを用いたダイデオキシターミネーター法によるプライマーウォーキング法によって決定した。すなわち、

カスタム合成DNAプライマーを用い、PE Biosystem社製のDNAシーケンシング試薬でマニュアルに従ってシーケンシング反応後、同社製のシーケンサーを用いてDNA塩基配列を解析した。一部のクローンについては、Licor社製DNAシーケンサーも利用した。

また、一部のクローンについてはカスタムプライマーを用いずcDNA が含まれるプラスミドをランダムに切断するショットガン法を用いて同様にDNAシーケンサーでDNA塩基配列を決定した。全長塩基配列は上記方法により決定された部分塩基配列を完全にオーバーラップさせ最終的に確定した。

次に、決定された全長塩基配列から、蛋白質への翻訳領域を推定しアミノ酸配列を求めた。それぞれに対応する配列番号を表 1 に示す。

【 0 1 8 7 】

実施例 4． 相同性検索による機能予測

決定された塩基配列および蛋白質をコードすると推定されるORF部分のアミノ酸配列についてSwissProt、RefSeq、nrに対するBLAST検索を行った。P値またはE値が 10^{-4} 以下であり、かつアミノ酸データベースを対象にした解析においてはコンセンサス長×相同性 = 3 0 以上のBLAST検索ヒットデータの中から、相同性が高い、塩基配列及び推定アミノ酸配列に対して機能の予測が比較的容易なヒットデータの中から代表的なものを選択し、相同性検索結果データとして明細書の最後に示した。したがって示したデータはあくまで代表的なものであり、各クローンに相同性を示す分子が、これのみに限定されるというわけではない。また、一部のクローンにおいて、先に記した条件にあてはまらないBLAST検索ヒットデータについては示さなかった。

【 0 1 8 8 】

実施例 5． 推定アミノ酸配列に対するシグナル配列、膜貫通領域および機能ドメインの検索

全長塩基配列から推定されたアミノ酸配列に対して、アミノ末端のシグナル配列の有無と膜貫通領域の有無を予測、さらに蛋白質の機能ドメイン（モチーフ）検索を行った。アミノ末端のシグナル配列についてはPSORT [K. Nakai & M. Kanehisa, Genomics, 14: 897-911 (1992)]を、膜貫通領域についてはSOSUI [T.Hiro

kawa et.al. Bioinformatics, 14: 378-379 (1998)] (三井情報開発株式会社販売) を用いて解析を行った。機能ドメインの検索についてはPfam (Version 5.5) (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) を用いた。PSORTやSOSUIにより、アミノ末端のシグナル配列や膜貫通領域が予測されたアミノ酸配列は分泌、膜蛋白質であると予測された。また、Pfamによる機能ドメイン検索において、ある機能ドメインにヒットしたアミノ酸配列はヒットデータをもとに、例えばPROSITE(<http://www.expasy.ch/cgi-bin/prosite-list.pl>)にある機能カテゴリー分類を参照にしてその蛋白質の機能予測することができる。また、PROSITEでの機能ドメインの検索も可能である。

各ソフトウェアによる検索結果を以下に示す。

【 0 1 8 9 】

PSORTにより推定アミノ酸配列にシグナル配列を検出されたクローンは、以下の 1 3 0 クローンであった。

ADIPS2000069, ASTRO2015162, BEAST2000981, BLADE2001031, BRACE2017397, BRACE2023633, BRACE3009392, BRACE3013986, BRACE3014523, BRACE3026345, BRACE3032537, BRACE3037803, BRACE3051144, BRAMY2015516, BRAMY3002886, BRAMY3009556, BRAMY3016829, BRAWH2011958, BRAWH2016209, BRAWH3005886, BRAWH3012005, BRAWH3014609, BRAWH3016123, BRAWH3018063, BRAWH3020200, BRAWH3023421, BRAWH3028223, BRAWH3032298, BRAWH3034134, BRAWH3040695, BRAWH3042438, BRAWH3046196, BRAWH3049068, BRCAN2003269, BRCAN2006955, BRCAN2018269, BRHIP2006921, BRHIP2020930, BRHIP3000859, BRHIP3012997, BRHIP3016032, BRHIP3020046, BRHIP3020733, BRHIP3028742, BRHIP3030230, BRHIP3035754, BRSSN2018218, BRSTN2010089, BRSTN2011688, BRTHA2000969, BRTHA2014647, BRTHA2020400, BRTHA2020721, BRTHA2026290, BRTHA2030036, BRTHA2033320, BRTHA2033683, BRTHA3003225, BRTHA3014835, BRTHA3018623, BRTHA3026161, BRTHA3027820, COLON2005623, CTONG3002588, FEBRA2023498, FEKID2002493, HCHON2009766, JCMLC2002095, NETRP2004090, NETRP2005849, NT2RI3009524, NT2RP8008057, OCBBF3007704, OCBBF3021502, OCBBF3022123, OCBBF3028001, PEBLM2005615, SKMUS2008585, SPLEN2025012, SPLEN2035615,

SPLEN2042051, STOMA2004663, SYNOV4009139, TESTI2037657, TESTI2049041, TESTI4002072, TESTI4022158, TESTI4024494, TESTI4035872, TESTI4043371, TESTI4045168, THYMU3003350, THYMU3014173, THYMU3015457, THYMU3023107, THYMU3025118, THYMU3025313, THYMU3025642, THYMU3026532, THYMU3026869, THYMU3028461, THYMU3029795, THYMU3034099, THYMU3036310, THYMU3036953, THYMU3037772, THYMU3038158, THYMU3038167, THYMU3040068, THYMU3040746, THYMU3044188, THYMU3045510, THYMU3047542, TRACH3003872, TRACH3014580, TRACH3016368, TRACH3019058, TRACH3020930, TRACH3021023, TRACH3021544, TRACH3022758, TRACH3023203, TRACH3023516, TRACH3025346, TRACH3026542, TRACH3026650, TRACH3029670, TRACH3031316, TRACH3034680, TRACH3036278

【 0 1 9 0 】

SOSUIにより推定アミノ酸配列に膜貫通領域を検出されたクローンは、以下の455クローンであった。数字は推定アミノ酸配列中に検出された膜貫通領域の数を示している。検索結果は、クローン名と膜貫通領域の数を//で区切って示した。

3NB692004045//5, ADRGL2010315//3, ASTRO2015162//5, BEAST2000981//4, BLADE2002744//2, BLADE2007744//1, BRACE2003628//4, BRACE2012528//1, BRACE2013126//3, BRACE2017580//2, BRACE2017992//2, BRACE2023633//2, BRACE2030039//6, BRACE2035191//1, BRACE3001973//2, BRACE3002264//11, BRACE3002344//1, BRACE3004981//1, BRACE3007869//3, BRACE3009392//6, BRACE3013874//2, BRACE3015898//1, BRACE3018083//1, BRACE3021517//1, BRACE3021805//1, BRACE3022051//1, BRACE3024379//2, BRACE3024444//2, BRACE3024497//2, BRACE3024879//6, BRACE3026345//1, BRACE3026456//1, BRACE3026802//2, BRACE3028360//2, BRACE3029021//1, BRACE3030538//5, BRACE3031372//3, BRACE3031579//3, BRACE3031728//1, BRACE3032385//8, BRACE3032980//1, BRACE3033525//1, BRACE3034964//1, BRACE3034993//2, BRACE3037637//3, BRACE3037803//2, BRACE3038570//3, BRACE3039358//1, BRACE3039378//6, BRACE3040644//1, BRACE3040863//2, BRACE3042326//11, BRACE3042409//4, BRACE3042432//2, BRACE3044090//2, BRACE3046049//1, BRACE3046152//3

, BRACE3046466//2, BRACE3048565//2, BRACE3050504//7,
BRACE3051144//3, BRACE3051621//3, BRACE3052486//1, BRALZ2011337//1, BRAL
Z2013690//2, BRAMY2015516//4, BRAMY2021098//1, BRAMY2025495//2, BRAMY203
7609//2, BRAMY2040915//1, BRAMY2041507//2, BRAMY2044686//4, BRAMY2046537
//5, BRAMY3002886//5, BRAMY3004126//6, BRAMY3007449//2, BRAMY3009904//2,
BRAMY3010654//2, BRAMY3010902//2, BRAMY3015547//2,
BRAMY3015549//2, BRAMY3016829//3, BRAWH2000256//5, BRAWH2010364//2, BRAW
H2011812//1, BRAWH2012866//1, BRAWH2016209//5, BRAWH2016305//1, BRAWH300
1053//1, BRAWH3001783//1, BRAWH3001833//7, BRAWH3005892//1, BRAWH3008867
//2, BRAWH3010461//4, BRAWH3010657//1, BRAWH3011907//1, BRAWH3012662//1,
BRAWH3012779//3, BRAWH3013049//1, BRAWH3014609//2,
BRAWH3015175//1, BRAWH3018063//1, BRAWH3018969//5, BRAWH3019529//1, BRAW
H3019820//3, BRAWH3020200//3, BRAWH3020884//1, BRAWH3021012//2, BRAWH302
1641//2, BRAWH3022347//1, BRAWH3023156//1, BRAWH3023274//2, BRAWH3023415
//1, BRAWH3024186//1, BRAWH3024242//3, BRAWH3027574//1, BRAWH3027880//5,
BRAWH3028223//2, BRAWH3028754//2, BRAWH3029806//10,
BRAWH3030810//1, BRAWH3034114//1, BRAWH3034134//1, BRAWH3035914//1, BRAW
H3036270//1, BRAWH3038055//1, BRAWH3038324//3, BRAWH3040695//1, BRAWH304
0711//2, BRAWH3042132//1, BRAWH3042438//1, BRAWH3042772//2, BRAWH3042996
//2, BRAWH3043498//2, BRAWH3044676//1, BRAWH3046196//3, BRAWH3047063//1,
BRAWH3048374//2, BRAWH3048724//2, BRAWH3049068//2,
BRAWH3049544//1, BRCAN2002662//1, BRCAN2003269//3, BRCAN2018269//2, BRCA
N2019653//2, BRCAN2020412//2, BRCAN2020972//1, BRCAN2022126//5, BRCOC200
6164//8, BRCOC2006639//1, BRCOC2009638//3, BRHIP2021929//7, BRHIP3001878
//3, BRHIP3002000//10, BRHIP3002124//3, BRHIP3003306//2, BRHIP3003395//1
, BRHIP3004774//1, BRHIP3005801//1, BRHIP3006950//2,
BRHIP3007195//8, BRHIP3007960//1, BRHIP3008320//6, BRHIP3010289//2, BRHI
P3011831//1, BRHIP3012185//2, BRHIP3013078//1, BRHIP3016032//10, BRHIP30
17146//3, BRHIP3017558//11, BRHIP3019956//1, BRHIP3021019//1, BRHIP30257

95//11, BRHIP3025844//1, BRHIP3027160//1, BRHIP3027191//1, BRHIP3028742//2, BRHIP3029530//2, BRHIP3031733//1, BRHIP3033557//5, BRHIP3035222//2, BRHIP3036715//3, BRHIP3036936//1, BRHIP3037810//3, BRHIP3039430//4, BRHIP3041587//1, BRSSN2004710//1, BRSSN2018218//2, BRSTN2010089//11, BRSTN2011688//2, BRSTN2011899//1, BRTHA2000969//2, BRTHA2003759//3, BRTHA2012189//1, BRTHA2014647//2, BRTHA2018304//2, BRTHA2019726//1, BRTHA2019743//2, BRTHA2020566//1, BRTHA2020781//1, BRTHA2021212//1, BRTHA2021440//1, BRTHA2021450//1, BRTHA2022914//2, BRTHA2022968//1, BRTHA2023437//1, BRTHA2030036//3, BRTHA2031917//1, BRTHA2033469//2, BRTHA2033683//7, BRTHA2036055//1, BRTHA2036295//1, BRTHA3006593//1, BRTHA3010540//2, BRTHA3010717//4, BRTHA3011194//11, BRTHA3011998//3, BRTHA3012265//4, BRTHA3013882//3, BRTHA3014835//1, BRTHA3016616//2, BRTHA3018623//2, BRTHA3028505//1, CHONS2001797//1, CHONS2002419//2, COLON2005623//1, COLON2005735//10, CTONG2008989//4, CTONG2020582//1, CTONG2027150//1, CTONG3001605//5, CTONG3002588//1, CTONG3008223//2, FCBBF3012443//1, FEBRA2023498//1, FEBRA2026977//1, FEHRT2002708//4, FEKID2002231//1, FELNG2000720//1, FELNG2001706//1, HCHON2009766//12, HSYRA2004550//6, JCMLC2000273//1, KIDNE2004531//6, KIDNE2015987//2, KIDNE2017153//1, LYMPB1000158//1, LYMPB2002236//12, LYMPB2002478//2, MESAN2014624//5, N1ESE2000698//1, NETRP2004090//3, NETRP200434//1, NETRP2005282//2, NETRP2005849//2, NT2RI3005861//1, NT2RI3009524//1, NT2RP7019682//2, NT2RP8001605//2, NT2RP8003787//6, NT2RP8008057//1, OCBBF2004478//4, OCBBF2018229//2, OCBBF2018618//6, OCBBF2036019//2, OCBBF3003745//2, OCBBF3007704//1, OCBBF3022123//1, OCBBF3022576//2, OCBBF3023175//3, OCBBF3023993//3, OCBBF3025475//13, OCBBF3025887//1, OCBBF3028001//2, PEBLM2003935//1, PEBLM2005615//9, PLACE5000522//2, PLACE6000012//3, PLACE6010936//6, PLACE6019674//1, PLACE7000266//1, PLACE7000707//2, PLACE7003639//3, PLACE7008136//2, PLACE7011269//2, PLACE7014247//3, PLACE7016321//3, PLACE7016454//2, PUAEN200

0684//4, SKMUS2008585//2, SMINT2003641//1, SPLEN2007689//2, SPLEN2011252
//3, SPLEN2031004//1, SPLEN2034551//1, SPLEN2035615//1, STOMA2004663//1,
TIESE2002665//12, TBAES2005361//1, TBAES2007428//2,
TESOP2008556//1, TESTI2007490//2, TESTI2018335//10, TESTI2022323//6, TES
TI2024267//9, TESTI2028613//3, TESTI2036822//5, TESTI2037085//1, TESTI20
37877//1, TESTI2046188//1, TESTI4001037//2, TESTI4002072//6, TESTI400288
9//2, TESTI4003602//6, TESTI4004539//8, TESTI4004653//9, TESTI4005399//1
1, TESTI4007671//1, TESTI4010544//13, TESTI4010721//6,
TESTI4013774//2, TESTI4014415//14, TESTI4014932//2, TESTI4014977//1, TES
TI4017647//1, TESTI4017854//2, TESTI4019149//1, TESTI4021377//4, TESTI40
21569//4, TESTI4022158//2, TESTI4023096//9, TESTI4023654//1, TESTI402668
0//1, TESTI4027170//1, TESTI4028042//2, TESTI4031818//1, TESTI4032128//1
, TESTI4033177//2, TESTI4034973//3, TESTI4035989//1,
TESTI4036012//3, TESTI4037949//2, TESTI4038047//2, TESTI4039575//1, TEST
I4040559//4, TESTI4041049//2, TESTI4043067//1, TESTI4043371//3, TESTI404
6073//1, TESTI4046450//2, TESTI4047119//11, TESTI4048296//2, TESTI404854
5//1, TESTI4051015//3, TESTI4051858//1, TESTI4052219//2, TESTI4052430//1
, TESTI4052598//1, THYMU3002825//1, THYMU3003007//1,
THYMU3008935//1, THYMU3009755//2, THYMU3011360//2, THYMU3013197//1, THYM
U3014173//1, THYMU3015647//9, THYMU3016518//2, THYMU3018151//2, THYMU301
9605//1, THYMU3021404//7, THYMU3021586//3, THYMU3022211//2, THYMU3022528
//3, THYMU3022668//1, THYMU3023107//5, THYMU3023400//9, THYMU3025313//1,
THYMU3025642//2, THYMU3026306//1, THYMU3026532//2,
THYMU3026869//1, THYMU3027540//2, THYMU3031878//4, THYMU3032032//2, THYM
U3033649//2, THYMU3034616//2, THYMU3036310//1, THYMU3036934//2, THYMU303
8158//1, THYMU3040126//3, THYMU3040146//2, THYMU3040172//2, THYMU3040746
//2, THYMU3040816//2, THYMU3041918//1, THYMU3042321//1, THYMU3043688//4,
THYMU3043779//2, THYMU3044188//2, THYMU3047115//7,
THYMU3047156//3, THYMU3047542//2, THYMU3047760//2, TLIVE2008797//1, TRAC

H3003872//2, TRACH3004747//12, TRACH3005274//1, TRACH3005699//1, TRACH3007274//2, TRACH3007625//7, TRACH3009008//2, TRACH3009061//6, TRACH3010382//1, TRACH3011184//1, TRACH3012891//2, TRACH3013900//1, TRACH3014063//3, TRACH3015346//1, TRACH3016368//1, TRACH3016885//1, TRACH3016992//1, TRACH3017409//1, TRACH3018191//2, TRACH3018240//1, TRACH3018943//1, TRACH3019370//6, TRACH3019621//10, TRACH3020930//2, TRACH3022109//3, TRACH3023063//3, TRACH3023203//3, TRACH3023945//1, TRACH3024081//2, TRACH3024671//2, TRACH3025346//5, TRACH3026542//2, TRACH3026650//1, TRACH3027681//2, TRACH3029670//2, TRACH3031316//1, TRACH3031678//8, TRACH3032480//1, TRACH3038399//1, TSTOM2002682//1, UTERU3005422//3, UTERU3010029//3, UTERU3011092//8, UTERU3011837//1, UTERU3012414//1, UTERU3015647//1, UTERU3016273//5, UTERU3017626//6, UTERU3022168//1, UTERU3022922//2, UTERU3023413//1

【 0 1 9 1 】

Pfamにより推定アミノ酸配列に機能ドメインを検出されたクローンは以下の 7 9 6 クローンであった。検索結果は、クローン名//機能ドメイン名のように示し、複数の機能ドメインがヒットした場合には//で区切って並記した。なお同一の機能ドメインが複数ヒットした場合も省略せずに記載した。

3NB692004045//Sodium Bile acid symporter family// FecCD transport family
ADIPS2000069//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain

ASTRO2016114//Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BEAST2000981//PA domain// Zinc finger, C3HC4 type (RING finger)// PHD-finger

BLADE2001031//Thrombospondin type 1 domain

BLADE2002310//RhoGAP domain
BLADE2008809//PH domain
BRACE1000475//Enoyl-CoA hydratase/isomerase family
BRACE2003628//NADH-Ubiquinone oxidoreductase (complex I), chain 5 C-term
inus
BRACE2010336//TPR Domain// TPR Domain// TPR Domain// TPR Domain// TPR Do
main// TPR Domain// TPR Domain
BRACE2012528//alpha/beta hydrolase fold
BRACE2012625//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognitio
n motif. (a.k.a. RRM, RBD, or RNP domain)
BRACE2013009//EF hand
BRACE2013132//Adenosine/AMP deaminase
BRACE2016896//tRNA synthetases class II (F)// tRNA synthetases class II
(F)// tRNA synthetases class II (D, K and N)
BRACE2017397//von Willebrand factor type A domain
BRACE2017872//PWWP domain
BRACE2019348//Zinc finger, C2H2 type// Zinc finger, C2H2 type
BRACE2023744//Translationally controlled tumor protein
BRACE2034434//Protein of unknown function
BRACE2035120//Inositol polyphosphate phosphatase family, catalytic domai
n
BRACE2042541//Ank repeat// Ank repeat// Glutathione S-transferases.
BRACE2046976//Collagen triple helix repeat (20 copies)
BRACE2047975//Eukaryotic protein kinase domain
BRACE3001973//EGF-like domain// Laminin G domain// EGF-like domain// EGF
-like domain// EGF-like domain
BRACE3002264//GNS1/SUR4 family// Ion transport protein// Ion transport p
rotein

BRACE3002344//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// PQQ enzyme repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

BRACE3002756//SAM domain (Sterile alpha motif)

BRACE3003866//Src homology domain 2

BRACE3004767//PH domain

BRACE3005903//K-box region// TSC-22/dip/bun family

BRACE3009392//Aminotransferases class-III pyridoxal-phosphate// Sodium:dicarboxylate symporter family

BRACE3013418//Ank repeat// Ank repeat// ZU5 domain// Death domain// TGF-beta propeptide// Fatty acid desaturase// Isocitrate lyase

BRACE3013874//Leucine rich repeat C-terminal domain// Immunoglobulin domain// Fibronectin type III domain

BRACE3014523//Wiskott Aldrich syndrome homology region 2

BRACE3015898//PI3-kinase family, ras-binding domain

BRACE3017253//Adenylate kinase// Transferrin

BRACE3019570//Troponin

BRACE3019941//TPR Domain// TPR Domain// DNA-dependent RNA polymerase// TPR Domain// TPR Domain// TPR Domain// 7-fold repeat in Clathrin and VPS// TPR Domain// TPR Domain// TPR Domain// TPR Domain

BRACE3022303//BRCA1 C Terminus (BRCT) domain// BRCA1 C Terminus (BRCT) domain

BRACE3022340//Troponin

BRACE3024444//Copper/zinc superoxide dismutase (SODC)

BRACE3024879//7 transmembrane receptor (Secretin family)

BRACE3025719//Zinc finger, C3HC4 type (RING finger)// Filamin/ABP280 repeat.// NHL repeat// NHL repeat// NHL repeat// NHL repeat// Squash family of serine protease inhibitors

BRACE3026345//Insulin/IGF/Relaxin family

BRACE3026844//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 t
ype// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zin
c finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Z
inc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type/
/ Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc fing
er, C2H2 type

BRACE3026947//FYVE zinc finger

BRACE3029021//Zinc finger, C2H2 type

BRACE3031315//Serine hydroxymethyltransferase// UBA domain

BRACE3031372//D-isomer specific 2-hydroxyacid dehydrogenases

BRACE3031743//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

BRACE3032385//Ion transport protein

BRACE3032537//Luteovirus (ORF3) RNA-directed RNA-polymerase

BRACE3033525//Prolyl oligopeptidase family

BRACE3034183//Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 ty
pe// Plant PEC family metallothionein// Transcription factor S-II (TFIIS
)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
type// FYVE zinc finger// Zinc finger, C2H2 type// RNA polymerases M/15
Kd subunits// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-typ
e zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc f
inger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zin
c finger, C2H2 type

BRACE3034964//alpha/beta hydrolase fold

BRACE3036283//DnaJ domain

BRACE3039288//Viral RNA dependent RNA polymerase

BRACE3039358//Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich r
epeat C-terminal domain// Immunoglobulin domain// Immunoglobulin domain/

/ Immunoglobulin domain

BRACE3039378//Pentaxin family// Receptor family ligand binding region//
7 transmembrane receptor (metabotropic glutamate family)

BRACE3039454//Aminotransferases class-III pyridoxal-phosphate

BRACE3040239//Zinc finger, C3HC4 type (RING finger)

BRACE3040644//Low-density lipoprotein receptor domain class A// EB modul
e// Low-density lipoprotein receptor domain class A// CUB domain// Low-d
ensity lipoprotein receptor domain class A// Low-density lipoprotein rec
eptor domain class A

BRACE3041059//Ubiquitin carboxyl-terminal hydrolases family 2// Ubiquiti
n carboxyl-terminal hydrolase family 2

BRACE3041162//Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-fing
er// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2
type// Zinc finger, C2H2 type// Putative zinc finger in N-recognin

BRACE3042046//RhoGEF domain// PH domain

BRACE3042409//AMP-binding enzyme

BRACE3042432//7 transmembrane receptor (Secretin family)

BRACE3043597//KOW motif

BRACE3044172//Phosphatidylinositol 3- and 4-kinases

BRACE3045424//PH domain

BRACE3046466//EGF-like domain// EGF-like domain// Laminin G domain// Lam
inin G domain// EGF-like domain// Laminin G domain// EGF-like domain// L
aminin G domain// Laminin G domain// EGF-like domain// EGF-like domain//
Laminin EGF-like (Domains III and V)// EB module// EGF-like domain// EG
F-like domain

BRACE3046491//PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also
known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).// SH3
domain// Guanylate kinase

BRACE3047482//Zinc finger, C3HC4 type (RING finger)// Zinc finger, C3HC4

type (RING finger)// B-box zinc finger// CONSTANS family zinc finger//
B-box zinc finger// Fibronectin type III domain// SPRY domain
BRACE3048615//Leucine Rich Repeat// Leucine Rich Repeat
BRACE3049714//Dihydroneopterin aldolase
BRACE3050270//Reverse transcriptase (RNA-dependent DNA polymerase)
BRACE3050504//Ion transport protein
BRACE3051621//Latrophilin/CL-1-like GPS domain// PLAT/LH2 domain// Regul
ator of G protein signaling domain
BRACE3051819//Myosin head (motor domain)// IQ calmodulin-binding motif//
IQ calmodulin-binding motif// Myosin tail// KE2 family protein// Myosin
tail// lactate/malate dehydrogenase// Troponin// Myosin tail
BRACE3052321//SH3 domain
BRACE3052410//Viral methyltransferase
BRACE3052595//C2 domain
BRALZ2010842//Mitochondrial carrier proteins
BRALZ2013621//KH domain
BRAMY2031516//wnt family of developmental signaling proteins
BRAMY2040915//Immunoglobulin domain
BRAMY2041347//Mov34/MPN/PAD-1 family
BRAMY2041384//Annexin// Annexin// Annexin// Annexin// Annexin// Annexin
BRAMY2046537//PMP-22/EMP/MP20/Claudin family
BRAMY3000692//Zinc finger, C2H2 type// Zinc finger, C2H2 type
BRAMY3002886//Domain of unknown function// CBS domain// CBS domain
BRAMY3004126//Transmembrane 4 family// 7 transmembrane receptor (rhodops
in family)
BRAMY3005184//ZU5 domain// Death domain
BRAMY3007078//Inositol monophosphatase family// PHD-finger// PHD-finger
BRAMY3009491//Phosphatidylinositol 3- and 4-kinases
BRAMY3010321//SAM domain (Sterile alpha motif)// PH domain// PH domain//

Putative GTP-ase activating protein for Arf

BRAMY3011501//SAP domain// SPRY domain

BRAMY3011581//Prokaryotic DNA topoisomerase// Topoisomerase DNA binding

C4 zinc finger// PHD-finger// Zinc finger, CCHC class

BRAMY3014027//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 t
ype// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H
2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finge
r, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fi
nger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2
type

BRAMY3014613//RhoGAP domain// haloacid dehalogenase-like hydrolase

BRAMY3015086//FERM domain (Band 4.1 family)

BRAMY3015547//RhoGEF domain

BRAMY3015549//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain// Immunoglobulin domain// Fibronecti
n type III domain// Fibronectin type III domain// Fibronectin type III d
omain// Fibronectin type III domain

BRAMY3017920//RhoGEF domain// PH domain// RhoGAP domain

BRAMY3018754//Protein of unknown function// Domain of unknown function

BRAMY4000915//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank re
peat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//
Glutamine amidotransferases class-II// Ank repeat// Ank repeat// Ank rep
eat// Ank repeat// Ank repeat// Ank repeat// Hantavirus nucleocapsid pro
tein// Ank repeat// Ank repeat

BRAMY4000962//Tudor domain

BRAMY4001652//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank re
peat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat//

Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ribosomal protein L3
4// Ank repeat// Ank repeat// Ank repeat// Uncharacterized protein famil
y UPF0028

BRAMY4002575//Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)
// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRAWH2000256//Progesterone receptor// Cytochrome c oxidase subunit III//
Sulfate transporter family

BRAWH2002333//3'5'-cyclic nucleotide phosphodiesterase

BRAWH2011796//S-100/ICaBP type calcium binding domain// EF hand

BRAWH2011812//Syndecan domain// BNR repeat// BNR repeat// BNR repeat// B
NR repeat// BNR repeat// PKD domain

BRAWH2012866//C2 domain// C2 domain

BRAWH2014053//Sigma-54 transcription factors// ATPases associated with v
arious cellular activities (AAA)

BRAWH2016209//Zinc finger, C3HC4 type (RING finger)// PHD-finger

BRAWH2016223//TPR Domain

BRAWH2016785//Pyridine nucleotide-disulphide oxidoreductase

BRAWH3000446//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fin
ger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRAWH3001783//Cadherin domain// Cadherin domain// Cadherin domain// Cadh
erin domain// Cadherin domain

BRAWH3003573//EF hand// EF hand// EF hand

BRAWH3005886//Rubredoxin// PHD-finger

BRAWH3008167//Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR
repeat)// CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi d
omain (SCR repeat)// CUB domain

BRAWH3009961//PHD-finger// Glycophorin A// PDZ domain (Also known as DHR
or GLGF).// C2 domain// C2 domain

BRAWH3010657//Ubiquitin carboxyl-terminal hydrolases family 2// Ubiquiti

BRAWH3017477//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fin

ger, C2H2 type

BRAWH3018063//Rap/ran-GAP

BRAWH3018548//Intermediate filament proteins// Vinculin family

BRAWH3019026//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Protein phosphatase 2A regulatory subunit PR55// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

BRAWH3021574//Wiskott Aldrich syndrome homology region 2

BRAWH3021580//Intermediate filament proteins// Zinc finger, CCHC class

BRAWH3021724//Transglutaminase-like superfamily

BRAWH3022347//Leucine Rich Repeat

BRAWH3022431//FGGY family of carbohydrate kinases

BRAWH3022651//PHD-finger// Zn-finger in ubiquitin-hydrolases and other proteins

BRAWH3022719//Eukaryotic initiation factor 4E

BRAWH3023156//Neurotransmitter-gated ion-channel

BRAWH3023415//Glycosyl hydrolase family 47

BRAWH3024186//Fibronectin type III domain// Protein-tyrosine phosphatase // Dual specificity phosphatase, catalytic domain// Protein-tyrosine phosphatase

BRAWH3024231//TPR Domain// TPR Domain// TPR Domain

BRAWH3024506//I/LWEQ domain

BRAWH3025157//Ank repeat// Ank repeat// Ank repeat// BTB/POZ domain// K+ channel tetramerisation domain

BRAWH3026349//PX domain

BRAWH3026938//PDZ domain (Also known as DHR or GLGF).

BRAWH3027440//TPR Domain// TPR Domain// TPR Domain// TPR Domain// PPR repeat

BRAWH3027533//AN1-like Zinc finger// PHD-finger// FYVE zinc finger

BRAWH3027574//TBC domain// EF hand

BRAWH3027607//DNA binding domain with preference for A/T rich regions

BRAWH3027806//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Arenavirus nucleocapsid protein// WD domain, G-beta repeat// WD domain, G-beta repeat

BRAWH3027880//Integral membrane protein// AN1-like Zinc finger// DHHC zinc finger domain

BRAWH3028796//Zinc finger C-x8-C-x5-C-x3-H type (and similar).// Zinc finger C-x8-C-x5-C-x3-H type (and similar).// Zinc finger C-x8-C-x5-C-x3-H type (and similar).// Zinc finger, C3HC4 type (RING finger)// Integrase Zinc binding domain// Zinc finger C-x8-C-x5-C-x3-H type (and similar).// Protein phosphatase 2A regulatory B subunit (B56 family)

BRAWH3029385//PH domain// Dynamin GTPase effector domain

BRAWH3029806//Copper/zinc superoxide dismutase (SODC)// Adenylate and Guanylate cyclase catalytic domain// NADH-ubiquinone oxidoreductase chain 4, amino terminus// Endothelin family

BRAWH3030772//Ank repeat// Ank repeat// Ank repeat

BRAWH3030910//SAM domain (Sterile alpha motif)

BRAWH3031342//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Putative zinc finger in N-recogin// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Src homology domain 2// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Src homology domain 2// Zinc finger, C2H2 type

BRAWH3031710//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

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BRAWH3041928//Wilm's tumour protein
BRAWH3042438//'Paired box' domain// EF hand// Phorbol esters/diacylglycerol binding domain (C1 domain)
BRAWH3042568//Homeobox domain
BRAWH3042772//Cation efflux family
BRAWH3042787//Gag P30 core shell protein// Zinc finger, CCHC class
BRAWH3043295//Inorganic pyrophosphatase
BRAWH3044122//C2 domain// Sigma-70 factor
BRAWH3044151//Thrombospondin type 1 domain// Thrombospondin type 1 domain// Thrombospondin type 1 domain// Keratin, high sulfur B2 protein// Thrombospondin type 1 domain
BRAWH3044985//Phosphotriesterase family
BRAWH3045118//DnaJ domain
BRAWH3046424//Histone deacetylase family
BRAWH3047692//Shikimate kinase// ATPases associated with various cellular activities (AAA)
BRAWH3048374//Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Sushi domain (SCR repeat)// Keratin, high sulfur B2 protein// Sushi domain (SCR repeat)
BRAWH3048724//Subtilase family
BRAWH3049544//Glycosyl transferases// Similarity to lectin domain of ricin beta-chain, 3 copies.
BRCAN2000923//ADP-ribosylation factor family// Ras family
BRCAN2002892//ADP-ribosylation factor family// Ras family
BRCAN2003269//ABC transporter
BRCAN2003814//Phosphatidylinositol-specific phospholipase C, X domain
BRCAN2006051//Peptidase family M41
BRCAN2010665//PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also

known as DHR or GLGF).// PDZ domain (Also known as DHR or GLGF).

BRCAN2015402//Cytochrome P450

BRCAN2019907//EF hand

BRCAN2020234//Lipocalin / cytosolic fatty-acid binding protein family

BRCAN2020331//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//

RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

BRCAN2021325//Zinc carboxypeptidase// Zinc carboxypeptidase

BRCAN2021452//Zinc finger, CCHC class// Zinc finger, CCHC class

BRCAN2021718//Ribosomal protein L10

BRCAN2022126//IstB-like ATP binding protein// Receptor family ligand binding region// Bacterial extracellular solute-binding proteins, family 3/ / Ligand-gated ion channel

BRCAN2025093//Ank repeat// Flagellar FliJ protein// Ank repeat

BRCOC2001355//GTP1/OBG family// Phosphoribulokinase// Adenylylsulfate kinase

BRCOC2006164//ATP synthase subunit C// Nucleoside transporter// Sugar (and other) transporter// Influenza RNA-dependent RNA polymerase subunit P A

BRCOC2006639//Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

BRCOC2012386//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type // Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRHIP2008756//MAS20 protein import receptor// BRCA1 C Terminus (BRCT) domain

BRHIP2013958//Domain of unknown function// MSP (Major sperm protein) domain

BRHIP2026346//Formin Homology 2 Domain
BRHIP2027077//Zinc finger, C2H2 type// Zinc finger, C2H2 type
BRHIP2027563//Kelch motif
BRHIP2029663//TPR Domain// Zinc finger, C3HC4 type (RING finger)// ATP-dependent protease La (LON) domain
BRHIP3000859//Wilm's tumour protein
BRHIP3001481//Protein-tyrosine phosphatase
BRHIP3001878//POT family
BRHIP3002000//Peptidase family M20/M25/M40// Sugar (and other) transporter
BRHIP3002114//Mandelate racemase / muconate lactonizing enzyme family
BRHIP3002141//DNA polymerase (viral) C-terminal domain
BRHIP3003063//cAMP phosphodiesterases class-II// Vinculin family
BRHIP3003126//HECT-domain (ubiquitin-transferase).
BRHIP3003306//Uncharacterized protein family// Rap/ran-GAP
BRHIP3003340//Actin
BRHIP3003795//Cytochrome P450
BRHIP3004710//TPR Domain// TPR Domain// TPR Domain
BRHIP3004725//tRNA synthetases class I (C)
BRHIP3005037//BAH domain// ELM2 domain// Myb-like DNA-binding domain// GATA zinc finger
BRHIP3005142//Adaptin N terminal region
BRHIP3005231//TPR Domain// TPR Domain
BRHIP3005307//Glutathione S-transferases.// Uncharacterized protein family UPF0028
BRHIP3005673//Glutathione S-transferases.
BRHIP3005944//Scavenger receptor cysteine-rich domain// Scavenger receptor cysteine-rich domain
BRHIP3006294//SH3 domain// RhoGAP domain

BRHIP3006449//Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats

BRHIP3006786//Sec7 domain

BRHIP3007195//Type I restriction modification DNA specificity domain// E1-E2 ATPase// E1-E2 ATPase// Neuraxin and MAP1B proteins// E1-E2 ATPase// Cof family

BRHIP3007223//Ubiquitin carboxyl-terminal hydrolases family 2// Ubiquitin carboxyl-terminal hydrolase family 2

BRHIP3007424//wnt family of developmental signaling proteins

BRHIP3007609//PHD-finger

BRHIP3008320//Transmembrane region cyclic Nucleotide Gated Channel

BRHIP3009753//CUB domain// Low-density lipoprotein receptor domain class A

BRHIP3010289//Delta serrate ligand// Kelch motif// Kelch motif// Plexin repeat// Plexin repeat// Lectin C-type domain// Plexin repeat// Plexin repeat// Laminin EGF-like (Domains III and V)// Keratin, high sulfur B2 protein// Laminin EGF-like (Domains III and V)

BRHIP3011082//HECT-domain (ubiquitin-transferase).

BRHIP3011460//RhoGEF domain// PH domain// SH3 domain

BRHIP3011567//Dihydropyridine sensitive L-type calcium channel (Beta subunit)// Dihydropyridine sensitive L-type calcium channel (Beta subunit)

BRHIP3012289//Flavin containing amine oxidase

BRHIP3012736//Collagen triple helix repeat (20 copies)

BRHIP3014675//Ank repeat// Ank repeat// Ank repeat// BTB/POZ domain// K+ channel tetramerisation domain

BRHIP3016032//Integral membrane protein// Divalent cation transporter// TPR Domain// TPR Domain// TPR Domain

BRHIP3017109//Src homology domain 2

BRHIP3017256//LIM domain containing proteins// AN1-like Zinc finger
BRHIP3017558//eubacterial secY protein// FecCD transport family// Domain
of unknown function// Sugar (and other) transporter// Sodium:galactosid
e symporter family// Monocarboxylate transporter
BRHIP3019643//Biopterin-dependent aromatic amino acid hydroxylase
BRHIP3019824//Prokaryotic transcription elongation factor, GreA/GreB
BRHIP3020733//Keratin, high sulfur B2 protein
BRHIP3021019//Protein-tyrosine phosphatase// Dual specificity phosphatas
e, catalytic domain
BRHIP3025795//Sugar (and other) transporter// Protein of unknown functio
n// Sodium:galactoside symporter family// Herpesvirus glycoprotein M// M
onocarboxylate transporter
BRHIP3027191//Hsp70 protein
BRHIP3027651//PHD-finger// PHD-finger
BRHIP3028246//CXXC zinc finger// PHD-finger// Beta type Zein
BRHIP3028570//PH domain// Fibroblast growth factor
BRHIP3029409//NTR/C345C module
BRHIP3030230//Pentaxin family
BRHIP3032374//Glutathione S-transferases.// Uncharacterized protein fami
ly UPF0028
BRHIP3033557//Pyridoxamine 5'-phosphate oxidase// Ligand-gated ion chann
el
BRHIP3033734//Keratin, high sulfur B2 protein
BRHIP3035006//Sialyltransferase family
BRHIP3036371//Immunoglobulin domain// Kunitz/Bovine pancreatic trypsin i
nhibitor domain// Kunitz/Bovine pancreatic trypsin inhibitor domain
BRHIP3036715//Class I Histocompatibility antigen, domains alpha 1 and 2/
/ Immunoglobulin domain
BRHIP3036936//Fibronectin type III domain

BRHIP3037543//Eukaryotic protein kinase domain
BRHIP3038030//Pyridine nucleotide-disulphide oxidoreductase// Phytoene d
ehydrogenase related enzyme
BRHIP3038735//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain
BRHIP3039509//Notch (DSL) domain// Amiloride-sensitive sodium channel
BRHIP3039592//Zinc finger, C3HC4 type (RING finger)
BRHIP3041587//Eukaryotic protein kinase domain
BRSSN2004710//3'5'-cyclic nucleotide phosphodiesterase
BRSSN2011843//bZIP transcription factor// RNA polymerase alpha subunit
BRSSN2015497//Tudor domain
BRSTN2006638//EF hand// EF hand// Pancreatic hormone peptides
BRSTN2010089//Cell cycle protein// 7 transmembrane receptor (Secretin fa
mily)
BRSTN2011961//Thioredoxin
BRSTN2012069//Elongation factor Tu family
BRSTN2016918//Transposase// Ezrin/radixin/moesin family// Intermediate f
ilament proteins
BRTHA2001304//Exonuclease
BRTHA2005448//Calpain family cysteine protease// Calpain large subunit,
domain III// EF hand
BRTHA2019726//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
BRTHA2020400//Immunoglobulin domain
BRTHA2020721//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
BRTHA2020910//Tubulin/FtsZ family
BRTHA2025869//Intermediate filament proteins// Intermediate filament pro
teins

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type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRTHA3011187//EF hand

BRTHA3011194//Voltage gated chloride channels// CBS domain

BRTHA3011361//Calponin homology (CH) domain// LIM domain containing proteins

BRTHA3012265//Sulfate transporter family// Ribosomal protein S3, C-terminal domain.

BRTHA3014000//Birnavirus VP3 protein// Zinc finger, C2H2 type// ELM2 domain// Myb-like DNA-binding domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type

BRTHA3014547//Adenylate kinase// Viral (Superfamily 1) RNA helicase// Arsenical pump membrane protein// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Dehydrogenase E1 component// Ank repeat// Shikimate / quinate 5-dehydrogenase// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat

BRTHA3017791//Lectin (probable mannose binding)

BRTHA3018409//Wilm's tumour protein

BRTHA3020771//PH domain

BRTHA3021708//PH domain

BRTHA3021786//Protein prenyltransferase alpha subunit repeat

BRTHA3021971//Putative peptidoglycan binding domain

BRTHA3023403//Phosphatidylinositol-specific phospholipase C, X domain// Phosphatidylinositol-specific phospholipase C, X domain// C2 domain

BRTHA3025073//Calponin homology (CH) domain

BRTHA3026161//Adenosine-deaminase (editase) domain

BRTHA3026916//Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif// RasGEF domain// Ras association (RalGDS/AF-6) domain

BRTHA3027171//Scorpion short toxins
BRTHA3027638//Matrix protein (MA), p15
BRTHA3028339//Zn-finger in Ran binding protein and others.
CERVX2000968//Immunoglobulin domain
CHONS2000797//T-box
CHONS2001287//Insulin-like growth factor binding proteins// Thyroglobulin type-1 repeat
CHONS2001834//Plexin repeat
CHONS2002829//F5/8 type C domain// Zinc carboxypeptidase// Zinc carboxypeptidase// Zinc carboxypeptidase
COLON2004351//Galactosyltransferase
COLON2005735//CbiM// Ammonium Transporter Family
CTONG2003517//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
CTONG2006235//Zn-finger in ubiquitin-hydrolases and other proteins
CTONG2008989//Connexin
CTONG2009570//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
CTONG2010330//Lysophospholipase catalytic domain
CTONG2011801//BTB/POZ domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type
CTONG2020582//AMP-binding enzyme
CTONG2026987//Reverse transcriptase (RNA-dependent DNA polymerase)
D90ST2003106//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
D90ST2004417//Ribosomal protein L13e
DFNES2011221//Rotavirus NS26

ERLTF2002178//Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif// Kelch motif

ERLTF2002369//PH domain// RhoGAP domain// Tropomyosins

FCBBF3001018//HMGL-like

FCBBF3012443//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine rich repeat C-terminal domain

FCBBF3020030//B-box zinc finger.// B-box zinc finger.// Putative zinc finger in N-recognin

FCBBF3021191//Protein phosphatase 2C// Protein phosphatase 2C

FCBBF3024911//PWWP domain

FCBBF5000384//BAF60b domain of the SWIB complex

FEBRA2000805//Uncharacterized protein family UPF0054

FEBRA2002260//CXXC zinc finger

FEBRA2013570//Dehydrogenase E1 component

FEBRA2023498//Leucine rich repeat N-terminal domain// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

FEBRA2026582//PPIC-type PPIASE domain.

FEBRA2028457//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)// RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

FEHRT2002708//DNA gyrase/topoisomerase IV, subunit A

FEKID2001001//SH3 domain// WW domain// WW domain// PH domain

FEKID2002493//wnt family of developmental signaling proteins

FEKID2002637//Ser/Thr protein phosphatase

FELNG2000720//Immunoglobulin domain// Immunoglobulin domain

FELNG2001953//Src homology domain 2

HCASM2008154//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)//

Zn-finger in Ran binding protein and others.

HCHON2009766//eIF4-gamma/eIF5/eIF2-epsilon

HHGPC2008185//Helper component proteinase// Site-specific recombinases

HSYRA2004550//E1-E2 ATPase// E1-E2 ATPase

HSYRA2007338//Fibronectin type III domain

JCMLC2000273//Lysosome-associated membrane glycoprotein (Lamp)// Integrin alpha cytoplasmic region

JCMLC2002751//von Willebrand factor type D domain// Plant PEC family metalloproteinase// Trypsin Inhibitor like cysteine rich domain// von Willebrand factor type C domain// von Willebrand factor type D domain

KIDNE2004531//Prion protein// Integral membrane protein// Cytochrome c oxidase subunit III// Uncharacterized protein family

KIDNE2010049//FGFY family of carbohydrate kinases// FGFR family of carbohydrate kinases

KIDNE2015987//EGF-like domain// Keratin, high sulfur B2 protein// Zona pellucida-like domain

KIDNE2018268//Zinc finger, C2H2 type

LYMPB2002236//ABC 3 transport family// CblM// NADH-ubiquinone oxidoreductase chain 4, amino terminus// UDP-glucuronosyl and UDP-glucosyl transferases

LYMPB2002344//TBC domain

LYMPB2002458//Fibronectin type III domain// Fibronectin type III domain// Fibrinogen beta and gamma chains, C-terminal globular domain

N1ESE2000698//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

NETRP2003103//Zinc finger, C3HC4 type (RING finger)// PHD-finger

NETRP2003448//ADP-ribosylation factor family// Ras family

i domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)// CUB domain// Sushi domain (SCR repeat)// CUB domain

NT2RP8003490//Hemagglutinin-neuraminidase// LIM domain containing proteins// LIM domain containing proteins// Homeobox domain

NT2RP8003787//Thermophilic metalloprotease (M29)// Ank repeat// Ion transport protein// Sodium:galactoside symporter family

NT2RP8005546//Viral (Superfamily 1) RNA helicase

NT2RP8006452//African swine fever virus multigene family 360 protein// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

NT2RP8007920//PPR repeat// LIM domain containing proteins

NT2RP8008057//Thrombospondin type 1 domain// Immunoglobulin domain// Transforming growth factor beta like domain

NT2RP8009119//Picornavirus 2B protein

NTONG2003805//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

NTONG2008483//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Zinc finger, C2H2 type

OCBBF2000831//WAP-type (Whey Acidic Protein) 'four-disulfide core'// Kazal-type serine protease inhibitor domain// Immunoglobulin domain// Kunitz/Bovine pancreatic trypsin inhibitor domain// Kunitz/Bovine pancreatic trypsin inhibitor domain// Furin-like cysteine rich region// Respiratory-chain NADH dehydrogenase, 49 Kd subunit// NTR/C345C module

OCBBF2003518//Transient receptor// Transient receptor

OCBBF2004478//Trypanosome variant surface glycoprotein// 7 transmembrane receptor (Secretin family)

OCBBF2007039//Reprolysin family propeptide// Reprolysin (M12B) family zinc metalloprotease// Thrombospondin type 1 domain// EB module

OCBBF2009536//Amiloride-sensitive sodium channel

OCBBF2014745//Zinc finger, C2H2 type// Zinc finger, C2H2 type

OCBBF2016928//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

OCBBF2018618//7 transmembrane receptor (Secretin family)// 7 transmembrane receptor (rhodopsin family)

OCBBF2024589//Glutamine amidotransferases class-II// Dihydroorotase-like

OCBBF2030927//Neuregulin family// von Willebrand factor type A domain// EGF-like domain// Response regulator receiver domain// von Willebrand factor type A domain// von Willebrand factor type A domain

OCBBF3001202//DENN (AEX-3) domain

OCBBF3001333//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

OCBBF3001616//Reverse transcriptase (RNA-dependent DNA polymerase)

OCBBF3004487//Platelet-derived growth factor (PDGF)// DEAD/DEAH box helicase

OCBBF3005330//Domain found in Dishevelled, Egl-10, and Pleckstrin// TCP-1/cpn60 chaperonin family// TCP-1/cpn60 chaperonin family

OCBBF3006986//Beige/BEACH domain// WD domain, G-beta repeat// WD domain, G-beta repeat

OCBBF3008392//DNA binding domain with preference for A/T rich regions//

PHD-finger// Bromodomain
OCBBF3008835//Collagen triple helix repeat (20 copies)
OCBBF3019269//CXXC zinc finger
OCBBF3020263//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription facto
r S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
finger, C2H2 type// Zinc finger, C2H2 type
OCBBF3021086//Influenza RNA-dependent RNA polymerase subunit PA// Reprol
ysin family propeptide// Leptin
OCBBF3021361//ELM2 domain// Myb-like DNA-binding domain
OCBBF3021502//Leptin
OCBBF3022827//A20-like zinc finger// Vacuolar sorting protein 9 (VPS9) d
omain
OCBBF3023175//Protein phosphatase 2C// Beige/BEACH domain// WD domain, G
-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD
domain, G-beta repeat
OCBBF3023913//R3H domain// Retroviral Vif (Viral infectivity) protein
OCBBF3025475//Sodium:sulfate symporter transmembrane region// Sodium:sul
fate symporter transmembrane region
OCBBF3025503//Vesiculovirus phosphoprotein// haloacid dehalogenase-like
hydrolase
OCBBF3026088//Fatty acid desaturase
OCBBF3026361//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fin
ger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zi
nc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
RNA polymerases M/15 Kd subunits
OCBBF3026979//Laminin G domain// Thrombospondin N-terminal -like domains
// von Willebrand factor type C domain// von Willebrand factor type C do

main// EGF-like domain// EB module// EGF-like domain// Plant PEC family
metallothionein// EGF-like domain// Trypsin Inhibitor like cysteine rich
domain// Metallothionein// EGF-like domain// EGF-like domain// EGF-like
domain// EGF-like domain// von Willebrand factor type C domain// von Wi
llebrand factor type C domain
OCBBF3027969//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Myosin
head (motor domain)
OCBBF3028001//Transmembrane region cyclic Nucleotide Gated Channel
PEBLM2001803//Vacuolar sorting protein 9 (VPS9) domain
PEBLM2005615//7 transmembrane receptor (rhodopsin family)// Herpesvirus
glycoprotein M
PEBLM2006298//Kinesin motor domain
PLACE5000492//Viral RNA dependent RNA polymerase// Phosphatidylinositol-
specific phospholipase C, X domain// Phosphatidylinositol-specific phospho
lipase C, X domain// C2 domain
PLACE6000055//WD domain, G-beta repeat// WD domain, G-beta repeat// WD d
omain, G-beta repeat
PLACE6001933//Receptor L domain
PLACE6003004//Signal peptidase I// Mandelate racemase / muconate lactoni
zing enzyme family
PLACE6010925//Ribosomal protein S11
PLACE6010936//7 transmembrane receptor (rhodopsin family)
PLACE6019600//Ras family
PLACE7000266//Fibronectin type III domain// Fibronectin type III domain/
/ Fibronectin type III domain// Fibronectin type III domain// Fibronecti
n type III domain// Fibronectin type III domain// Fibronectin type III d
omain// Fibronectin type III domain// Fibronectin type III domain
PLACE7002303//Homeobox domain
PLACE7003985//Prokaryotic molybdopterin oxidoreductases// short chain de

hydrogenase

PLACE7004103//KH domain// KH domain// KH domain// KH domain// Dynamin central region// Domain of unknown function// KH domain// KH domain// KH domain// Small cytokines (intecrine/chemokine), interleukin-8 like// Fanci
oni anaemia group C protein// KH domain// KH domain// AIR carboxylase//
KH domain

PLACE7004961//Dynamin GTPase effector domain

PLACE7005169//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PLACE7006090//Glycosyl hydrolases family 31

PLACE7006498//ADP-ribosylation factor family// G-protein alpha subunit

PLACE7007379//Zinc carboxypeptidase

PLACE7007973//Matrix protein (MA), p15// Matrix protein (MA), p15// Gag P30 core shell protein// Zinc finger, CCHC class

PLACE7008136//Reverse transcriptase (RNA-dependent DNA polymerase)

PLACE7009563//Arginase family// MAGE family

PLACE7009757//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type

PLACE7009936//RhoGAP domain

PLACE7011559//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank repeat// Integrin alpha cytoplasmic region

PLACE7012111//Reprolysin family propeptide// Reprolysin (M12B) family zinc metalloprotease// Keratin, high sulfur B2 protein// Disintegrin// EGF-like domain

PLACE7014247//Phosphatidylinositol 3- and 4-kinases

PLACE7016526//ATP-dependent protease La (LON) domain// NB-ARC domain// Adenylylsulfate kinase// IstB-like ATP binding protein// Shikimate kinase

// Isopentenyl transferase// ATPases associated with various cellular activities (AAA)

PLACE7018304//PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain// PLAT/LH2 domain

PLACE7018512//Zinc finger, C2H2 type// Zinc finger, C2H2 type

PROST2002078//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

PUAEN2000594//Poly-adenylate binding protein, unique domain.

PUAEN2000684//Geminivirus AL2 protein// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat// Leucine Rich Repeat

PUAEN2006639//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat

SKMUS2008585//Dual specificity phosphatase, catalytic domain

SKMUS2009557//Hydroxyethylthiazole kinase family

SMINT2010753//TPR Domain// TPR Domain// TPR Domain// TPR Domain// PPR repeat// TPR Domain

SMINT2011406//Dynammin GTPase effector domain

SMINT2011509//DNA polymerase X family

SMINT2014721//E2 (early) protein, N terminal// Carnitine acyltransferase

SMINT2017964//PH domain

SPLEN2007689//PX domain// SH3 domain

SPLEN2012571//SCAN domain// KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type

SPLEN2022785//Polyomavirus coat protein

SPLEN2025012//Immunoglobulin domain// Immunoglobulin domain// Immunoglob

ulin domain// Immunoglobulin domain// Immunoglobulin domain
SPLEN2028417//Homeobox domain
SPLEN2036608//Zinc finger C-x8-C-x5-C-x3-H type (and similar).
STOMA2004663//Immunoglobulin domain
SYNOV2003326//TSC-22/dip/bun family
SYNOV2017179//Hepatitis C virus non-structural protein NS4a// TBC domain
SYNOV4003174//Phosphoribulokinase// Myosin head (motor domain)
SYNOV4009139//Hyaluronidase
SYNOV4009575//WD domain, G-beta repeat// Gram-negative pili assembly cha
perone// WD domain, G-beta repeat// WD domain, G-beta repeat
TIESE2000609//DNA polymerase (viral) C-terminal domain// G-patch domain/
/ Double-stranded RNA binding motif
TIESE2000904//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 t
ype// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription fa
ctor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zi
nc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type//
Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 typ
e// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TIESE2002665//Amino acid permease
TBAES2003917//Ank repeat// Ank repeat// Ank repeat// Ank repeat
TBAES2007428//Scorpion short toxins// EGF-like domain// EGF-like domain
TESOP2002005//E7 protein, Early protein
TESTI2001364//Pyridine nucleotide-disulphide oxidoreductase// lactate/ma
late dehydrogenase
TESTI2005112//Respiratory-chain NADH dehydrogenase, 30 Kd subunit
TESTI2005564//EF hand
TESTI2006543//Collagen triple helix repeat (20 copies)
TESTI2007490//UDP-glucuronosyl and UDP-glucosyl transferases

TESTI2009739//Tropomyosins// Domain of unknown function
TESTI2011020//Keratin, high sulfur B2 protein
TESTI2018335//NADH-ubiquinone/plastoquinone oxidoreductase chain 4L// Transmembrane amino acid transporter protein// Amino acid permease
TESTI2018867//FF domain
TESTI2021112//Carbamoyl-phosphate synthase (CPSase)
TESTI2021654//Glycosyl hydrolases family 11
TESTI2022323//7 transmembrane receptor (rhodopsin family)
TESTI2023903//Ubiquitin family// Gram-negative pili assembly chaperone
TESTI2024267//Transmembrane amino acid transporter protein// Ion transport protein
TESTI2030901//Glutathione S-transferases.
TESTI2034913//Intermediate filament proteins// Intermediate filament proteins
TESTI2036285//Ubiquitin family// Ubiquitin family// Ubiquitin family
TESTI2036822//Integral membrane protein// AN1-like Zinc finger// DHHC zinc finger domain
TESTI2037877//Flavin containing amine oxidase
TESTI2040377//Phorbol esters/diacylglycerol binding domain (C1 domain)// Zinc finger, C3HC4 type (RING finger)// PHD-finger// Zinc finger present in dystrophin, CBP/p300// Zinc finger, C3HC4 type (RING finger)
TESTI2049041//TPR Domain// TPR Domain
TESTI2049062//short chain dehydrogenase
TESTI2052670//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
TESTI4000370//Keratin, high sulfur B2 protein// Bacterial regulatory proteins, gntR family
TESTI4000621//SNF2 and others N-terminal domain// 6-O-methylguanine DNA methyltransferase// Rel homology domain (RHD).// Helicases conserved C-t

finger, C2H2 type// Zinc finger, C2H2 type
TESTI4004031//Domain of unknown function
TESTI4004539//Integral membrane protein// Sodium Bile acid symporter family
TESTI4004695//Leptin
TESTI4005322//KRAB box// Fungal cellulose binding domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// TRAF-type zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TESTI4005399//Divalent cation transporter// Divalent cation transporter
TESTI4005470//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TESTI4005653//Collagen triple helix repeat (20 copies)
TESTI4007671//Thioredoxin
TESTI4007965//Adaptin N terminal region// Gamma-adaptin, C-terminus
TESTI4008305//Collagen triple helix repeat (20 copies)// Herpesvirus Glycoprotein B
TESTI4010544//Cytochrome C and Quinol oxidase polypeptide I// Sodium/hydrogen exchanger family// Ion transport protein// Cyclic nucleotide-binding domain
TESTI4010721//Ribonucleotide reductase
TESTI4010902//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
TESTI4011926//Gag P30 core shell protein
TESTI4012960//Influenza RNA-dependent RNA polymerase subunit PA// Repol

ysin family propeptide// Leptin

TESTI4013474//Nuclear transition protein 2// Phorbol esters/diacylglycerol binding domain (C1 domain)// RhoGAP domain

TESTI4013742//Leucine Rich Repeat// Leucine Rich Repeat// Hantavirus nucleocapsid protein// Troponin// Formin Homology 2 Domain// Apolipoprotein A1/A4/E family

TESTI4014415//Ribosomal protein S8// Uncharacterized protein family// Domain of unknown function// Sodium/hydrogen exchanger family// Ion transport protein// Cyclic nucleotide-binding domain

TESTI4017854//Hepatitis C virus non-structural protein E2/NS1

TESTI4020342//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// Protein phosphatase 2A regulatory subunit PR55// WD domain, G-beta repeat

TESTI4020596//Calpain family cysteine protease// Calpain large subunit, domain III// C2 domain

TESTI4020819//Clq domain

TESTI4021129//GAF domain

TESTI4021197//C2 domain// PDZ domain (Also known as DHR or GLGF).// Regulator of G protein signaling domain// Regulator of G protein signaling domain

TESTI4021569//ABC transporter transmembrane region.

TESTI4022158//Immunoglobulin domain// Thrombospondin type 1 domain// Thrombospondin type 1 domain// ZU5 domain// Death domain

TESTI4023096//ABC 3 transport family// Amino acid permease// Cystatin domain

TESTI4024294//Chorion protein

TESTI4024494//Zinc finger, C3HC4 type (RING finger)// Peroxidase// Zinc finger, C3HC4 type (RING finger)// B-box zinc finger.// Scorpion short t

oxins

TESTI4026080//Nucleosome assembly protein (NAP)// Lipoate-protein ligase
B// Asparaginase// ABC transporter

TESTI4028042//WD domain, G-beta repeat// WD domain, G-beta repeat// WD d
omain, G-beta repeat// Fibrillar collagen C-terminal domain

TESTI4028182//3'5'-cyclic nucleotide phosphodiesterase// Elongation fact
or Tu family

TESTI4029731//Ras family

TESTI4030864//Ribosomal protein L36

TESTI4031066//Lipoate-protein ligase B// KE2 family protein

TESTI4031173//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain

TESTI4032128//Amyloid A4 extracellular domain// Kunitz/Bovine pancreatic
trypsin inhibitor domain

TESTI4032913//Zinc finger present in dystrophin, CBP/p300// Ank repeat//
Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank re
peat

TESTI4033177//K-box region// Dual specificity phosphatase, catalytic dom
ain// Penicillin amidase

TESTI4035898//Kelch motif// Kelch motif// Kelch motif

TESTI4036048//PX domain

TESTI4037949//BTB/POZ domain// Kelch motif// Kelch motif// Kelch motif//
Kelch motif// Glycophorin A// Kelch motif// Kelch motif

TESTI4039451//Adaptin N terminal region

TESTI4039904//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fin
ger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc
finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H
2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger,
C2H2 type// Zinc finger, C2H2 type

TESTI4040559//Transmembrane region cyclic Nucleotide Gated Channel// Cyclic nucleotide-binding domain

TESTI4040598//Cytochrome P450

TESTI4041049//Calponin homology (CH) domain

TESTI4041482//Archaeal ATPase

TESTI4041984//EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// EB module// EGF-like domain// EGF-like domain// EGF-like domain// EGF-like domain// TB domain// EGF-like domain// EGF-like domain// TB domain// EGF-like domain// EGF-like domain

TESTI4043166//Formin Homology 2 Domain

TESTI4046073//Dockerin domain type I// RhoGAP domain

TESTI4046873//TPR Domain// TPR Domain// TPR Domain// TPR Domain

TESTI4047328//von Willebrand factor type D domain// Trypsin Inhibitor like cysteine rich domain// Chitin binding domain// von Willebrand factor type D domain// Trypsin Inhibitor like cysteine rich domain// Metallothionein

TESTI4047569//Keratin, high sulfur B2 protein

TESTI4047808//Eukaryotic protein kinase domain// Eukaryotic protein kinase domain

TESTI4049786//Mur ligase family// Hexokinase// Hexokinase

TESTI4049899//Scavenger receptor cysteine-rich domain// CUB domain

TESTI4051015//Major intrinsic protein// Major intrinsic protein

TESTI4051054//B-box zinc finger.

TESTI4051424//Immunoglobulin domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Fibronectin type III domain// Aldo/keto reductase family// Immunoglobulin domain// Thioredoxin// Immunoglobulin domain// Immunoglobulin domain

TESTI4051865//PDZ domain (Also known as DHR or GLGF).// Collagen triple

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THYMU3014173//Class I Histocompatibility antigen, domains alpha 1 and 2
THYMU3014372//Integrase Zinc binding domain// Aldo/keto reductase family
// MCM2/3/5 family
THYMU3015042//Polyomavirus coat protein
THYMU3015571//Chaperonins 10 Kd subunit
THYMU3015647//Domain of unknown function// Latrophilin/CL-1-like GPS domain// CbiM// 7 transmembrane receptor (Secretin family)
THYMU3016518//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
THYMU3017761//Gag P30 core shell protein
THYMU3019476//Matrix protein (MA), p15
THYMU3020221//Immunoglobulin domain// Fibronectin type II domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
THYMU3021404//Sugar (and other) transporter
THYMU3021586//Helix-loop-helix DNA-binding domain
THYMU3021755//HC03- transporter family
THYMU3022434//Zinc finger, C2H2 type// MOZ/SAS family
THYMU3023400//Transmembrane amino acid transporter protein// Large-conductance mechanosensitive channel, MscL// CbiM// DNA gyrase/topoisomerase IV, subunit A
THYMU3025118//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
THYMU3025642//von Hippel-Lindau disease tumor suppressor protein
THYMU3025683//Heavy-metal-associated domain// Vacuolar sorting protein 9 (VPS9) domain// chorismate binding enzyme// Ras association (RalGDS/AF-6) domain
THYMU3026000//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc

finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
THYMU3026306//FliP family// Glycosyl hydrolase family 47
THYMU3026479//Glutathione S-transferases.
THYMU3026532//Plexin repeat// Integrins, beta chain
THYMU3030072//KRAB box// Zinc finger, C2H2 type// Zinc finger, C2H2 type
// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 t
ype// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H
2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type//
Zinc finger, C2H2 type// Zinc finger, C2H2 type// DnaJ central domain (4
repeats)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finge
r, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
THYMU3030752//K+ channel tetramerisation domain
THYMU3031878//PAP2 superfamily
THYMU3032798//Eukaryotic protein kinase domain
THYMU3033626//NOL1/NOP2/sun family
THYMU3033649//Immunoreceptor tyrosine-based activation motif
THYMU3034671//Histone deacetylase family
THYMU3036953//Trypsin
THYMU3037617//FYVE zinc finger// AN1-like Zinc finger
THYMU3037772//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
THYMU3038158//Collagen triple helix repeat (20 copies)// Collagen triple
helix repeat (20 copies)// Collagen triple helix repeat (20 copies)
THYMU3040126//Metallothionein
THYMU3040172//Scavenger receptor cysteine-rich domain// Scavenger recept
or cysteine-rich domain// Scavenger receptor cysteine-rich domain
THYMU3040746//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
THYMU3040829//RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

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TRACH3005699//SEA domain// SEA domain
TRACH3006379//Intermediate filament proteins
TRACH3006800//Fungalysin metallopeptidase (M36)// SEA domain// SEA domain// SEA domain
TRACH3007689//Ank repeat// Ank repeat// Ank repeat// TPR Domain// TPR Domain// TPR Domain
TRACH3009008//Pyridine nucleotide-disulphide oxidoreductase
TRACH3009061//Papain family cysteine protease// ABC transporter
TRACH3010079//Mov34/MPN/PAD-1 family
TRACH3010167//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TRACH3011082//Immunoglobulin domain
TRACH3011184//Immunoglobulin domain
TRACH3011313//Aminotransferase class IV
TRACH3011538//RhoGEF domain// PH domain
TRACH3012106//FERM domain (Band 4.1 family)
TRACH3012460//Collagen triple helix repeat (20 copies)
TRACH3012659//Immunoglobulin domain
TRACH3015346//Uncharacterized protein family UPF0004// Uncharacterized protein family UPF0004
TRACH3015354//Lectin (probable mannose binding)
TRACH3015951//BTB/POZ domain// Zinc finger, C2H2 type// Zinc finger, C3H4 type (RING finger)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TRACH3016455//Calpain family cysteine protease// Calpain large subunit, domain III
TRACH3016805//Ank repeat// Ank repeat// Ank repeat// Ank repeat// Ank re

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TRACH3022296//DnaJ domain

TRACH3022758//EF hand// EF hand

TRACH3023203//Flavivirus polyprotein propeptide

TRACH3023373//EF hand// EF hand// Reovirus viral attachment protein sigma 1// Peptide hormone

TRACH3023516//FKBP-type peptidyl-prolyl cis-trans isomerases// FKBP-type peptidyl-prolyl cis-trans isomerases// FKBP-type peptidyl-prolyl cis-trans isomerases// FKBP-type peptidyl-prolyl cis-trans isomerases// EF hand// EF hand

TRACH3024020//Eukaryotic protein kinase domain

TRACH3024081//E1-E2 ATPase

TRACH3024342//Metallo-beta-lactamase superfamily

TRACH3024512//Chitin synthase// von Willebrand factor type A domain

TRACH3025316//Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats// Armadillo/beta-catenin-like repeats// Beta-lactamase// Armadillo/beta-catenin-like repeats

TRACH3026299//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain

TRACH3026303//Rhodanese-like domain// Integrase Zinc binding domain// Integrase Zinc binding domain

TRACH3026650//IPT/TIG domain// IPT/TIG domain// IPT/TIG domain// Clq domain// EF hand// EF hand// Growth-Arrest-Specific Protein 2 Domain// Potyvirus P1 protease

TRACH3027229//Acyltransferase

TRACH3027701//Thermophilic metalloprotease (M29)

TRACH3028180//SCAN domain// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// PHD-finger// Zinc finger, C2H2 type// Zinc finger, C

2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger
, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc fin
ger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
TRACH3028441//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
TRACH3028837//Calponin homology (CH) domain
TRACH3028855//R3H domain// Uncharacterized protein family UPF0024
TRACH3029329//Fes/CIP4 homology domain// Hrl repeat motif// ENV polyprot
ein (coat polyprotein)// ATP synthase Alpha chain, C terminal
TRACH3029462//Spectrin repeat// Spectrin repeat// Protein of unknown fun
ction// Spectrin repeat// Bacterial flagellin N-terminus// Spectrin repe
at// Spectrin repeat// Spectrin repeat// Caulimovirus movement protein//
Spectrin repeat// Spectrin repeat// Spectrin repeat// UvrB/uvrC motif//
Spectrin repeat// Spectrin repeat// Spectrin repeat// KE2 family protei
n
TRACH3029670//Immunoglobulin domain// Immunoglobulin domain// Immunoglob
ulin domain// Immunoglobulin domain
TRACH3030176//Beige/BEACH domain// WD domain, G-beta repeat// WD domain,
G-beta repeat
TRACH3030855//Serpins (serine protease inhibitors)
TRACH3031316//Immunoglobulin domain
TRACH3031660//Regulatory subunit of type II PKA R-subunit// Cyclic nucle
otide-binding domain// Cyclic nucleotide-binding domain
TRACH3031678//Natural resistance-associated macrophage protein
TRACH3032150//Calcium channel extracellular region// Pyridoxal-dependent
decarboxylase conserved domain
TRACH3032570//PDZ domain (Also known as DHR or GLGF).// PDZ domain (Also
known as DHR or GLGF).
TRACH3034680//Immunoglobulin domain// Immunoglobulin domain// Immunoglob

ulin domain// Immunoglobulin domain
TRACH3036103//Immunoglobulin domain
TRACH3036750//BTK motif// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// GATA zinc finger// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Ribonuclease T2 family
TRACH3037505//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
TRACH3038399//Eukaryotic protein kinase domain// Eukaryotic protein kinase domain
TSTOM2001571//Eukaryotic protein kinase domain
TUTER2001433//Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain// Immunoglobulin domain
UTERU2016669//Helix-hairpin-helix motif.// Helix-hairpin-helix motif.
UTERU2024042//Eukaryotic protein kinase domain
UTERU2037423//Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Transcription factor S-II (TFIIIS)// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type// Zinc finger, C2H2 type
UTERU3001029//WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat// WD domain, G-beta repeat
UTERU3001394//EGF-like domain
UTERU3001946//Fungalsin metalloproteinase (M36)// SEA domain// SEA domain
UTERU3006720//RhoGAP domain
UTERU3009775//PDZ domain (Also known as DHR or GLGF).
UTERU3010409//Immunoglobulin domain

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rmadillo/beta-catenin-like repeats

UTERU3017626//Ion transport protein// Transmembrane region cyclic Nucleotide Gated Channel

UTERU3017995//UBX domain

UTERU3018172//Bacterial regulatory proteins, crp family

UTERU3018255//Thrombospondin type 1 domain

UTERU3019708//Viral (Superfamily 1) RNA helicase

UTERU3020090//DNA polymerase (viral) C-terminal domain

UTERU3021231//PX domain

UTERU3021850//Thrombospondin type 1 domain// DnaJ central domain (4 repeats)

UTERU3022168//DNA polymerase family B// C2 domain// C2 domain// C2 domain// C2 domain// C2 domain

UTERU3022588//bZIP transcription factor

UTERU3023141//Double-stranded RNA binding motif

【 0 1 9 2 】

実施例 6 . 全長塩基配列および推定アミノ酸配列の相同性検索による機能カテゴリー分類

全長塩基配列および推定アミノ酸配列のSwiss-Prot、nr、RefSeqの各データベースを対象に行った相同性検索の結果（相同性検索結果データ参照）から、クローン中にコードされる蛋白質の機能予測、カテゴリー分類を行った。

【 0 1 9 3 】

分泌・膜蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中に growth factor, cytokine, hormone, signal, transmembrane, membrane, extracellular matrix, receptor, G-protein coupled receptor, ionic channel, voltage-gated channel, calcium channel, cell adhesion, collagen, connective tissue 等、分泌・膜蛋白質と推定される記載があった、もしくはPsortとSOSUIによる推定ORFの解析の結果、シグナルシーケンスや膜貫通領域があったクローンである。

【0194】

糖蛋白質関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中に glycoprotein 等、糖蛋白質関連蛋白質と推定される記載があったクローンである。

【0195】

シグナル伝達関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中に serine/threonine-protein kinase, tyrosine-protein kinase, SH3 domain, SH2 domain等、シグナル伝達関連蛋白質と推定される記載があったクローンである。

【0196】

転写関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中に transcription regulation, zinc finger, homeobox 等、転写関連蛋白質と推定される記載があったクローンである。

【0197】

疾患関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中に disease mutation, syndrome 等、疾患関連蛋白質と推定される記載があった、あるいは全長塩基配列に対するSwiss-Protヒットデータ、及びnr、RefSeq ヒットデータが、ヒトの遺伝子と疾患のデータベースであるOnline Mendelian Inheritance in Man (OMIM)に登録されている遺伝子、蛋白質であったクローンである。

【0198】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にmetabolism, oxidoreductase, E.C.No. (Enzyme commission number)等、酵素・代謝関連蛋白質と推定される記載があったクローンである。

【0199】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンとは、cell division, cell cycle, mitosis, chromosomal protein, cell growth, apoptosis等、細胞分裂・増殖関連蛋白質と推定される記載があったクローンである。

【0200】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にstructural protein, cytoskeleton, actin-binding, microtubules等、細胞骨格関連蛋白質と推定される記載があったクローンである。

【0201】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にnuclear protein, RNA splicing, RNA processing, RNA helicase, polyadenylation等、核蛋白質・RNA合成関連蛋白質と推定される記載があったクローンである。

【0202】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にtranslation regulation, protein biosynthesis, amino-acid biosynthesis, ribosomal protein, protein transport, signal recognition particle等、蛋白質合成・輸送関連蛋白質と推定される記載があったクローンである。

【0203】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にheat shock, DNA repair, DNA damage等、細胞防御関連蛋白質と推定される記載があったクローンである。

【0204】

発生・分化関連蛋白質のカテゴリーに属すると推定されたクローンとは、developmental protein等、発生・分化関連蛋白質と推定される記載があったクローンである。

【0205】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にDNA-binding, RNA-binding等と記載があったクローンである。

【0206】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンとは、ヒットデータ中にATP-binding, GTP-binding等と記載があったクローンである。

【 0 2 0 7 】

この機能カテゴリー分類では一つのクローンが上記の複数のカテゴリーに該当する場合は、そのまま複数のカテゴリーに分類した。ただし、蛋白質の機能は必ずしも分類された機能カテゴリーに限定されるわけではなく、今後その他の機能も明らかになる可能性がある。

【 0 2 0 8 】

分泌・膜蛋白質に属すると推定されたクローンは、以下の 5 5 1 クローンであった。

3NB692004045, ADIPS2000069, ADRGL2010315, ASTRO2015162, BLADE2001031, BLADE2002744, BLADE2007744, BRACE2003628, BRACE2012528, BRACE2013126, BRACE2017397, BRACE2017580, BRACE2017992, BRACE2023633, BRACE2030039, BRACE2035191, BRACE3001403, BRACE3001973, BRACE3002264, BRACE3002756, BRACE3004767, BRACE3004981, BRACE3007869, BRACE3009392, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3015898, BRACE3018083, BRACE3021517, BRACE3021805, BRACE3022051, BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024879, BRACE3026345, BRACE3026456, BRACE3026802, BRACE3028360, BRACE3029021, BRACE3030538, BRACE3031372, BRACE3031579, BRACE3031728, BRACE3032385, BRACE3032537, BRACE3032980, BRACE3033525, BRACE3034964, BRACE3034993, BRACE3037637, BRACE3037803, BRACE3038570, BRACE3039358, BRACE3039378, BRACE3040644, BRACE3040863, BRACE3042326, BRACE3042409, BRACE3042432, BRACE3044090, BRACE3046049, BRACE3046466, BRACE3048565, BRACE3050504, BRACE3051144, BRACE3051621, BRACE3052486, BRALZ2010842, BRALZ2011337, BRALZ2013690, BRAMY2015516, BRAMY2021098, BRAMY2025495, BRAMY2037609, BRAMY2041507, BRAMY2044686, BRAMY2046537, BRAMY3002886, BRAMY3004126, BRAMY3007449, BRAMY3009556, BRAMY3009904, BRAMY3010654, BRAMY3010902, BRAMY3015549, BRAMY3016829, BRAMY3018248, BRAWH2000256, BRAWH2010364, BRAWH2011812, BRAWH2011958, BRAWH2012866, BRAWH2014053, BRAWH2016209, BRAWH2016305, BRAWH3001053, BRAWH3001783, BRAWH3001833, BRAWH3003573, BRAWH3005892, BRAWH3008867, BRAWH3010461, BRAWH3010657, BR

AWH3011907, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013049, BRAWH3014609, BRAWH3015175, BRAWH3016123, BRAWH3017259, BRAWH3018063, BRAWH3018548, BRAWH3018969, BRAWH3019529, BRAWH3019820, BRAWH3020200, BRAWH3020884, BRAWH3021012, BRAWH3021641, BRAWH3022347, BRAWH3023156, BRAWH3023274, BRAWH3023415, BRAWH3023421, BRAWH3024186, BRAWH3024242, BRAWH3027574, BRAWH3027880, BRAWH3028223, BRAWH3028754, BRAWH3029806, BRAWH3030810, BRAWH3032298, BRAWH3034114, BRAWH3034134, BRAWH3035914, BRAWH3036270, BRAWH3038055, BRAWH3038324, BRAWH3040711, BRAWH3040900, BRAWH3042132, BRAWH3042772, BRAWH3042996, BRAWH3043498, BRAWH3043623, BRAWH3044151, BRAWH3044676, BRAWH3046196, BRAWH3047063, BRAWH3048374, BRAWH3048724, BRAWH3049068, BRAWH3049544, BRCAN2002662, BRCAN2003269, BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2015402, BRCAN2018269, BRCAN2019653, BRCAN2019907, BRCAN2020234, BRCAN2020412, BRCAN2020972, BRCAN2021325, BRCAN2022126, BRCOC2006164, BRCOC2006639, BRCOC2009638, BRHIP2006921, BRHIP2020930, BRHIP2021929, BRHIP3000859, BRHIP3001878, BRHIP3002000, BRHIP3002124, BRHIP3003063, BRHIP3003306, BRHIP3003395, BRHIP3004774, BRHIP3005801, BRHIP3005944, BRHIP3006950, BRHIP3007195, BRHIP3007424, BRHIP3007960, BRHIP3008320, BRHIP3010289, BRHIP3011269, BRHIP3011831, BRHIP3012185, BRHIP3012357, BRHIP3012997, BRHIP3013078, BRHIP3016032, BRHIP3017146, BRHIP3017558, BRHIP3019956, BRHIP3020733, BRHIP3021019, BRHIP3025795, BRHIP3025844, BRHIP3027160, BRHIP3027191, BRHIP3028742, BRHIP3029530, BRHIP3030230, BRHIP3031733, BRHIP3035222, BRHIP3035754, BRHIP3036715, BRHIP3036936, BRHIP3037810, BRHIP3039430, BRHIP3039509, BRSSN2004710, BRSSN2018218, BRSTN2010089, BRSTN2011688, BRSTN2011899, BRSTN2011961, BRTHA2000969, BRTHA2003759, BRTHA2012189, BRTHA2014647, BRTHA2018304, BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566, BRTHA2020721, BRTHA2020781, BRTHA2021212, BRTHA2021440, BRTHA2021450, BRTHA2022914, BRTHA2022968, BRTHA2023437, BRTHA2026311, BRTHA2027250, BRTHA2030036, BRTHA2031917, BRTHA2033155, BRTHA2033320, BRTH

A2033469, BRTHA2033683, BRTHA2036055, BRTHA2036295, BRTHA3003225, BRTHA3006593, BRTHA3010135, BRTHA3010540, BRTHA3010717, BRTHA3011194, BRTHA3011998, BRTHA3012265, BRTHA3013882, BRTHA3014835, BRTHA3016616, BRTHA3018623, BRTHA3026161, BRTHA3027820, BRTHA3028505, CHONS2001287, CHONS2001797, CHONS2002419, COLON2004351, COLON2005623, COLON2005735, CTONG2008989, CTONG2020582, CTONG2027150, CTONG3001605, CTONG3002588, CTONG3008223, FCBBF3012443, FEBRA2023498, FEBRA2026977, FEHRT2002708, FEKID2002231, FEKID2002493, FELNG2000720, FELNG2001706, HCHON2009766, HSYR A2004550, JCMLC1000159, JCMLC2000273, JCMLC2002095, JCMLC2002751, KIDNE2004531, KIDNE2015987, KIDNE2017153, LYMPB1000158, LYMPB2002236, LYMPB2002458, LYMPB2002478, MESAN2014624, NETRP2004090, NETRP2004434, NETRP2005282, NETRP2005849, NETRP2008582, NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3009524, NT2RP7019682, NT2RP8001605, NT2RP8003787, NT2RP8008057, OCBBF2000831, OCBBF2004478, OCBBF2007039, OCBBF2009536, OCBBF2018229, OCBBF2018618, OCBBF2036019, OCBBF3003745, OCBBF3007704, OCBBF3021502, OCBBF3022123, OCBBF3022576, OCBBF3023175, OCBBF3023993, OCBBF3025475, OCBBF3025887, OCBBF3026979, OCBBF3028001, PEBLM2003935, PEBLM2005615, PLACE5000522, PLACE6000012, PLACE6010936, PLACE6019674, PLACE7000266, PLACE7000707, PLACE7001759, PLACE7003639, PLACE7006090, PLACE7006498, PLACE7008136, PLACE7011269, PLACE7012111, PLACE7016321, PLACE7016454, PUAEN2000684, SMINT2003641, SPLEN2011252, SPLEN2025012, SPLEN2031004, SPLEN2034551, SPLEN2035615, SPLEN2042051, STOMA2004663, SYNOV4009139, TIESE2002665, TBAES2005361, TBAES2007428, TESOP2008556, TESTI2003768, TESTI2007490, TESTI2018335, TESTI2022323, TESTI2024267, TESTI2028613, TESTI2036822, TESTI2037085, TESTI2037657, TESTI2037877, TESTI2046188, TESTI2049041, TESTI2052670, TESTI4001037, TESTI4002072, TESTI4002889, TESTI4003602, TESTI4004539, TESTI4004653, TESTI4005399, TESTI4007671, TESTI4010544, TESTI4010721, TESTI4013774, TESTI4014415, TESTI4014932, TESTI4014977, TESTI4017647, TESTI4017854, TESTI4019149, TESTI4

021197, TESTI4021377, TESTI4021569, TESTI4022158, TESTI4023096,
TESTI4023654, TESTI4024494, TESTI4026680, TESTI4027170, TESTI4028042, TE
STI4031173, TESTI4031818, TESTI4032128, TESTI4034973, TESTI4035872, TEST
I4035989, TESTI4036012, TESTI4037949, TESTI4038047, TESTI4040559, TESTI4
041049, TESTI4043067, TESTI4043371, TESTI4045168, TESTI4046450,
TESTI4047119, TESTI4048296, TESTI4048545, TESTI4051015, TESTI4051858, TE
STI4052219, TESTI4052430, TESTI4052598, THYMU3002825, THYMU3003007, THYM
U3003350, THYMU3008935, THYMU3009755, THYMU3011360, THYMU3013197, THYMU3
014173, THYMU3015457, THYMU3015647, THYMU3016518, THYMU3018151,
THYMU3019605, THYMU3021404, THYMU3022211, THYMU3022528, THYMU3022668, TH
YMU3023107, THYMU3023400, THYMU3025118, THYMU3025313, THYMU3025642, THYM
U3026306, THYMU3026532, THYMU3026869, THYMU3027540, THYMU3028461, THYMU3
029795, THYMU3031878, THYMU3032032, THYMU3033649, THYMU3033754,
THYMU3034099, THYMU3034616, THYMU3036310, THYMU3036934, THYMU3036953, TH
YMU3037192, THYMU3037772, THYMU3038158, THYMU3038167, THYMU3040068, THYM
U3040126, THYMU3040146, THYMU3040172, THYMU3040746, THYMU3040816, THYMU3
041918, THYMU3042321, THYMU3043688, THYMU3043779, THYMU3044188,
THYMU3045510, THYMU3047115, THYMU3047156, THYMU3047542, THYMU3047760, TK
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TRACH3013900, TRACH3014063, TRACH3014580, TRACH3015136, TRACH3015346, TR
ACH3016368, TRACH3016885, TRACH3016992, TRACH3017409, TRACH3018191, TRAC
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019621, TRACH3019807, TRACH3020930, TRACH3021023, TRACH3021544,
TRACH3022758, TRACH3023063, TRACH3023203, TRACH3023516, TRACH3023945, TR
ACH3024081, TRACH3024671, TRACH3025346, TRACH3026542, TRACH3027681, TRAC
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036103, TRACH3036278, TSTOM2002682, UTERU3005422, UTERU3010029,

UTERU3011092, UTERU3011398, UTERU3011837, UTERU3012414, UTERU3015647, UTERU3016273, UTERU3017626, UTERU3021850, UTERU3022168, UTERU3022922, UTERU3023413

【 0 2 0 9 】

糖蛋白質関連蛋白質に属すると推定されたクローンは、以下の 1 1 4 クローンであった。

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3001403, BRACE3001973, BRACE3002264, BRACE3009392, BRACE3026345, BRACE3032385, BRACE3039358, BRACE3039378, BRACE3042432, BRACE3046466, BRACE3051621, BRAMY3004126, BRAWH2012866, BRAWH3001783, BRAWH3003573, BRAWH3014609, BRAWH3023156, BRAWH3024186, BRAWH3029806, BRAWH3040900, BRAWH3043623, BRAWH3044151, BRAWH3049544, BRCAN2003269, BRCAN2021325, BRHIP3005944, BRHIP3007424, BRHIP3010289, BRHIP3011269, BRHIP3011567, BRHIP3030230, BRHIP3036715, BRHIP3036936, BRHIP3039509, BRTHA2019726, BRTHA2020721, BRTHA2022968, BRTHA2025869, BRTHA2027250, BRTHA2031917, BRTHA2033155, BRTHA2033683, BRTHA3010135, CHONS2001287, COLON2004351, FEKID2002493, FELNG2000720, JCMLC1000159, JCMLC2000273, JCMLC2002095, JCMLC2002751, KIDNE2015987, LYMPB2002458, NT2RI3005923, NT2RI3009524, OCBBF2000831, OCBBF2004478, OCBBF2007039, OCBBF2018618, OCBBF3026979, PEBLM2005615, PLACE6001933, PLACE6010936, PLACE7006090, PLACE7012111, SPLEN2025012, STOMA2004663, TIESE2002665, TESTI2007490, TESTI2022323, TESTI2037657, TESTI2052670, TESTI4001517, TESTI4014932, TESTI4031173, THYMU3014173, THYMU3015647, THYMU3016518, THYMU3020221, THYMU3025118, THYMU3026532, THYMU3032032, THYMU3037772, THYMU3040172, TKIDN2011160, TLUNG2001445, TRACH3005274, TRACH3009061, TRACH3015136, TRACH3018524, TRACH3018907, TRACH3019058, TRACH3019370, TRACH3019621, TRACH3019807, TRACH3020930, TRACH3021023, TRACH3023516, TRACH3025346, TRACH3026299, TRACH3028441, TRACH3029670, TRACH3031678, TRACH3034680, TRACH3037505, TRACH3038399, TATER2001433, UTERU3011398, UTERU3011837, UTERU3015647, UTERU3021850

【 0 2 1 0 】

シグナル伝達関連蛋白質に属すると推定されたクローンは、以下の 7 1 クローンであった。

BRACE3002344, BRACE3017253, BRACE3031315, BRACE3036283, BRACE3042046, BRACE3044172, BRACE3046491, BRACE3046609, BRAMY3009491, BRAMY3015547, BRAMY3017920, BRAWH3017180, BRAWH3019026, BRAWH3027806, BRAWH3032340, BRAWH3042438, BRAWH3047644, BRCAN2010665, BRHIP3006294, BRHIP3011460, BRHIP3011567, BRHIP3033557, BRHIP3037543, BRHIP3041587, BRTHA2026290, BRTHA2035743, BRTHA3011187, BRTHA3021708, BRTHA3025073, BRTHA3026916, KIDNE2010049, N1ESE2000698, OCBBF3005330, OCBBF3006986, OCBBF3009244, OCBBF3025630, PLACE6000055, PLACE6001933, PLACE7009936, PLACE7011559, PLACE7014247, PUAEN2006639, SKMUS2008585, SPLEN2007689, TESTI2021654, TESTI2040377, TESTI4010902, TESTI4013474, TESTI4046073, TESTI4049786, TESTI4051865, THYMU3013785, THYMU3025683, THYMU3032798, TRACH3003037, TRACH3003357, TRACH3005173, TRACH3018519, TRACH3018606, TRACH3024020, TRACH3026650, TRACH3027701, TRACH3029462, TRACH3030176, TRACH3038399, TS TOM2001571, TSTOM2002611, UTERU2024042, UTERU3001029, UTERU3010919, UTERU3021231

【 0 2 1 1 】

転写関連蛋白質に属すると推定されたクローンは、以下の 1 0 6 クローンであった。

ASTRO2016114, BEAST2000981, BRACE2012947, BRACE2019348, BRACE3025719, BRACE3026844, BRACE3034183, BRACE3041162, BRACE3046152, BRAMY2040915, BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027, BRAMY3018754, BRAWH3000446, BRAWH3005886, BRAWH3011577, BRAWH3013009, BRAWH3013264, BRAWH3017477, BRAWH3023172, BRAWH3028796, BRAWH3031342, BRAWH3032571, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3038827, BRCOC2012386, BRHIP2023735, BRHIP2027077, BRHIP2029529, BRHIP3004725, BRHIP3027651, BRHIP3028246, BRTHA2024712, BRTHA3000456, BRTHA3003736, BRTHA3010212,

BRTHA3014000, BRTHA3028339, CHONS2000797, CHONS2002829, CTONG2001932, CTONG2011801, D9OST2003106, FCBBF3020030, FCBBF5000384, HCASM2008154, NETRP2004017, NT2RI3008179, NT2RI3009480, NT2RP8003490, NTONG2003805, NTONG2008483, OCBBF2016928, OCBBF3005330, OCBBF3008392, OCBBF3020263, OCBBF3021361, OCBBF3022166, PLACE7002303, PLACE7005169, PLACE7009757, SPLEN2012571, SPLEN2028417, SYNOV2003326, TIESE2000904, TESTI2040377, TESTI4001679, TESTI4002799, TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4039904, TESTI4052775, THYMU3008105, THYMU3012983, THYMU3014372, THYMU3020869, THYMU3021586, THYMU3022434, THYMU3026000, THYMU3030072, THYMU3037052, THYMU3043200, TLIVE2001616, TRACH3003037, TRACH3003458, TRACH3004424, TRACH3010079, TRACH3010167, TRACH3010342, TRACH3015951, TRACH3021883, TRACH3022109, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3016070, UTERU3019708, UTERU3022588

【 0 2 1 2 】

疾患関連蛋白質に属すると推定されたクローンは、以下の 3 9 1 クローンであった。

ADIPS2000069, ASTRO2015162, ASTRO2016114, ASTRO3000154, BLADE2000256, BRACE1000475, BRACE2012838, BRACE2012947, BRACE2013009, BRACE2016896, BRACE2017397, BRACE2023744, BRACE2027382, BRACE3001403, BRACE3001973, BRACE3002756, BRACE3004767, BRACE3009392, BRACE3013418, BRACE3018083, BRACE3019941, BRACE3020669, BRACE3025719, BRACE3026345, BRACE3026802, BRACE3028998, BRACE3036283, BRACE3039378, BRACE3040644, BRACE3041059, BRACE3041162, BRACE3042046, BRACE3042432, BRACE3043597, BRACE3044172, BRACE3046152, BRACE3046466, BRACE3046609, BRACE3051621, BRACE3052321, BRALZ2010842, BRALZ2013621, BRAMY2041384, BRAMY3000692, BRAMY3004126, BRAMY3007078, BRAMY3009491, BRAMY3011501, BRAMY3011581, BRAMY3014027, BRAMY3015086, BRAMY3017920, BRAMY3018248, BRAWH2002333, BRAWH2012866, BRAWH2014053, BRAWH3001638, BRAWH3001783, BRAWH3004335, BRAWH3010602,

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【 0 2 1 3 】

このうち、Swiss-Protヒットデータ、及びnr、RefSeqヒットデータが、ヒトの遺伝子と疾患のデータベースであるOnline Mendelian Inheritance in Man (OMIM)に登録されている遺伝子、蛋白質であったクローンは以下の390クローンであった(クローン名の後ろのカッコ内は対象となったOMIM Number)。

ADIPS2000069(146900), ASTRO2015162(606106), ASTRO2016114(603899), ASTRO3000154(601594), BLADE2000256(140750), BRACE1000475(600696), BRACE2012838(605032), BRACE2012947(140580), BRACE2013009(605888), BRACE2016896(601421), BRACE2017397(115437), BRACE2023744(600763), BRACE2027382(606019), BRACE3001403(126141), BRACE3001973(600976), BRACE3002756(603143), BRACE3004767(182790), BRACE3009392(600229), BRACE3013418(182900), BRACE3018083(605268),

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BRALZ2010842(212138), BRALZ2013621(600712), BRAMY2041384(114070), BRAMY3

000692(603971), BRAMY3004126(603071), BRAMY3007078(602410), BRAMY3009491
(600286), BRAMY3011501(602869), BRAMY3011581(601243), BRAMY3014027(19454
2), BRAMY3015086(602879), BRAMY3017920(600365), BRAMY3018248(605464), BR
AWH2002333(171891), BRAWH2012866(185605), BRAWH2014053(604581), BRAWH300
1638(605003), BRAWH3001783(605514), BRAWH3004335(603244), BRAWH3010602(6
03216),

BRAWH3011577(601139), BRAWH3011623(164020), BRAWH3017180(601441), BRAWH3
017259(603143), BRAWH3018548(193065), BRAWH3019026(602033), BRAWH3021580
(179838), BRAWH3023156(137190), BRAWH3023172(603755), BRAWH3023415(60434
6), BRAWH3024186(179590), BRAWH3029385(602378), BRAWH3029538(600948), BR
AWH3031342(603971), BRAWH3032298(601995), BRAWH3032571(603277), BRAWH303
3513(604054;261510), BRAWH3034668(603486), BRAWH3034775(605800), BRAWH30
34890(606265),

BRAWH3036334(603971), BRAWH3038324(604249), BRAWH3038827(600574), BRAWH3
040900(604265), BRAWH3041492(130500), BRAWH3041556(172460), BRAWH3042438
(125855), BRAWH3042447(606323), BRAWH3042772(602878), BRAWH3043295(17903
0), BRAWH3043623(600976), BRAWH3044151(605421), BRAWH3046424(300272), BR
AWH3047565(606277), BRAWH3047644(605216), BRAWH3049544(602273), BRCAN200
3269(171060;602347), BRCAN2006051(604581), BRCAN2010665(603583), BRCAN20
20331(604851),

BRCAN2021325(114855), BRCOC2012386(602277), BRHIP2008756(605819), BRHIP2
023735(601670), BRHIP2029529(189972), BRHIP3001076(604673), BRHIP3001481
(176889), BRHIP3003984(603722;223900), BRHIP3004215(603294), BRHIP300472
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85), BRHIP3005801(605704), BRHIP3006449(604275), BRHIP3007609(426000), B
RHIP3010289(603130), BRHIP3011567(114207), BRHIP3017146(602878), BRHIP30
17855(606406),

BRHIP3021019(176879), BRHIP3023922(156570;250940), BRHIP3025795(603877),
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3029409(604156), BRHIP3030230(602367), BRHIP3032374(603197), BRHIP303500
6(604402), BRHIP3036715(142800), BRHIP3037543(602052), BRHIP3039509(6013
28), BRSSN2004710(600127), BRSTN2006466(138275), BRSTN2008475(605178), B
RSTN2011961(176790), BRSTN2012069(130590), BRSTN2016918(137780), BRTHA20
19726(147100),
BRTHA2020721(147100), BRTHA2020910(602661), BRTHA2024712(600747), BRTHA2
025869(162280), BRTHA2026071(605297), BRTHA2026290(602306), BRTHA2031917
(118946), BRTHA2033155(601873), BRTHA2033683(111000), BRTHA3003736(13351
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37), BRTHA3011998(603264), BRTHA3012265(605646), BRTHA3014547(182900), B
RTHA3021708(602654), BRTHA3021971(605609), BRTHA3023403(600597), BRTHA30
26916(601619),
BRTHA3027957(606078), CHONS2001287(146732), CHONS2002829(602981), COLON2
001829(604399), COLON2004911(603937;180100), COLON2005735(111690;111700)
, CTONG2001932(605683), CTONG2010330(606088), CTONG2011801(603971), CTON
G2014206(605609), D90ST2004417(113703), FCBBF3020030(603406), FCBBF30211
91(605119), FCBBF5000384(601737), FEBRA2013570(248600), FEBRA2026582(300
252), FEBRA2028457(164035), FEKID2002637(176875), FELNG2000720(601662),
FELNG2001953(603597),
HCASM2008154(133450), JCMLC1000159(107470;209950), JCMLC2000273(120980),
JCMLC2002095(600738), KIDNE2015987(191845), NIESE2000698(604734), NETRP
2000961(600417), NETRP2003448(179551), NETRP2004017(605344), NETRP200858
2(103195), NT2RI3008179(603808), NT2RI3009480(601804), NT2RI3009524(6042
10;600105), NT2RP8003787(605427), NT2RP8008057(603489), NTONG2003805(601
781), OCBBF2004478(604265), OCBBF2007039(605009), OCBBF2018618(102775),
OCBBF2024589(602462),
OCBBF2030927(603897), OCBBF2036019(601825;256000), OCBBF3001202(140750),
OCBBF3004487(142560), OCBBF3008392(605682), OCBBF3020263(604077), OCBBF
3022166(600848), OCBBF3025475(604148), OCBBF3025503(601653;113650), OCBB

F3025630(604141), OCBBF3026979(602319), PEBLM2005615(600242), PLACE50004
92(602142), PLACE6001933(131550), PLACE6016030(605442), PLACE7000266(188
840), PLACE7001759(600338), PLACE7002303(601542;180500;137600;604229), P
LACE7003985(109684), PLACE7004103(142695),
PLACE7006090(154360), PLACE7006268(603053), PLACE7006498(604394), PLACE7
007379(603105), PLACE7009563(300344), PLACE7009757(601804), PLACE7009936
(600365), PLACE7011559(600831), PLACE7012111(602714), PLACE7014247(60123
2), PLACE7016526(605490), PUAEN2000594(604679), SKNSH2007306(118990), SM
INT2011406(147890), SMINT2011509(606343), SMINT2014721(606090), SPLEN200
7689(233700), SPLEN2012571(603430), SPLEN2025012(146900), SPLEN2028417(1
42995),
SPLEN2033996(603853), SYNOV2003326(602960), SYNOV4009139(603551), TIESE2
000609(182465), TESTI2005112(603846), TESTI2007490(601291), TESTI2009739
(160745), TESTI2023903(605046), TESTI2030901(600436), TESTI2034913(14806
0), TESTI2052670(142461), TESTI4001517(148070), TESTI4001679(602850), TE
STI4002868(601863;209920), TESTI4003796(603132), TESTI4003944(603971), T
ESTI4004653(606106), TESTI4005322(603899), TESTI4005653(182465), TESTI40
07965(603533),
TESTI4017382(605689), TESTI4017647(603211), TESTI4018436(601754), TESTI4
020596(602537), TESTI4021197(602189), TESTI4021569(605464), TESTI4021713
(604105), TESTI4023096(604878), TESTI4026080(605575), TESTI4028182(60389
2), TESTI4031173(190197), TESTI4032128(104776), TESTI4032834(300188), TE
STI4032913(106410), TESTI4033177(602038), TESTI4036048(601272), TESTI403
9575(600951), TESTI4039904(603899), TESTI4041984(604710), TESTI4046073(3
00118;309801),
TESTI4047119(606202), TESTI4049786(142600;235700), TESTI4049899(601969),
TESTI4051015(602974), TESTI4052775(165250), THYMU3002825(604346), THYMU
3008105(194548), THYMU3012402(600686), THYMU3012983(194556), THYMU301378
5(604722), THYMU3014173(143010), THYMU3014372(116945), THYMU3014620(6056

57), THYMU3016518(147100), THYMU3020221(147100), THYMU3020869(602550), THYMU3021586(184756), THYMU3021755(605024), THYMU3022434(601408), THYMU3023400(605180),

THYMU3025118(155735), THYMU3026306(604346), THYMU3026532(600065;116920), THYMU3027671(604143), THYMU3032032(604463), THYMU3032798(601212), THYMU3033649(186780), THYMU3033759(600495), THYMU3037052(300346), THYMU3037772(147100), THYMU3038158(603033;603034), THYMU3038375(181590), THYMU3040172(186720), THYMU3040746(147110), THYMU3040816(605704), THYMU3040829(602649), THYMU3043200(605596), THYMU3047115(108730), THYMU3047760(604783), TKIDN2011160(605011),

TLIVE2007736(604990), TLUNG2000654(148059), TLUNG2001445(146900), TLUNG2001600(147130), TRACH2024730(605611), TRACH3004424(603971), TRACH3005173(151410), TRACH3005191(605333), TRACH3005699(606154), TRACH3006379(148059), TRACH3006800(606154), TRACH3008042(166945), TRACH3009008(601112), TRACH3009701(603330), TRACH3010079(604850), TRACH3010167(601804), TRACH3010342(602943), TRACH3011282(601833), TRACH3011313(113520), TRACH3011503(602862),

TRACH3012891(602397), TRACH3015951(604084), TRACH3016455(605286), TRACH3016805(106410), TRACH3018524(176882), TRACH3018907(146900), TRACH3019058(147170), TRACH3019621(191350), TRACH3020769(160776), TRACH3020930(147100), TRACH3021023(147170), TRACH3021373(606030), TRACH3021778(164035), TRACH3021883(603347), TRACH3023373(159350), TRACH3023960(603337), TRACH3024081(605867), TRACH3024671(605942), TRACH3025346(603377;212140), TRACH3026283(601517),

TRACH3026299(147170), TRACH3028441(147170), TRACH3028597(604310), TRACH3028837(602127), TRACH3029670(147170), TRACH3030855(173321), TRACH3031660(176912), TRACH3031678(600523), TRACH3032570(602217), TRACH3034680(147170), TRACH3036750(604077), TRACH3037505(147170), TRACH3038399(604032;226980), TUTER2001433(146900), UTERU2024042(602214), UTERU2037423(604077), U

TERU3001946(606154), UTERU3004635(103390), UTERU3011398(120240;158810;254090), UTERU3012293(194556),
UTERU3012414(604394), UTERU3012999(605567), UTERU3015011(602505), UTERU3015299(601825;256000), UTERU3016308(602127), UTERU3017441(604276), UTERU3017626(603788), UTERU3019708(601430), UTERU3021850(605009), UTERU3022588(123811)

【 0 2 1 4 】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の
1 6 4 クローンであった。

ASTRO2008972, BRACE1000475, BRACE2013132, BRACE2016896, BRACE2035120, BRACE3017253, BRACE3021805, BRACE3028998, BRACE3031315, BRACE3036283, BRACE3041059, BRACE3042409, BRACE3044172, BRACE3046609, BRAMY3009491, BRAMY3011581, BRAWH2002333, BRAWH2014053, BRAWH3001638, BRAWH3004335, BRAWH3011331, BRAWH3017180, BRAWH3020928, BRAWH3023415, BRAWH3023421, BRAWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3029806, BRAWH3032571, BRAWH3033513, BRAWH3034668, BRAWH3037428, BRAWH3037979, BRAWH3041556, BRAWH3042438, BRAWH3043295, BRAWH3044151, BRAWH3046424, BRAWH3047692, BRAWH3049544, BRCAN2003814, BRCAN2006051, BRCAN2015402, BRCAN2021325, BRHIP3001481, BRHIP3003126, BRHIP3005307, BRHIP3005673, BRHIP3007195, BRHIP3007223, BRHIP3011082, BRHIP3011269, BRHIP3021019, BRHIP3023922, BRHIP3032374, BRHIP3035006, BRHIP3037543, BRHIP3041587, BRSSN2004710, BRSTN2006466, BRSTN2011961, BRTHA2005448, BRTHA2010672, BRTHA2025869, BRTHA2026311, BRTHA2033155, BRTHA2035743, BRTHA3003736, BRTHA3010135, BRTHA3010469, BRTHA3023403, CHONS2002829, COLON2004351, CTONG2010330, CTONG2020582, CTONG3001605, FCBBF3001018, FCBBF3021191, FCBBF5000384, FEBRA2013570, FEBRA2026582, FEKID2002637, HSYRA2004550, KIDNE2010049, NETRP2000961, NT2RI2004818, NT2RP7016508, OCBBF2007039, OCBBF2024589, OCBBF2036019, OCBBF3004487, OCBBF3005330, OCBBF3009244, PLACE5000492, PLACE6001933, PLACE7001759, PLACE7003985, PLACE7004103, PLACE7004961,

PLACE7006090, PLACE7006268, PLACE7007379, PLACE7011559, PLACE7012111, PLACE7014247, PLACE7016526, SKMUS2008585, SMINT2011509, SMINT2012179, SMINT2014721, SPLEN2007689, SYNOV4009139, TBAES2007428, TESTI2005112, TESTI2007490, TESTI2021654, TESTI2040377, TESTI2049062, TESTI4000621, TESTI4002799, TESTI4007671, TESTI4020596, TESTI4033177, TESTI4049786, TESTI4052219, THYMU3002825, THYMU3026306, THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428, THYMU3047115, THYMU3047891, TKIDN2011160, TRACH3005173, TRACH3005274, TRACH3009008, TRACH3011313, TRACH3011503, TRACH3012891, TRACH3015136, TRACH3016455, TRACH3018108, TRACH3018261, TRACH3018524, TRACH3019621, TRACH3021544, TRACH3022758, TRACH3023516, TRACH3024020, TRACH3024081, TRACH3027229, TRACH3027701, TRACH3032150, TRACH3038399, TSTOM2001571, TSTOM2002611, UTERU2024042, UTERU3010604, UTERU3010919, UTERU3015299, UTERU3019708, UTERU3021850

【 0 2 1 5 】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 2 7 クローンであった。

BLADE2000256, BRACE2002392, BRACE3030538, BRACE3036283, BRACE3044495, BRAMY3002886, BRAMY3009556, BRAWH2016209, BRAWH3004350, BRAWH3027574, BRCAN2019907, BRHIP3001076, BRHIP3029409, BRSTN2008475, BRTHA3011265, FEKID2002637, NT2RP8005546, OCBBF3001202, PLACE7011559, SPLEN2033996, TESTI2023903, TESTI4020819, TESTI4049899, THYMU3014372, THYMU3021586, UTERU3010919, UTERU3012999

【 0 2 1 6 】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 6 0 クローンであった。

BRACE3004767, BRACE3013418, BRACE3051819, BRAMY3005184, BRAMY3015086, BRAMY4000915, BRAMY4001652, BRAWH3001783, BRAWH3015175, BRAWH3018548, BRAWH3019026, BRAWH3021580, BRAWH3021724, BRAWH3027440, BRAWH3027806, BRAWH3029385, BRAWH3040900, BRAWH3041492, BRCAN2020467, BRHIP3003063,

BRHIP3003340, BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA3014547, BRTHA3025073, CERVX2000968, JCMLC2000273, NIESE2000698, NT2RI3005923, OCBBF2003518, OCBBF2004478, OCBBF3027969, PLACE7000266, PLACE7004961, SMINT2010753, SPLEN2034934, SYNOV4003174, TESTI2001915, TESTI2009739, TESTI2034913, TESTI4001517, TESTI4004917, TESTI4010902, TESTI4032913, TESTI4051424, THYMU3026532, TLUNG2000654, TRACH3006379, TRACH3016805, TRACH3020769, TRACH3022960, TRACH3026650, TRACH3028837, TRACH3029462, TRACH3032570, UTERU3000670, UTERU3001029, UTERU3015011, UTERU3016308

【 0 2 1 7 】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 0 クローンであった。

ASTRO3000154, BRACE3014714, BRACE3036283, BRALZ2013621, BRAMY3009556, BRAMY3011501, BRAWH3011623, BRAWH3017180, BRAWH3022651, BRAWH3038252, BRAWH3040695, BRAWH3046424, BRHIP3004215, BRHIP3007223, BRHIP3020046, BRTHA3010530, CTONG2006235, FEBRA2028457, NT2RP7016508, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006268, TESTI2036285, TESTI2037657, TESTI4014932, TESTI4028182, TESTI4032128, TESTI4033177, TESTI4039575, THYMU3012402, THYMU3040829, THYMU3041428, TRACH3002752, TRACH3018108, TRACH3021778, UTERU3004635, UTERU3010409, UTERU3010919, UTERU3013302

【 0 2 1 8 】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 0 クローンであった。

BRACE2016896, BRACE2023744, BRACE3020669, BRACE3030538, BRACE3041059, BRACE3043597, BRAWH2014053, BRAWH3001638, BRAWH3010602, BRAWH3024506, BRAWH3026349, BRAWH3034668, BRAWH3037979, BRAWH3041556, BRAWH3044151, BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2006051, BRCAN2021325, BRHIP3007223, BRSTN2012069, BRTHA2005448, BRTHA2010672, CHONS2002829, CTONG3001605, D9OST2004417, OCBBF2000831, OCBBF2007039, PLACE6019600, PLACE7007379, PLACE7012111, PLACE7016526, TESTI4018436, TESTI4020596, TESTI4

032128, TESTI4036048, THYMU3012402, THYMU3033759, THYMU3036953,
THYMU3046360, TKIDN2011160, TRACH3016455, TRACH3018519, TRACH3021544, TRACH3025316, TRACH3030855, TRACH3038399, UTERU3014647, UTERU3021850

【 0 2 1 9 】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 クローンであった。

BRACE2012947, BRHIP2029529, BRTHA3003736, THYMU3015571, TRACH3022296

【 0 2 2 0 】

発生、分化関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 6 クローンであった。

ASTR03000154, BRACE3034964, BRAWH3004350, BRAWH3029538, BRAWH3038252, BRHIP3007424, BRTHA2024712, BRTHA3011265, FEKID2002493, NT2RP8003490, NT2RP8006452, OCBBF3025503, PLACE7002303, TESTI2026024, TRACH3028180, UTERU3016070

【 0 2 2 1 】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 9 クローンであった。

ASTR02016114, BEAST2000981, BRACE2012947, BRACE2019348, BRACE3020669, BRACE3025719, BRACE3026844, BRACE3031743, BRACE3034183, BRACE3041162, BRACE3046152, BRALZ2013621, BRAMY2040915, BRAMY2046537, BRAMY3000692, BRAMY3007078, BRAMY3011501, BRAMY3011581, BRAMY3014027, BRAMY3018754, BRAMY4000962, BRAWH3000446, BRAWH3011577, BRAWH3011623, BRAWH3013009, BRAWH3013264, BRAWH3017477, BRAWH3028796, BRAWH3031342, BRAWH3032571, BRAWH3034775, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3038827, BRCAN2020331, BRCOC2012386, BRHIP2027077, BRHIP3004725, BRHIP3028246, BRSSN2015497, BRTHA2024712, BRTHA3000456, BRTHA3003736, BRTHA3010212, BRTHA3014000, BRTHA3028339, CHONS2000797, CHONS2002829, CTONG2001932, CTONG2011801, D9OST2003106, FCBBF3020030, FCBBF5000384, FEBRA2028457, HCASM2008154, NETRP2004017, NT2RI3008179, NT2RI3009480, NT2RP7016508,

NT2RP8003490, NTONG2003805, NTONG2008483, OCBBF2016928, OCBBF3004487, OCBBF3008392, OCBBF3020263, OCBBF3021361, OCBBF3022166, PLACE7002303, PLACE7004103, PLACE7005169, PLACE7009757, PROST2002078, PUAEN2000594, SMINT2011509, SPLEN2012571, SPLEN2028417, TIESE2000609, TIESE2000904, TESTI4002868, TESTI4003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4005653, TESTI4032128, TESTI4039575, TESTI4039904, TESTI4052775, THYMU3008105, THYMU3012983, THYMU3014372, THYMU3020869, THYMU3021586, THYMU3026000, THYMU3030072, THYMU3033759, THYMU3037052, THYMU3040829, TLIVE2001616, TRACH3003458, TRACH3004424, TRACH3005191, TRACH3008508, TRACH3010079, TRACH3010167, TRACH3010342, TRACH3015951, TRACH3021778, TRACH3021883, TRACH3022109, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3013302, UTERU3016070, UTERU3022588

【 0 2 2 2 】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 68 クローンであった。

BRACE2013009, BRACE2016896, BRACE3002344, BRACE3014714, BRACE3017253, BRACE3036283, BRACE3051819, BRAMY3011501, BRAMY3018248, BRAWH2014053, BRAWH3015175, BRAWH3024506, BRAWH3029385, BRAWH3032571, BRAWH3037428, BRAWH3041556, BRAWH3047692, BRCAN2000923, BRCAN2002892, BRCAN2003269, BRCAN2006051, BRHIP3007195, BRHIP3027191, BRHIP3041587, BRSTN2012069, BRTHA2020910, BRTHA3003736, HSYRA2004550, KIDNE2010049, NETRP2003448, NT2RP7016508, OCBBF2003518, OCBBF3004487, PLACE6001933, PLACE6019600, PLACE7004961, PLACE7006498, PLACE7011559, PLACE7016526, PUAEN2006639, SMINT2011406, TESTI2009739, TESTI2040377, TESTI4004917, TESTI4013474, TESTI4021569, TESTI4028182, TESTI4049786, TESTI4052219, THYMU3014372, THYMU3032798, THYMU3041428, THYMU3047115, TRACH3005191, TRACH3009061, TRACH3009701, TRACH3012891, TRACH3019370, TRACH3020769, TRACH3022960, TRACH3023960, TRACH3024081, TRACH3038399, TSTOM2001571, UTERU2024042, UTERU3010919, UTERU3012414, UTERU3019708

【 0 2 2 3 】

以下の 1 0 4 クローンについては、上記のいずれのカテゴリーに属するか明らかでないクローンであったが、全長配列に対する相同性検索で何らかの機能が予測されているクローンである。クローン名と相同性検索結果のDefinitionを//で区切り、以下に示した。

BLADE2002310//SH3-domain binding protein 1 [Homo sapiens]

BLADE2007799//Hepatocellular carcinoma-associated antigen 66.

BRACE2017359//Mus musculus suppressor of Ty 6 homolog (S. cerevisiae) (Supt6h)

BRACE2017872//nuclear receptor-binding SET-domain protein 1 [Mus musculus]

BRACE3009416//testis specific ankyrin-like protein 1 [Homo sapiens]

BRACE3016020//SBB131 protein [Homo sapiens]

BRACE3019570//SNAP-25-interacting protein [Rattus norvegicus]

BRACE3022303//Pax transcription activation domain interacting protein [Mus musculus]

BRACE3022340//SNAP-25-interacting protein [Rattus norvegicus]

BRACE3026290//Homo sapiens lethal giant larvae homolog 2 [Homo sapiens]

BRACE3032631//F-box protein FBX13 [Mus musculus].

BRACE3040239//Deltex3 [Mus musculus]

BRACE3047482//tripartite motif-containing 9 [Homo sapiens]

BRACE3049714//NYD-TSPG protein [Homo sapiens]

BRACE3052410//IDN3 protein [Homo sapiens]

BRACE3052595//Nim2 [Rattus norvegicus]

BRALZ2014054//cenexin 2 [Rattus norvegicus].

BRAMY3007471//gene trap locus F3b; transcript expressed during hematopoiesis 2 [Mus musculus]

BRAMY3010321//MRIP-1 protein [Homo sapiens]

BRAMY3014613//SH3-domain binding protein 1 [Homo sapiens]

BAMY4001863//Mus musculus enabled homolog (Drosophila) (Enah), mRNA
BRAWH2011796//S-100 protein, alpha chain.
BRAWH3008167//CUB and Sushi multiple domains 1 [Homo sapiens]
BRAWH3009961//Nim2 [Rattus norvegicus]
BRAWH3010726//phosphatidylinositol transfer protein, membrane-associated
; Drosophila retinal degeneration B [Homo sapiens]
BRAWH3015017//axonemal dynein light chain p33.
BRAWH3024231//Tetratricopeptide repeat protein 4.
BRAWH3026938//semaF cytoplasmic domain associated protein 3; semaphorin
cytoplasmic domain-associated protein 3A [Mus musculus]
BRAWH3027533//rap2 interacting protein x [Homo sapiens].
BRAWH3030910//Sec23-interacting protein p125 [Homo sapiens]
BRAWH3031710//serologically defined colon cancer antigen 33 [Homo sapien
s]
BRAWH3033293//synaptopodin [Homo sapiens]
BRAWH3042568//ventral anterior homeobox containing gene 1 [Mus musculus]
BRAWH3043034//Mus musculus neuregulin 1 (Nrg1)
BRAWH3044122//Munc13-1 [Rattus norvegicus]
BRHIP2026346//lymphocyte specific formin related protein; formin-related
gene in leukocytes [Mus musculus]
BRHIP2027563//host cell factor homolog [Homo sapiens]
BRHIP3002114//rTS beta protein [Homo sapiens]
BRHIP3003795//cytochrome P450 retinoid metabolizing protein [Homo sapien
s]
BRHIP3006786//peptidylprolyl isomerase (cyclophilin)-like 2; cyclophilin
-like protein CyP-60 [Homo sapiens]
BRHIP3017109//Socs-5 [Mus musculus]
BRHIP3019643//Homo sapiens gamma tubulin ring complex protein (76p gene)
(76P), mRNA

BRHIP3032148//brain-enriched guanylate kinase-associated [Rattus norvegicus]

BRSTN2006638//synaptotagmin interacting protein 1 [Rattus norvegicus]

BRSTN2016892//BUP protein [Homo sapiens]

BRSTN2016992//DRR1 protein (TU3A protein).

BRSTN2017151//COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis); COP9 complex S7a [Mus musculus]

BRTHA2020642//DRR1 protein (TU3A protein).

BRTHA3018409//synaptotagmin-like 4; granuphilin-a; granuphilin-b; granuphilin

BRTHA3019183//Ca²⁺-dependent activator protein for secretion; Ca²⁺-dependent activator protein for secretion [Mus musculus]

CHONS2001834//tumor endothelial marker.7 precursor [Homo sapiens]

CTONG2009570//rab11 binding protein [Bos taurus].

CTONG2012123//Mus musculus enabled homolog (Drosophila) (Enah), mRNA

CTONG2027591//Mus musculus pecanex homolog (Drosophila) (Pcnx), mRNA.

CTONG3003669//high-glucose-regulated protein 8 [Homo sapiens]

ERLTF2002178//Kelch-like protein X.

HHDPC2008185//jerky [Mus musculus]

NT2RI3001573//F-box protein FBL10 [Mus musculus].

NT2RI3007095//Mus musculus neuregulin 1 (Nrg1), mRNA.

NT2RP8001363//signal peptide, CUB domain, EGF-like 1 [Mus musculus]

NT2RP8001584//alpha integrin binding protein 63 [Homo sapiens]

NT2RP8001604//CUB and Sushi multiple domains 1 [Homo sapiens]

OCBBF3019269//Homo sapiens Dvl-binding protein IDAX (inhibition of the Dvl and Axin complex) (IDAX)

OCBBF3022827//putative Rab5 GDP/GTP exchange factor homologue [Homo sapiens]

OCBBF3023913//Mus musculus protein phosphatase 1, regulatory (inhibitor)

subunit 1C (Ppplr1c)
PLACE6003004//rTS beta protein [Homo sapiens]
PLACE6008315//similar to ALPHA-ACTININ, SARCOMERIC (F-ACTIN CROSS LINKIN
G PROTEIN) (D. melanogaster) [Homo sapiens].
PLACE6010925//NY-REN-50 antigen [Homo sapiens]
PLACE7012127//AAA-ATPase TOB3 [Homo sapiens]
PROST2016566//erythroblast macrophage protein [Mus musculus]
SYNOV2017179//EBP50-PDZ interactor of 64 kD [Homo sapiens]
SYNOV3000345//upregulated by 1,25-dihydroxyvitamin D-3 [Homo sapiens]
TBAES2003917//NG28 protein [Mus musculus]
TESTI2001364//lactate dehydrogenase A -like [Homo sapiens]
TESTI2004601//NYD-TSPG protein [Homo sapiens]
TESTI2009497//GPI-anchored protein p137 (p137GPI).
TESTI4002774//oxysterol binding protein 2 [Mus musculus]
TESTI4003579//FH1/FH2 domains-containing protein (Formin homolog overexp
ressed in spleen) (FHOS).
TESTI4003703//retinoblastoma-associated protein RAP140 [Homo sapiens]
TESTI4013742//antigen identified by monoclonal antibody 2A8 [Mus muscul
s]
TESTI4014908//dedicator of cyto-kinesis 2 [Mus musculus]
TESTI4018506//tomosyn [Rattus norvegicus]
TESTI4020342//H326 [Homo sapiens]
TESTI4024294//WW domain binding protein 2 [Mus musculus]
TESTI4039451//B29 protein [Homo sapiens]
TESTI4041482//Rattus norvegicus SEC15 homolog (S. cerevisiae) (Sec15), m
RNA
TESTI4043166//lymphocyte specific formin related protein; formin-related
gene in leukocytes [Mus musculus]
TESTI4047328//otogelin [Mus musculus]

THYMU3011717//exocyst component protein 70 kDa homolog (S. cerevisiae)
THYMU3016822//erythroblast macrophage protein [Mus musculus]
THYMU3026479//secretory pathway component Sec31B-1 [Homo sapiens]
THYMU3028702//chromosome condensation-related SMC-associated protein 1;
chromosome condensation-related SMC-associated protein 1; KIAA0159 gene
product [Homo sapiens]
THYMU3029719//AAA-ATPase TOB3 [Homo sapiens]
THYMU3038347//tumor stroma and activated macrophage protein DLM-1 [Homo
sapiens]
THYMU3038603//WW domain binding protein 2 [Mus musculus]
THYMU3040830//AD-012 protein [Homo sapiens]
THYMU3041603//gamma-tubulin complex protein 2 [Homo sapiens]
TKIDN2003396//Homo sapiens paternally expressed 10 (PEG10), mRNA
TRACH2011057//D-type cyclin-interacting protein 1; MAID protein [Homo sa
piens]
TRACH3004412//clusterin-like 1 (retinal); unknown prepropeptide specific
to rod photoreceptor [Homo sapiens]
TRACH3012106//erythrocyte protein band 4.1-like 3 [Mus musculus]
UTERU3009775//PAPIN [Rattus norvegicus]
UTERU3010892//adaptor-related protein complex 3, delta 1 subunit; adapti
n, delta [Homo sapiens]
UTERU3017995//p47 [Homo sapiens]

【 0 2 2 4 】

残る 8 7 9 クローンについては、現在のところ相同性検索の情報からは機能を推定できる情報の得られないクローンであった。これらクローンについては今後、データベースのアップデートによって機能が明らかになる可能性がある。クローン名を以下に示した。

ADRGL2010594, AHMSC1000138, BLADE2004849, BLADE2006043, BLADE2007735, BLADE2008809, BRACE2005991, BRACE2010336, BRACE2012625, BRACE2012833, BRAC

E2012936, BRACE2017844, BRACE2025452, BRACE2026404, BRACE2027312, BRACE2028956, BRACE2032584, BRACE2033128, BRACE2034434, BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975, BRACE3002541, BRACE3003866, BRACE3004046, BRACE3004371, BRACE3004887, BRACE3005870, BRACE3005903, BRACE3006553, BRACE3007649, BRACE3009075, BRACE3009265, BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774, BRACE3015090, BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810, BRACE3016862, BRACE3019611, BRACE3019817, BRACE3020356, BRACE3021430, BRACE3022312, BRACE3022847, BRACE3023604, BRACE3024537, BRACE3025627, BRACE3026161, BRACE3026947, BRACE3027256, BRACE3027931, BRACE3028895, BRACE3029005, BRACE3029205, BRACE3029447, BRACE3031161, BRACE3031184, BRACE3031185, BRACE3031843, BRACE3032538, BRACE3034389, BRACE3035168, BRACE3036156, BRACE3036271, BRACE3037612, BRACE3038012, BRACE3038030, BRACE3038760, BRACE3039288, BRACE3039454, BRACE3040012, BRACE3040504, BRACE3041827, BRACE3042210, BRACE3042594, BRACE3044247, BRACE3044377, BRACE3045078, BRACE3045145, BRACE3045424, BRACE3045708, BRACE3045981, BRACE3046294, BRACE3046837, BRACE3046855, BRACE3046966, BRACE3047018, BRACE3047801, BRACE3048483, BRACE3048615, BRACE3048677, BRACE3048756, BRACE3048904, BRACE3048905, BRACE3049186, BRACE3050270, BRACE3051627, BRACE3051722, BRACE3051879, BRALZ2003119, BRALZ2007661, BRALZ2008930, BRAMY2022320, BRAMY2023939, BRAMY2031516, BRAMY2033895, BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2039630, BRAMY2041347, BRAMY2046489, BRAMY3001409, BRAMY3002329, BRAMY3002508, BRAMY3004364, BRAMY3005656, BRAMY3005912, BRAMY3008436, BRAMY3009158, BRAMY3010603, BRAMY3011865, BRAMY3014555, BRAMY3017827, BRAMY3017965, BRAMY3018121, BRAMY3018340, BRAMY4001234, BRAMY4001913, BRAMY4002575, BRAMY4002628, BRAWH2004078, BRAWH2010619, BRAWH2012054, BRAWH2013955, BRAWH2016223, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000884, BRAWH3003244, BRAWH3003975, BRAWH3005037, BRAWH3005896, BRAWH3008559, BRAWH3010833, BRAWH3011101, BRAWH3

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BRAWH3027616, BRAWH3027675, BRAWH3028202, BRAWH3028461, BRAWH3029313, BR
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AWH3043944, BRAWH3044487, BRAWH3044585, BRAWH3044985, BRAWH3045118, BRAW
H3045229, BRAWH3045625, BRAWH3046209, BRAWH3046802, BRAWH3046959, BRAWH3
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BRCAN2007525, BRCAN2008701, BRCAN2009168, BRCAN2010547, BRCAN2010581, BR
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N2021718, BRCAN2025093, BRCAN2027593, BRCAN2028702, BRCOC2001355, BRCOC2
002777, BRCOC2006942, BRCOC2010115, BRHIP2006819, BRHIP2009177,
BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125, BRHIP2017714, BR
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BRHIP3016421, BRHIP3017256, BRHIP3018784, BRHIP3019824, BRHIP3019880, BR
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2RP7017139, NT2RP7020343, NT2RP8000633, NT2RP8001407, NT2RP8003657, NT2RP8006521, NT2RP8007416, NT2RP8007503, NT2RP8007920, NT2RP8009119, NT2RP8009248, NTONG2002278, NTONG2004829, NTONG2009468, OCBBF2014745, OCBBF2019761, OCBBF2024779, OCBBF2025631, OCBBF3000743, OCBBF3000830, OCBBF3001076, OCBBF3001616, OCBBF3004908, OCBBF3005843, OCBBF3007078, OCBBF3008835, OCBBF3020414, OCBBF3021086, OCBBF3021166, OCBBF3021515, OCBBF3023543, OCBBF3025127, OCBBF3025131, OCBBF3025901, OCBBF3026088, OCBBF3026361, PEBLM2001803, PEBLM2006298, PERIC2003349, PLACE5000527, PLACE6019542, PLACE7003684, PLACE7005671, PLACE7005840, PLACE7006240, PLACE7006540, PLACE7007973, PLACE7008766, PLACE7010567, PLACE7013060, PLACE7014396, PLACE7015238, PLACE7015647, PLACE7016214, PLACE7018304, PLACE7018349, PLACE7018452, PLACE7018479, PLACE7018512, PROST2007444, PROST2017578, PROST2017729, PROST2017749, PROST2017910, RECTM2001519, SKMUS2009479, SKMUS2009557, SKNMC2003639, SMINT2009292, SMINT2009895, SMINT2012040, SMINT2014166, SMINT2017964, SMINT2019105, SPLEN2001227, SPLEN2017999, SPLEN2019092, SPLEN2019480, SPLEN2021231, SPLEN2021991, SPLEN2022785, SPLEN2022920, SPLEN2024571, SPLEN2027852, SPLEN2028593, SPLEN2032677, SPLEN2034601, SPLEN2036608, SPLEN2037077, STOMA2003894, SYNOV4000598, SYNOV4004210, SYNOV4009575, TBAES2007548, TBAES2007862, TESOP2002005, TESOP2003308, TESOP2004110, TESTI1000459, TESTI2004452, TESTI2004971, TESTI2005153, TESTI2005564, TESTI2006543, TESTI2008636, TESTI2011020, TESTI2011033, TESTI2018687, TESTI2018867, TESTI2021112, TESTI2023053, TESTI2026284, TESTI2030519, TESTI2033905, TESTI2035962, TESTI2037209, TESTI2037572, TESTI2038733, TESTI2039342, TESTI2039732, TESTI2039738, TESTI2040372, TESTI2041362, TESTI2041976, TESTI2051742, TESTI2052110, TESTI2052202, TESTI2052799, TESTI4000370, TESTI4000534, TESTI4000600, TESTI4000703, TESTI4000957, TESTI4001348, TESTI4001569, TESTI4002003, TESTI4002141, TESTI4002195, TESTI4002520, TESTI4003179, TESTI4003279, TESTI4003319, TESTI4003404, TESTI4003565, TESTI4003574, TEST

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022955, UTERU2023941, UTERU2027369, UTERU2028377, UTERU2029660,
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018172, UTERU3018255, UTERU3020090, UTERU3023141

【 0 2 2 5 】

実施例 7. 推定アミノ酸配列に対する機能ドメインの検索による機能カテゴリー分類

ドメイン、モチーフはタンパク質の最小限の機能構造である。一タンパク質の構造はこの最小限構造の寄せ集めで成り立ち、その結果、タンパク質全体としての機能が決定される。よってドメインやモチーフ構造の解析から全体としてのタンパク質が持つ機能を比較的正確に予測することが可能である。また、この結果を機能別にデータベース化することは、特定の機能を持つクローンが容易に選択可能ということであり、個々のクローンの機能解析の際に非常に有用である。

全長塩基配列から推定されたアミノ酸配列のPfamに対するドメイン検索の結果（実施例 5 参照）から、ヒットデータのドメイン、モチーフ名やアクセッション番号、Pfam (<http://www.sanger.ac.uk/Software/Pfam/index.shtml>) における詳細な記述データや、PROSITE (<http://www.expasy.ch/cgi-bin/prosite-list.pl>) にある機能カテゴリー分類を参照に、ヒットした 6 6 4 クローン中にコードされるタンパク質の機能予測、カテゴリー分類を行った。

【 0 2 2 6 】

分泌・膜蛋白質のカテゴリーに属すると推定されたクローンとは、受容体、イオンチャンネル、ホルモン、成長因子などと推測されるような例えば 7 transmembrane receptor, Pancreatic hormone peptides, Ion transport protein, Fibroblast growth factor等のドメイン、モチーフを持つクローンである。

【 0 2 2 7 】

糖蛋白質関連蛋白質のカテゴリーに属すると推定されたクローンとは、糖タンパク質、糖転移酵素などGlycobiologyに関わると推測されるような例えばImmunoglobulin domain, Glycosyl transferases group 1等のドメイン、モチーフを持つクローンである。

【 0 2 2 8 】

シグナル伝達関連蛋白質のカテゴリーに属すると推定されたクローンとは、タンパク質リン酸化酵素、脱リン酸化酵素、SH2ドメイン、Small Gタンパク質などと推測されるような例えばEukaryotic protein kinase domain, Protein phos

phatase 2C, Ras family等のドメイン、モチーフを持つクローンである。

【0229】

転写関連蛋白質のカテゴリーに属すると推定されたクローンとは、転写因子、転写調節に関わるタンパク質などと推測されるような例えばbZIP transcription factor, Zinc finger, C2H2 type等のドメイン、モチーフを持つクローンである。

【0230】

疾患関連蛋白質のカテゴリーに属すると推定されたクローンとは、特定の疾患で発現が見られるようなタンパク質や、疾患で発現が上昇したり減少したりすると推測されるような例えばWilm's tumour protein, von Hippel-Lindau disease tumor suppressor protein等のドメイン、モチーフを持つクローンである。

【0231】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンとは、転移酵素、合成酵素、加水分解酵素などと推測されるような例えばAldehyde dehydrogenase family, Chitin synthase, Glucose-6-phosphate dehydrogenase等のドメイン、モチーフを持つクローンである。

【0232】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンとは、サイクリン、細胞増殖制御タンパク質などと推測されるような例えばCyclin, Cell division protein等のドメイン、モチーフを持つクローンである。

【0233】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンとは、アクチン、キネシン、フィブロネクチンなどと推測されるような例えばActin, Fibronectin type I domain, Kinesin motor domain等のドメイン、モチーフを持つクローンである。

【0234】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンとは、スプライシング因子、RNA合成酵素、ヘリカーゼなどと推測されるような例えばHepatitis C virus RNA dependent RNA polymerase, DEAD/DEAH box helica

se等のドメイン、モチーフを持つクローンである。

【0235】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンとは、翻訳関連タンパク質、ユビキチン関連タンパク質、Ribosomal proteinなどと推測されるような例えばTranslation initiation factor SUI1, Ubiquitin family, Ribosomal protein L16等のドメイン、モチーフを持つクローンである。

【0236】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンとは、分子シャペロン、DNA修復タンパク質などと推測されるような例えばHsp90 protein, DNA mismatch repair protein等のドメイン、モチーフを持つクローンである。

【0237】

発生・分化関連蛋白質のカテゴリーに属すると推定されたクローンとは、器官形成関連タンパク質などと推測されるような例えばFloricaula / Leafy protein等のドメイン、モチーフを持つクローンである。

【0238】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンとは、転写因子、DNAリガーゼをはじめとしたDNA・RNA関連酵素類、Zinc-finger関連タンパク質などと推測されるような例えばTranscription factor WhiB, B-box zinc finger, tRNA synthetases class I (C)等のドメイン、モチーフを持つクローンである。

【0239】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンとは、ATPase等をはじめとしたATP・GTP関連酵素類、Gタンパク質などと推測されるような例えばE1-E2 ATPase, Ras family等のドメイン、モチーフを持つクローンである。

【0240】

なお、この機能カテゴリー分類では一つのクローンが上記の複数のカテゴリーに該当する場合は、そのまま複数のカテゴリーに分類した。ただし、蛋白質の機能は必ずしも分類された機能カテゴリーに限定されるわけではない。

【0241】

分泌・膜蛋白質に属すると推定されたクローンは、以下の 9 2 クローンであった。

3NB692004045, BRACE3002264, BRACE3009392, BRACE3013418, BRACE3024879, BRACE3032385, BRACE3039378, BRACE3042432, BRACE3050504, BRACE3051621, BRAMY2046537, BRAMY3004126, BRAWH2000256, BRAWH2011812, BRAWH3023156, BRAWH3025157, BRAWH3027880, BRAWH3036270, BRAWH3037265, BRAWH3042772, BRCAN2003269, BRCAN2022126, BRCOC2006164, BRHIP3002000, BRHIP3005944, BRHIP3008320, BRHIP3011567, BRHIP3014675, BRHIP3016032, BRHIP3017558, BRHIP3025795, BRHIP3033557, BRHIP3039509, BRSTN2010089, BRTHA2031917, BRTHA3011194, BRTHA3012265, BRTHA3014547, COLON2005735, JCMLC2000273, KIDNE2004531, LYMPB2002236, NT2RP7019682, NT2RP8001363, NT2RP8003787, OCBBF2003518, OCBBF2004478, OCBBF2009536, OCBBF2018618, OCBBF3004487, OCBBF3025475, OCBBF3028001, PEBLM2005615, PLACE6010936, PLACE7004103, PLACE7011559, PLACE7018304, TESTI2018335, TESTI2022323, TESTI2024267, TESTI2036822, TESTI4003602, TESTI4004539, TESTI4005399, TESTI4008305, TESTI4010544, TESTI4014415, TESTI4021569, TESTI4023096, TESTI4026080, TESTI4040559, TESTI4049899, THYMU3015647, THYMU3021404, THYMU3023400, THYMU3026532, THYMU3030752, THYMU3040172, THYMU3044075, TRACH3003357, TRACH3004113, TRACH3004747, TRACH3005699, TRACH3006800, TRACH3009061, TRACH3019370, TRACH3023373, TRACH3031678, TRACH3032150, UTERU3001946, UTERU3016273, UTERU3017626

【 0 2 4 2 】

糖蛋白質関連蛋白質に属すると推定されたクローンは、以下の 8 1 クローンであった。

3NB692004045, ADIPS2000069, BRACE2017397, BRACE3013874, BRACE3017253, BRACE3039358, BRAMY2040915, BRAMY3015549, BRAWH3009961, BRAWH3023415, BRAWH3049544, BRHIP3017558, BRHIP3025795, BRHIP3036371, BRHIP3036715, BRHIP3038735, BRTHA2019726, BRTHA2020400, BRTHA2020721, BRTHA3017791, CERVX2000968, FELNG2000720, JCMLC2000273, KIDNE2004531, NT2RP8008057, OC

BBF2000831, OCBBF2004478, OCBBF2030927, PEBLM2005615, PLACE7006090, SPLE
N2025012, STOMA2004663, TESTI2021654, TESTI2052670, TESTI4008305, TESTI4
022158, TESTI4031173, TESTI4032128, TESTI4037949, TESTI4051424,
THYMU3002825, THYMU3014173, THYMU3016518, THYMU3020221, THYMU3025118, TH
YMU3026306, THYMU3026532, THYMU3037772, THYMU3040746, TLUNG2001445, TLUN
G2001600, TRACH3003357, TRACH3004113, TRACH3004412, TRACH3005274, TRACH3
005699, TRACH3006800, TRACH3011082, TRACH3011184, TRACH3012659,
TRACH3015354, TRACH3018261, TRACH3018907, TRACH3019058, TRACH3019621, TR
ACH3019807, TRACH3020930, TRACH3021023, TRACH3024512, TRACH3026299, TRAC
H3028441, TRACH3029670, TRACH3031316, TRACH3034680, TRACH3036103, TRACH3
037505, TUTER2001433, UTERU3001946, UTERU3010409, UTERU3011398,
UTERU3015647

【 0 2 4 3 】

シグナル伝達関連蛋白質に属すると推定されたクローンは、以下の 1 2 5 クロ
ーンであった。

BLADE2002310, BLADE2008809, BRACE2047975, BRACE3002344, BRACE3003866, BR
ACE3004767, BRACE3013418, BRACE3015898, BRACE3017253, BRACE3042046, BRAC
E3044172, BRACE3045424, BRACE3046491, BRACE3051621, BRACE3052321, BRACE3
052595, BRAMY3005184, BRAMY3009491, BRAMY3010321, BRAMY3014613,
BRAMY3015547, BRAMY3017920, BRAWH2012866, BRAWH3009961, BRAWH3017180, BR
AWH3018063, BRAWH3019026, BRAWH3022431, BRAWH3024186, BRAWH3026349, BRAW
H3027574, BRAWH3027806, BRAWH3029385, BRAWH3031342, BRAWH3032340, BRAWH3
035914, BRAWH3037428, BRAWH3044122, BRAWH3047692, BRCAN2000923,
BRCAN2002892, BRCOC2001355, BRHIP3003306, BRHIP3006294, BRHIP3006786, BR
HIP3011460, BRHIP3017109, BRHIP3021019, BRHIP3028570, BRHIP3037543, BRHI
P3041587, BRTHA2026290, BRTHA2027250, BRTHA3014547, BRTHA3020771, BRTHA3
021708, BRTHA3023403, BRTHA3026916, CTONG2009570, ERLTF2002369,
FEKID2001001, FEKID2002637, FELNG2001953, KIDNE2010049, LYMPB2002344, N1
ESE2000698, NETRP2003448, NT2RI2004818, NTONG2008483, OCBBF3006986, OCBB

F3021086, OCBBF3021502, OCBBF3023175, PLACE5000492, PLACE6000055, PLACE6019600, PLACE7009936, PLACE7014247, PLACE7016526, PUAEN2006639, SKMUS2008585, SKMUS2009557, SMINT2017964, SPLEN2007689, SYNOV2017179, SYNOV4009575, TESTI4002774, TESTI4004695, TESTI4010902, TESTI4012960, TESTI4013474, TESTI4020342, TESTI4020596, TESTI4021197, TESTI4022158, TESTI4028042, TESTI4029731, TESTI4033177, TESTI4036048, TESTI4046073, TESTI4047808, TESTI4049786, TESTI4051865, THYMU3013785, THYMU3025683, THYMU3032798, TRACH2024730, TRACH3003037, TRACH3003357, TRACH3005173, TRACH3011538, TRACH3018519, TRACH3020605, TRACH3024020, TRACH3030176, TRACH3031660, TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042, UTERU3001029, UTERU3006720, UTERU3010919, UTERU3021231, UTERU3022168

【 0 2 4 4 】

転写関連蛋白質に属すると推定されたクローンは、以下の 1 4 1 クローンであった。

ASTRO2016114, BEAST2000981, BRACE2019348, BRACE3025719, BRACE3026844, BRACE3026947, BRACE3029021, BRACE3034183, BRACE3040239, BRACE3041162, BRACE3047482, BRAMY2041347, BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027, BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209, BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3013009, BRAWH3013264, BRAWH3015175, BRAWH3015610, BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAWH3027533, BRAWH3027880, BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3032571, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3042787, BRAWH3044122, BRAWH3046424, BRCAN2021452, BRCOC2012386, BRHIP2027077, BRHIP2029663, BRHIP3005037, BRHIP3007609, BRHIP3017256, BRHIP3019824, BRHIP3027651, BRHIP3028246, BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA3000456, BRTHA3003225, BRTHA3010212, BRTHA3014000, BRTHA3028339, CHONS2000797, CTONG2006235, CTONG2011801, FCBBF3020030, FEBRA2002260, HCASM2008154, KIDNE2018268, NETRP2003103, NETRP2004017, NT2RI3009480, NTONG2003805, NTONG2008483, OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3

008392, OCBBF3019269, OCBBF3020263, OCBBF3022827, OCBBF3025503,
OCBBF3026361, PLACE7005169, PLACE7007973, PLACE7009757, PLACE7018512, SM
INT2014721, SPLEN2012571, SPLEN2036608, TIESE2000904, TESTI2036822, TEST
I2040377, TESTI4000370, TESTI4000621, TESTI4001679, TESTI4002799, TESTI4
003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4024494,
TESTI4028182, TESTI4032913, TESTI4039904, TESTI4051054, TESTI4052775, TH
YMU2008207, THYMU2038199, THYMU3008105, THYMU3012983, THYMU3014372, THYM
U3021586, THYMU3022434, THYMU3026000, THYMU3030072, THYMU3034671, THYMU3
037617, THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616,
TLUNG2000654, TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113, TR
ACH3004412, TRACH3004424, TRACH3005274, TRACH3010079, TRACH3010167, TRAC
H3015951, TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750, UTERU2
037423, UTERU3012293, UTERU3015011, UTERU3016070, UTERU3018172,
UTERU3022588

【 0 2 4 5 】

疾患関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 クロ
ーンであった。

BRAWH3041928, BRHIP3000859, BRTHA3018409, THYMU3025642

【 0 2 4 6 】

酵素・代謝関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の
2 6 4 クローンであった。

BRACE1000475, BRACE2003628, BRACE2012528, BRACE2013132, BRACE2016896, BR
ACE2035120, BRACE2042541, BRACE2047975, BRACE3002344, BRACE3009392, BRAC
E3013418, BRACE3015898, BRACE3017253, BRACE3019941, BRACE3024444, BRACE3
031315, BRACE3031372, BRACE3032537, BRACE3033525, BRACE3034183,
BRACE3034964, BRACE3039288, BRACE3039454, BRACE3041059, BRACE3042409, BR
ACE3044172, BRACE3046491, BRACE3049714, BRACE3050270, BRACE3051819, BRAC
E3052410, BRACE3052595, BRAMY3007078, BRAMY3009491, BRAMY3011581, BRAMY3
014613, BRAMY4000915, BRAWH2000256, BRAWH2002333, BRAWH2012866,

BRAWH2014053, BRAWH2016785, BRAWH3009961, BRAWH3010657, BRAWH3013264, BRAWH3015175, BRAWH3017180, BRAWH3017259, BRAWH3019026, BRAWH3021724, BRAWH3022431, BRAWH3023415, BRAWH3024186, BRAWH3028796, BRAWH3029385, BRAWH3029806, BRAWH3032571, BRAWH3033513, BRAWH3034668, BRAWH3034743, BRAWH3037979, BRAWH3041556, BRAWH3043295, BRAWH3044122, BRAWH3044985, BRAWH3046424, BRAWH3047692, BRAWH3048724, BRAWH3049544, BRCAN2003814, BRCA N2006051, BRCAN2015402, BRCAN2021325, BRCOC2001355, BRCOC2006164, BRHIP2029663, BRHIP3001481, BRHIP3002000, BRHIP3002114, BRHIP3002141, BRHIP3003063, BRHIP3003126, BRHIP3003795, BRHIP3004725, BRHIP3005307, BRHIP3005673, BRHIP3007195, BRHIP3007223, BRHIP3011082, BRHIP3012289, BRHIP3016032, BRHIP3019643, BRHIP3021019, BRHIP3032374, BRHIP3033557, BRHIP3035006, BRHIP3037543, BRHIP3038030, BRHIP3041587, BRSSN2004710, BRSSN2011843, BRSTN2011961, BRSTN2016918, BRTHA2001304, BRTHA2005448, BRTHA2026290, BRTHA2026311, BRTHA2027250, BRTHA2030036, BRTHA2033683, BRTHA2035743, BRTHA2036295, BRTHA2037247, BRTHA3003736, BRTHA3010135, BRTHA3014547, BRTHA3021786, BRTHA3023403, BRTHA3026916, CHONS2002829, COLON2004351, CTONG2010330, CTONG2020582, CTONG2026987, FCBBF3001018, FCBBF3021191, FEBRA2013570, FEBRA2026582, FEHRT2002708, FEKID2002637, HHDP C2008185, HSYRA2004550, KIDNE2004531, KIDNE2010049, LYMPB2002236, NT2RI2004818, NT2RI3001967, NT2RP7016508, NT2RP8003490, NT2RP8003787, NT2RP8005546, OCBBF2000831, OCBBF2007039, OCBBF2024589, OCBBF3001616, OCBBF3004487, OCBBF3021086, OCBBF3023175, OCBBF3025503, OCBBF3026088, OCBBF3026361, PLACE5000492, PLACE6003004, PLACE7003985, PLACE7004103, PLACE7004961, PLACE7006090, PLACE7007379, PLACE7008136, PLACE7012111, PLACE7014247, PLACE7016526, SKMUS2008585, SKMUS2009557, SMINT2011406, SMINT2011509, SYNOV2017179, SYNOV4003174, SYNOV4009139, TIESE2000609, TIESE2002665, TESTI2001364, TESTI2005112, TESTI2007490, TESTI2018335, TESTI2021112, TESTI2021654, TESTI2030901, TESTI2037877, TESTI2049062, TESTI4000621, TESTI4002774, TESTI4002799, TESTI4003404, TESTI4003565, TE

STI4003602, TESTI4003703, TESTI4005399, TESTI4007671, TESTI4010544, TESTI4010721, TESTI4012960, TESTI4017854, TESTI4020342, TESTI4020596, TESTI4020819, TESTI4021129, TESTI4021197, TESTI4023096, TESTI4024494, TESTI4026080, TESTI4028182, TESTI4031066, TESTI4033177, TESTI4040598, TESTI4041482, TESTI4046073, TESTI4047808, TESTI4049786, TESTI4051424, TESTI4051865, TESTI4052219, THYMU3000390, THYMU3002825, THYMU3014372, THYMU3023400, THYMU3025683, THYMU3026306, THYMU3026479, THYMU3031878, THYMU3032798, THYMU3034671, THYMU3036953, THYMU3041428, THYMU3047115, THYMU3047891, TRACH2022113, TRACH2024730, TRACH3003037, TRACH3005274, TRACH3006800, TRACH3009008, TRACH3009061, TRACH3011313, TRACH3016455, TRACH3017409, TRACH3018108, TRACH3018261, TRACH3019621, TRACH3021544, TRACH3023516, TRACH3024020, TRACH3024081, TRACH3024342, TRACH3024512, TRACH3025316, TRACH3026303, TRACH3026650, TRACH3027229, TRACH3027701, TRACH3029329, TRACH3032150, TRACH3036750, TRACH3038399, TSTOM2001571, UTERU2024042, UTERU3001946, UTERU3010604, UTERU3010919, UTERU3015299, UTERU3017441, UTERU3019708, UTERU3020090, UTERU3022168

【 0 2 4 7 】

細胞分裂・増殖関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 3 クローンであった。

BRACE3022303, BRAWH3017260, BRHIP2008756, BRHIP3028570, BRSTN2006638, NT2RI2004818, PLACE7009563, PLACE7016526, SMINT2014721, THYMU3025642, THYMU3033626, TRACH3029329, UTERU3010919

【 0 2 4 8 】

細胞骨格関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 1 クローンであった。

BRACE2046976, BRACE3013874, BRACE3047482, BRACE3051819, BRAMY3015549, BRAWH3015175, BRAWH3018548, BRAWH3021580, BRAWH3024186, BRAWH3024506, BRAWH3029385, BRAWH3032298, BRAWH3049544, BRHIP3003340, BRHIP3012736, BRHIP3036936, BRSTN2016918, BRTHA2020910, BRTHA2025869, BRTHA2031917,

BRTHA3011361, BRTHA3025073, CTONG2008989, HSYRA2007338, LYMPB2002458, OCBBF3008835, OCBBF3027969, PEBLM2006298, PLACE7000266, PLACE7004103, PLAC E7004961, SMINT2011406, SYNOV4003174, TESTI2006543, TESTI2034913, TESTI4 001517, TESTI4005653, TESTI4008305, TESTI4041049, TESTI4051424, TESTI4051865, THYMU3020221, THYMU3038158, TLUNG2000654, TRACH3002890, TRACH3006379, TRACH3012460, TRACH3018524, TRACH3020769, TRACH3028837, UTER U3011837

【 0 2 4 9 】

核蛋白質・RNA合成関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 2 9 クローンであった。

BRACE2016896, BRACE3032537, BRACE3034183, BRACE3039288, BRAWH3013264, BRAWH3032571, BRCOC2006164, BRHIP3004725, BRSSN2011843, BRTHA2026290, BRTHA3003736, BRTHA3014547, NT2RP7016508, NT2RP8005546, OCBBF3004487, OCBBF3 021086, OCBBF3026361, PLACE5000492, TESTI4000621, TESTI4002799, TESTI4010721, TESTI4012960, THYMU3014372, THYMU3033626, THYMU3041428, TRACH3017409, TRACH3029462, UTERU3010919, UTERU3019708

【 0 2 5 0 】

蛋白質合成・輸送関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 5 0 クローンであった。

BRACE3033525, BRACE3041059, BRAMY4001652, BRAWH3010657, BRAWH3013264, BRAWH3034668, BRAWH3036247, BRAWH3037428, BRAWH3037979, BRCAN2000923, BRCA N2002892, BRCAN2006051, BRCAN2021325, BRCAN2021718, BRHIP2029663, BRHIP3 002000, BRHIP3003126, BRHIP3007223, BRHIP3011082, BRSTN2010089, BRTHA2036295, BRTHA3012265, CHONS2002829, D9OST2004417, HHDPC2008185, NE TRP2003448, OCBBF2007039, OCBBF3021086, PLACE6003004, PLACE6010925, PLAC E7006498, PLACE7007379, PLACE7012111, PLACE7016526, TESTI2023903, TESTI2 036285, TESTI4003602, TESTI4012960, TESTI4014415, TESTI4030864, TESTI4051865, THYMU3036953, THYMU3047891, TRACH3004113, TRACH3006800, TRACH3009061, TRACH3021544, TRACH3026650, UTERU3001946, UTERU3012414

【 0 2 5 1 】

細胞防御関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 4 クローンであった。

BRHIP3027191, SYNOV4009575, TESTI2023903, TRACH3029462

【 0 2 5 2 】

発生、分化関連蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 クローンであった。

CHONS2000797

【 0 2 5 3 】

DNA・RNA結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 1 8 5 クローンであった。

ASTR02016114, BEAST2000981, BRACE2012625, BRACE2016896, BRACE2019348, BRACE3019941, BRACE3025719, BRACE3026844, BRACE3026947, BRACE3029021, BRACE3031743, BRACE3032537, BRACE3034183, BRACE3039288, BRACE3040239, BRACE3041162, BRACE3047482, BRACE3050270, BRALZ2013621, BRAMY2041347, BRAMY3000692, BRAMY3007078, BRAMY3011581, BRAMY3014027, BRAMY4002575, BRAWH2000256, BRAWH2014053, BRAWH2016209, BRAWH3000446, BRAWH3005886, BRAWH3009961, BRAWH3011623, BRAWH3013009, BRAWH3013264, BRAWH3015175, BRAWH3015610, BRAWH3017477, BRAWH3021580, BRAWH3022651, BRAWH3027533, BRAWH3027607, BRAWH3027880, BRAWH3028796, BRAWH3031342, BRAWH3031710, BRAWH3032571, BRAWH3035403, BRAWH3035936, BRAWH3036247, BRAWH3036334, BRAWH3038055, BRAWH3042787, BRAWH3044122, BRCAN2020331, BRCAN2021452, BRCOC2006164, BRCOC2012386, BRHIP2027077, BRHIP2029663, BRHIP3002141, BRHIP3004725, BRHIP3005037, BRHIP3007609, BRHIP3017256, BRHIP3019824, BRHIP3027651, BRHIP3028246, BRHIP3039592, BRSSN2011843, BRSTN2012069, BRTHA2026290, BRTHA2037247, BRTHA3000456, BRTHA3003225, BRTHA3003736, BRTHA3010212, BRTHA3014000, BRTHA3014547, BRTHA3028339, CHONS2000797, CTONG2003517, CTONG2006235, CTONG2011801, CTONG2026987, D90ST2003106, FCBBF3020030, FEBRA2002260, FEBRA2028457, FEHRT2002708, HCASM2008154, KIDN

E2018268, NETRP2003103, NETRP2004017, NT2RI3009480, NT2RP7016508, NT2RP8005546, NTONG2003805, NTONG2008483, OCBBF2014745, OCBBF2016928, OCBBF3001333, OCBBF3001616, OCBBF3004487, OCBBF3008392, OCBBF3019269, OCBBF3020263, OCBBF3021086, OCBBF3021361, OCBBF3022827, OCBBF3025503, OCBBF3026361, PLACE5000492, PLACE7004103, PLACE7005169, PLACE7007973, PLACE7008136, PLACE7009757, PLACE7018512, PROST2002078, SMINT2011509, SMINT2014721, SPLEN2012571, SPLEN2036608, TIESE2000609, TIESE2000904, TESTI2036822, TESTI2040377, TESTI4000370, TESTI4000621, TESTI4001679, TESTI4002799, TESTI4003796, TESTI4003944, TESTI4005322, TESTI4005470, TESTI4012960, TESTI4024494, TESTI4028182, TESTI4032913, TESTI4039904, TESTI4051054, TESTI4052775, THYMU2008207, THYMU2038199, THYMU3008105, THYMU3012983, THYMU3014372, THYMU3021586, THYMU3022434, THYMU3023400, THYMU3026000, THYMU3030072, THYMU3037617, THYMU3040829, THYMU3041428, THYMU3043200, THYMU3045704, TKIDN2003396, TLIVE2001616, TLUNG2000654, TRACH3002752, TRACH3003037, TRACH3003458, TRACH3004113, TRACH3004412, TRACH3004424, TRACH3005274, TRACH3010079, TRACH3010167, TRACH3015951, TRACH3017409, TRACH3021778, TRACH3022109, TRACH3026303, TRACH3028180, TRACH3036750, UTERU2037423, UTERU3012293, UTERU3015011, UTERU3016070, UTERU3019708, UTERU3020090, UTERU3022168, UTERU3022588, UTERU3023141

【 0 2 5 4 】

ATP・GTP結合蛋白質のカテゴリーに属すると推定されたクローンは、以下の 41 クローンであった。

BRACE3042409, BRAWH2002333, BRAWH2014053, BRAWH3015175, BRAWH3029385, BRAWH3029806, BRAWH3034743, BRAWH3037428, BRAWH3047692, BRCAN2000923, BRCA N2002892, BRCAN2022126, BRCOC2001355, BRCOC2006164, BRHIP3007195, BRSSN2004710, BRTHA2026290, BRTHA2033683, BRTHA3026916, CTONG2020582, HSYRA2004550, NETRP2003448, PLACE6019600, PLACE7004961, PLACE7006498, PLACE7016526, SMINT2011406, TESTI4010544, TESTI4014415, TESTI4028182, TESTI4029731, TESTI4040559, TESTI4041482, TESTI4052219, THYMU3013785, THYMU3

047115, TRACH2024730, TRACH3024081, TRACH3029329, TRACH3031660,
UTERU3012414

【 0 2 5 5 】

以下の 1 7 2 クローンについては、Pfamでヒットデータがあったものの、上記のいずれのカテゴリに属するか明らかでないクローンであった。今後同様のドメイン、モチーフを持つタンパク質のデータの蓄積と共に機能がより詳細に解明され、上記のカテゴリに分類できる可能性がある。クローン名と機能ドメイン名をクローン名//機能ドメイン名のように示し、複数の機能ドメインがヒットした場合には//で区切って並記した。

なお同一の機能ドメインが複数ヒットした場合も省略せずに記載した。

BLADE2001031// Thrombospondin type 1 domain

BRACE2010336// TPR Domain

BRACE2013009// EF hand

BRACE2017872// PWWP domain

BRACE2023744// Translationally controlled tumor protein

BRACE2034434// Protein of unknown function

BRACE3001973// EGF-like domain//Laminin G domain

BRACE3002756// SAM domain (Sterile alpha motif)

BRACE3005903// K-box region//TSC-22/dip/bun family

BRACE3014523// Wiskott Aldrich syndrome homology region 2

BRACE3019570// Troponin

BRACE3022340// Troponin

BRACE3026345// Insulin/IGF/Relaxin family

BRACE3036283// DnaJ domain

BRACE3040644// Low-density lipoprotein receptor domain class A//EB module//CUB domain

BRACE3043597// KOW motif

BRACE3046466// EGF-like domain//Laminin G domain//Laminin EGF-like (Domains III and V)//EB module

BRACE3048615// Leucine Rich Repeat
BRALZ2010842// Mitochondrial carrier proteins
BRAMY2031516// wnt family of developmental signaling proteins
BRAMY2041384// Annexin
BRAMY3002886// Domain of unknown function//CBS domain
BRAMY3011501// SAP domain//SPRY domain
BRAMY3015086// FERM domain (Band 4.1 family)
BRAMY3018754// Protein of unknown function//Domain of unknown function
BRAMY4000962// Tudor domain
BRAWH2011796// S-100/ICaBP type calcium binding domain//EF hand
BRAWH2016223// TPR Domain
BRAWH3001783// Cadherin domain
BRAWH3003573// EF hand
BRAWH3008167// Sushi domain (SCR repeat)//CUB domain
BRAWH3011331// Disintegrin
BRAWH3011577// KRAB box
BRAWH3014609// Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine rich repeat C-terminal domain
BRAWH3021574// Wiskott Aldrich syndrome homology region 2
BRAWH3022347// Leucine Rich Repeat
BRAWH3022719// Eukaryotic initiation factor 4E
BRAWH3024231// TPR Domain
BRAWH3026938// PDZ domain (Also known as DHR or GLGF).
BRAWH3027440// TPR Domain//PPR repeat
BRAWH3030772// Ank repeat
BRAWH3030910// SAM domain (Sterile alpha motif)
BRAWH3033448// TPR Domain
BRAWH3034775// SAP domain//SPRY domain
BRAWH3038252// Formin Homology 2 Domain

BRAWH3038324// Dehydrins
BRAWH3038827// Kelch motif//BTB/POZ domain
BRAWH3042438// 'Paired box' domain//EF hand//Phorbol esters/diacylglycerol binding domain (C1 domain)
BRAWH3042568// Homeobox domain
BRAWH3044151// Thrombospondin type 1 domain//Keratin, high sulfur B2 protein
BRAWH3045118// DnaJ domain
BRAWH3048374// Sushi domain (SCR repeat)//Keratin, high sulfur B2 protein
BRCAN2010665// PDZ domain (Also known as DHR or GLGF).
BRCAN2019907// EF hand
BRCAN2020234// Lipocalin / cytosolic fatty-acid binding protein family
BRCAN2025093// Ank repeat//Flagellar FliJ protein
BRCOC2006639// Leucine Rich Repeat
BRHIP2013958// Domain of unknown function//MSP (Major sperm protein) domain
BRHIP2026346// Formin Homology 2 Domain
BRHIP2027563// Kelch motif
BRHIP3001878// POT family
BRHIP3004710// TPR Domain
BRHIP3005142// Adaptin N terminal region
BRHIP3005231// TPR Domain
BRHIP3006449// Armadillo/beta-catenin-like repeats
BRHIP3007424// wnt family of developmental signaling proteins
BRHIP3009753// CUB domain//Low-density lipoprotein receptor domain class A
BRHIP3010289// Delta serrate ligand//Kelch motif//Plexin repeat//Lectin C-type domain//Laminin EGF-like (Domains III and V)//Keratin, high sulfur

r B2 protein

BRHIP3020733// Keratin, high sulfur B2 protein

BRHIP3029409// NTR/C345C module

BRHIP3030230// Pentaxin family

BRHIP3033734// Keratin, high sulfur B2 protein

BRSSN2015497// Tudor domain

BRTHA2038345// Ank repeat

BRTHA3011187// EF hand

BRTHA3021971// Putative peptidoglycan binding domain

BRTHA3026161// Adenosine-deaminase (editase) domain

BRTHA3027171// Scorpion short toxins

BRTHA3027638// Matrix protein (MA), p15

CHONS2001287// Insulin-like growth factor binding proteins//Thyroglobulin type-1 repeat

CHONS2001834// Plexin repeat

DFNES2011221// Rotavirus NS26

ERLTF2002178// Kelch motif

FCBBF3012443// Leucine rich repeat N-terminal domain//Leucine Rich Repeat//Leucine rich repeat C-terminal domain

FCBBF3024911// PWWP domain

FCBBF5000384// BAF60b domain of the SWIB complex

FEBRA2000805// Uncharacterized protein family UPF0054

FEBRA2023498// Leucine rich repeat N-terminal domain//Leucine Rich Repeat

FEKID2002493// wnt family of developmental signaling proteins

HCHON2009766// eIF4-gamma/eIF5/eIF2-epsilon

JCM LC2002751// von Willebrand factor type D domain//Plant PEC family metallothionein//Trypsin Inhibitor like cysteine rich domain//von Willebrand factor type C domain

KIDNE2015987// EGF-like domain//Keratin, high sulfur B2 protein//Zona pe
llucida-like domain

NT2RI3001573// Leucine Rich Repeat

NT2RI3005923// Cadherin domain

NT2RI3009524// EGF-like domain//Metallothionein//Laminin G domain

NT2RP7007387// Armadillo/beta-catenin-like repeats//picornavirus capsid
protein

NT2RP7020343// Transforming growth factor beta like domain//Keratin, hig
h sulfur B2 protein

NT2RP8000633// VPR/VPX protein

NT2RP8001604// CUB domain//Sushi domain (SCR repeat)

NT2RP8006452// African swine fever virus multigene family 360 protein//L
eucine Rich Repeat

NT2RP8007920// PPR repeat//LIM domain containing proteins

NT2RP8009119// Picornavirus 2B protein

OCBBF3001202// DENN (AEX-3) domain

OCBBF3005330// Domain found in Dishevelled, Egl-10, and Pleckstrin//TCP-
1/cpn60 chaperonin family

OCBBF3023913// R3H domain//Retroviral Vif (Viral infectivity) protein

OCBBF3026979// Laminin G domain//Thrombospondin N-terminal -like domains
//von Willebrand factor type C domain//EGF-like domain//EB module//Plant
PEC family metallothionein//Trypsin Inhibitor like cysteine rich domain
//Metallothionein

PEBLM2001803// Vacuolar sorting protein 9 (VPS9) domain

PLACE6001933// Receptor L domain

PLACE7002303// Homeobox domain

PUAEN2000594// Poly-adenylate binding protein, unique domain.

PUAEN2000684// Geminivirus AL2 protein//Leucine Rich Repeat

SMINT2010753// TPR Domain//PPR repeat

SPLEN2022785// Polyomavirus coat protein
SPLEN2028417// Homeobox domain
SYNOV2003326// TSC-22/dip/bun family
TBAES2003917// Ank repeat
TBAES2007428// Scorpion short toxins//EGF-like domain
TESOP2002005// E7 protein, Early protein
TESTI2005564// EF hand
TESTI2009739// Tropomyosins//Domain of unknown function
TESTI2011020// Keratin, high sulfur B2 protein
TESTI2018867// FF domain
TESTI2049041// TPR Domain
TESTI4001569// Leucine Rich Repeat//KE2 family protein
TESTI4002141// Keratin, high sulfur B2 protein
TESTI4002868// Metallothionein
TESTI4004031// Domain of unknown function
TESTI4007965// Adaptin N terminal region//Gamma-adaptin, C-terminus
TESTI4011926// Gag P30 core shell protein
TESTI4013742// Leucine Rich Repeat//Hantavirus nucleocapsid protein//Troponin//Formin Homology 2 Domain//Apolipoprotein A1/A4/E family
TESTI4024294// Chorion protein
TESTI4035898// Kelch motif
TESTI4039451// Adaptin N terminal region
TESTI4041984// EGF-like domain//EB module//TB domain
TESTI4043166// Formin Homology 2 Domain
TESTI4046873// TPR Domain
TESTI4047328// von Willebrand factor type D domain//Trypsin Inhibitor like cysteine rich domain//Chitin binding domain//Metallothionein
TESTI4047569// Keratin, high sulfur B2 protein
TESTI4051015// Major intrinsic protein

TESTI4052598// Lectin C-type domain
THYMU3003007// TPR Domain
THYMU3012402// Armadillo/beta-catenin-like repeats
THYMU3015042// Polyomavirus coat protein
THYMU3015571// Chaperonins 10 Kd subunit
THYMU3017761// Gag P30 core shell protein
THYMU3019476// Matrix protein (MA), p15
THYMU3021755// HCO3- transporter family
THYMU3033649// Immunoreceptor tyrosine-based activation motif
THYMU3040126// Metallothionein
THYMU3046360// F-box domain.
TKIDN2011051// Keratin, high sulfur B2 protein
TKIDN2011160// Thrombospondin type 1 domain
TLIVE2007736// PDZ domain (Also known as DHR or GLGF).
TRACH3007689// Ank repeat//TPR Domain
TRACH3012106// FERM domain (Band 4.1 family)
TRACH3015346// Uncharacterized protein family UPF0004
TRACH3016805// Ank repeat
TRACH3018606// SAM domain (Sterile alpha motif)
TRACH3022296// DnaJ domain
TRACH3022758// EF hand
TRACH3023203// Flavivirus polyprotein propeptide
TRACH3028855// R3H domain//Uncharacterized protein family UPF0024
TRACH3030855// Serpins (serine protease inhibitors)
TRACH3032570// PDZ domain (Also known as DHR or GLGF).
UTERU2016669// Helix-hairpin-helix motif.
UTERU3001394// EGF-like domain
UTERU3009775// PDZ domain (Also known as DHR or GLGF).
UTERU3011558// GTPase of unknown function

UTERU3011579// Plant PEC family metallothionein

UTERU3017995// UBX domain

UTERU3018255// Thrombospondin type 1 domain

UTERU3021850// Thrombospondin type 1 domain//DnaJ central domain (4 repeats)

【 0 2 5 6 】

またこれら以外にPfamでヒットデータがなかった残りのクローンについても、今後タンパク質のデータの蓄積と共に新たなドメイン、モチーフが見い出された場合、再びクローンの推定アミノ酸配列を新しいデータベースに対して解析することで新たな機能を有したドメイン、モチーフが発見され、カテゴリー分類できる可能性がある。

【 0 2 5 7 】

実施例 8. in silicoにおける発現頻度解析

実施例 1 に示した様々な組織・細胞由来のcDNAライブラリーを作製し、各ライブラリーからcDNAクローンを無作為に選択して、その5'末端領域の配列を決定し、データベース化した。本データベースは1,402,070個のクローンの塩基配列をデータベース化したものであり、解析母数としては十分なデータベースである。

次にこのデータベースにある各クローンの塩基配列を、塩基配列の相同性検索プログラムによって相同な配列同士をカテゴライズし（クラスター化）、各クラスターに属するクローン数を各ライブラリー毎に集計し規格化することによって、ある遺伝子のcDNAライブラリー内での存在比を解析した。この解析によって、cDNAライブラリーのソースとなっている組織や細胞における、ある遺伝子の発現頻度情報を得た。

【 0 2 5 8 】

次に本発明のcDNAの塩基配列を持つ遺伝子の、組織や細胞間での発現を解析するために、大量のcDNAクローンを解析した組織や細胞由来のライブラリーを組織・細胞間での発現量の比較の対象にした。すなわち600個以上のcDNAクローンの塩基配列を解析した組織や細胞について、先に規格化した数値を組織間や細胞

間で比較し、遺伝子の発現頻度の変化を解析した。この解析によって以下に続く病態や機能に関連する遺伝子であることが示された。なお、以降に示される表 2 ～ 2 4 中の各数値は、相対的な発現頻度を示し、数値が大きいほど発現量が多いことを示す。

【 0 2 5 9 】

骨粗鬆症に関連する遺伝子

骨粗鬆症とは、骨の成分が全体として減少し、骨折しやすくなった病態であるが、その発症には骨を産生する骨芽細胞と、骨を吸収する破骨細胞の働きのバランス、すなわち骨代謝が関与する。したがって単球／マクロファージ系の前駆細胞から分化する破骨細胞 (Molecular Medicine 38. 642-648. (2001)) の増加に関連する遺伝子は、骨代謝に関連した骨粗鬆症に関する遺伝子である。

【 0 2 6 0 】

単球／マクロファージ系の前駆細胞 (糖タンパク質CD34を発現している細胞：CD34+細胞) での発現頻度と比較して、CD34+細胞を破骨細胞分化因子 (Molecular Medicine 38. 642-648. (2001)) で処理した細胞で増加または減少する遺伝子を、塩基配列情報にしたがって解析し、探索した。CD34+細胞のRNAから作製したライブラリー (CD34C)、CD34+細胞を破骨細胞分化因子で処理した細胞のRNAから作製したライブラリー (D30ST, D60STまたはD90ST) のcDNAを解析して比較した結果 (表 2)、両方で発現変化のある遺伝子は以下の 1 2 クローンであった。BRAWH3018063, BRHIP3020046, BRSSN2013696, BRSTN2012069, BRTHA2027229, D90ST2003106, D90ST2003989, D90ST2004417, OCBBF2016928, TESTI4005653, TESTI4013474, THYMU3032798

これらのクローンは骨粗鬆症に関する遺伝子である。

【 0 2 6 1 】

神経細胞分化関連遺伝子

神経細胞の分化に関する遺伝子は、神経疾患の治療に有用な遺伝子である。神経系の細胞を分化誘導して発現変化する遺伝子は、神経疾患に関すると考えられている。

神経系の培養細胞NT2を分化誘導 (レチノイン酸(RA)刺激またはRA刺激後さら

に増殖阻害剤処理)して発現変化する遺伝子を探索した。未分化なNT2細胞由来のライブラリー (NT2RM) と分化誘導処理した細胞のライブラリー (NT2RP, NT2RIまたはNT2NE) のcDNAを解析して比較した結果 (表3)、両者で発現変化のある遺伝子は以下の102クローンであった。

BLADE2004849, BRACE2003628, BRACE2012528, BRAMY2023939, BRAMY2031516, BRAMY4002628, BRAWH3010461, BRAWH3017259, BRAWH3018063, BRAWH3022651, BRAWH3024186, BRCAN2019653, BRCAN2022126, BRCOC2012386, BRHIP3002000, BRHIP3007223, BRHIP3021019, BRSTN2011961, BRSTN2012069, BRTHA2033155, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3021971, CHONS2002829, CTONG2006235, FCBBF3012443, FEBRA2026582, LIVER2008465, NT2NE2011107, NT2NE2016041, NT2RI2004818, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI2023671, NT2RI2028537, NT2RI3001573, NT2RI3001967, NT2RI3005861, NT2RI3005923, NT2RI3007095, NT2RI3008179, NT2RI3009480, NT2RI3009524, NT2RP7003439, NT2RP7007387, NT2RP7014178, NT2RP7014778, NT2RP7016508, NT2RP7017139, NT2RP7019682, NT2RP7020343, NT2RP8000633, NT2RP8001363, NT2RP8001407, NT2RP8001584, NT2RP8001604, NT2RP8001605, NT2RP8003490, NT2RP8003657, NT2RP8003787, NT2RP8005546, NT2RP8006452, NT2RP8006521, NT2RP8007416, NT2RP8007503, NT2RP8007920, NT2RP8008057, NT2RP8009119, NT2RP8009248, NTONG2008483, OCBBF2003518, OCBBF3001333, OCBBF3004908, PLACE7004103, PROST2017910, SMINT2009292, SPLEN2012571, TIESE2000904, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4005653, TESTI4007965, TESTI4012960, TESTI4018436, THYMU3001776, THYMU3002887, THYMU3029795, THYMU3041428, THYMU3047115, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3009008, TRACH3016805, TRACH3016885, TRACH3026303, UTERU2016669

これらの遺伝子は神経疾患に関する遺伝子である。

【 0 2 6 2 】

アルツハイマー病関連遺伝子

アルツハイマー病とは記憶力が低下し、進行すれば生活が困難となり介護が必

要となる脳神経系の疾患であり、進行すれば脳そのものが萎縮する。その発症の要因はストレスなどの環境因子、高血圧やコレステロール血症などの血管因子も関わりがあるといわれているが、未だ不明である。したがって、正常脳組織とアルツハイマーの病態組織を比較した時、発現に差のある遺伝子はアルツハイマー病に関連する遺伝子であり、病態の発症メカニズムの解明や、遺伝子診断に有用であると考えられる。アルツハイマー患者の脳皮質由来のライブラリー（BRALZ、BRASW）と、正常全脳組織由来のライブラリー（BRAWH）のcDNAを解析して比較した結果（表4）、両者で発現変化のある遺伝子は以下の298クローンであった。

ASTR02016114, BRACE2002392, BRACE2012528, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRALZ2003119, BRALZ2007661, BRALZ2008930, BRALZ2010842, BRALZ2011337, BRALZ2013621, BRALZ2013690, BRALZ2014054, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548,

BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2019653, BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3003063, BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSTN2010089, BRSTN2012069, BRSTN2016992, BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, CTONG2006235, CTONG2009033, CTONG2020582, D90ST2003106, DFNES2001829, KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PL

ACE7006240, PROST2007444, PROST2017910, TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4013474, TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3041428, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3013167

これらの遺伝子はアルツハイマー病に関する遺伝子である。

【 0 2 6 3 】

パーキンソン病関連遺伝子

パーキンソン病とは脳内の黒質で作られるドーパミンという神経伝達物質が十分量作られなくなり、その結果、手が震え、筋肉の動きが固くなって身体の動きが鈍くなる等の運動障害を引き起こす脳神経系の疾患である。脳の神経細胞は通常、歳を取るにつれて少しずつ減少するが、パーキンソン病では黒質の神経細胞が普通よりも早く著しく減少する。よって脳組織全体と黒質とを比較した時、発現に差のある遺伝子は黒質特異的な変動をするパーキンソン病に関連する遺伝子であり、発症メカニズムの解明や遺伝子診断に有用であると考えられる。黒質由来のライブラリー (BRSSN) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 5)、両者で発現変化のある遺伝子は以下の 305 クローンであった。

ASTRO2016114, BRACE2012528, BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3025719, BRACE3026802, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BR

AWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH

H3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP2029643, BRHIP3001573, BRHIP3002000, BRHIP3003063, BRHIP3003984, BRHIP3004774, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSSN2004303, BRSSN2004710, BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198, BRSSN2013696, BRSSN2015497, BRSSN2018218, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016992, BRSTN2017104, BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, CTONG2006235, CTONG2009033, CTONG2011801, CTONG2020582, D90ST2003106, DFNES2001829, KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292, T1ESE2000904, TBAES2007428, TESTI2005112, TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3022198, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3013167

これらの遺伝子はパーキンソン病に関する遺伝子である。

【 0 2 6 4 】

短期記憶・痴呆症に関連する遺伝子

脳組織の中で海馬とは記憶を扱う非常に重要な部位であり、得た情報の情報の要・不要を判断して、他の脳部位に記憶を蓄えさせる、記憶固定の働きがある。臨床的知見より、海馬に異常をきたしたり最悪海馬が無くなると、5分程度しか新しいことを覚えていられなくなる。また痴呆症患者の一部はこの海馬に異常をきたしていると考えられている。脳組織全体と海馬とを比較した時、発現に差のある遺伝子は記憶に関与したり、痴呆症に関連する遺伝子であり、記憶のメカニズム解明や遺伝子診断に有用であると考えられる。海馬由来のライブラリー (BRHIP) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表6)、両者で発現変化のある遺伝子は以下の438クローンであった。

ASTRO2016114, BRACE2002392, BRACE2012528, BRACE2017359, BRACE2017397, BRACE2017844, BRACE3004046, BRACE3004371, BRACE3004767, BRACE3009416, BRACE3022340, BRACE3027931, BRACE3029021, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3036156, BRACE3039358, BRACE3040863, BRACE3042326, BRACE3042432, BRACE3045078, BRACE3045981, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005184, BRAMY3005912, BRAMY3007078, BRAMY3008436, BRAMY4000915, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3

016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260,
BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BR
AWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAW
H3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3
021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724,
BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BR
AWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAW
H3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3
024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420,
BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BR
AWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAW
H3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3
029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910,
BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BR
AWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAW
H3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3
034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914,
BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BR
AWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAW
H3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2
010665, BRCAN2019953, BRCAN2022126, BRCAN2025093, BRCOC2012386,
BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177, BRHIP2011199, BR
HIP2013958, BRHIP2015153, BRHIP2016125, BRHIP2017714, BRHIP2020930, BRHI
P2021929, BRHIP2023735, BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2
027563, BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626,
BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338, BRHIP3001360, BR
HIP3001481, BRHIP3001573, BRHIP3001878, BRHIP3002000, BRHIP3002114, BRHI
P3002124, BRHIP3002141, BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3
002931, BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340,

BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710, BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037, BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673, BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294, BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172, BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409, BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082, BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753, BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269, BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3012185, BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997, BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675, BRHIP3015854, BRHIP3016032, BRHIP3016421, BRHIP3017109, BRHIP3017146, BRHIP3017256, BRHIP3017558, BRHIP3017855, BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3019880, BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733, BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656, BRHIP3023922, BRHIP3024703, BRHIP3024820, BRHIP3025795, BRHIP3025844, BRHIP3026231, BRHIP3026651, BRHIP3027160, BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3028246, BRHIP3028570, BRHIP3028742, BRSTN2010089, BRSTN2012069, BRSTN2016992, BRTHA2001953, BRTHA2008502, BRTHA2031517, BRTHA2033155, BRTHA2035743, BRTHA3003417, BRTHA3003736, BRTHA3005988, BRTHA3007662, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BRTHA3012265, BRTHA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, CHONS2002829, CTONG2006235, CTONG2009033, CTONG2020582, D9OST2003106, DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2000831, OCBBF2003518, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240, PROST2007444, SMINT2012179, SYNOV4004210, TBAES2007428, TESTI2005112, TESTI2005564, TESTI2021654, TESTI4001569, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TE

STI4003944, TESTI4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158, TESTI4029297, THYMU3000776, THYMU3002887, THYMU3003007, THYMU3003350, THYMU3007308, THYMU3008105, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3034671, THYMU3037827, THYMU3038214, THYMU3044075, TKIDN2000319, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3022198, TRACH3024342, TRACH3024671, TRACH3025316, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, TSTOM2000235, UTERU3005422, UTERU3010409, UTERU3013167, UTERU3016273

これらの遺伝子は記憶および痴呆症に関する遺伝子である。

【 0 2 6 5 】

平衡感覚・運動機能に関する遺伝子

小脳は平衡感覚と筋肉運動、運動学習の中枢である。この領域は運動の調節に参与していると考えられており、小脳が動作することによって無意識的にスムーズな運動をすることが可能になる。また、運動だけでなく読み書きなどより高次の運動の慣れにも小脳が参与していることも最近の研究で解明されつつある。脳組織全体と小脳とを比較した時、発現に差のある遺伝子は平衡感覚や運動機能に参与する遺伝子であり、脳が制御する運動機能の分子メカニズム解明に有用であると考えられる。小脳由来のライブラリー (BRACE) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 7)、両者で発現変化のある遺伝子は以下の 5 0 2 クローンであった。

ASTRO2016114, BRACE1000475, BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956, BRAC

E2030039, BRACE2032584, BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973, BRACE3002344, BRACE3002541, BRACE3002756, BRACE3003866, BRACE3004046, BRACE3004371, BRACE3004767, BRACE3004887, BRACE3004981, BRACE3005870, BRACE3005903, BRACE3006553, BRACE3007649, BRACE3007869, BRACE3009075, BRACE3009265, BRACE3009392, BRACE3009416, BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774, BRACE3013418, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3014714, BRACE3015090, BRACE3015898, BRACE3016020, BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810, BRACE3016862, BRACE3017253, BRACE3018083, BRACE3019570, BRACE3019611, BRACE3019817, BRACE3019941, BRACE3020356, BRACE3020669, BRACE3021430, BRACE3021517, BRACE3021805, BRACE3022051, BRACE3022303, BRACE3022312, BRACE3022340, BRACE3022847, BRACE3023604, BRACE3024379, BRACE3024444, BRACE3024497, BRACE3024537, BRACE3024879, BRACE3025627, BRACE3025719, BRACE3026161, BRACE3026290, BRACE3026345, BRACE3026456, BRACE3026802, BRACE3026844, BRACE3026947, BRACE3027256, BRACE3027931, BRACE3028360, BRACE3028895, BRACE3028998, BRACE3029005, BRACE3029021, BRACE3029205, BRACE3029447, BRACE3030538, BRACE3031161, BRACE3031184, BRACE3031185, BRACE3031315, BRACE3031372, BRACE3031579, BRACE3031728, BRACE3031743, BRACE3031843, BRACE3032385, BRACE3032537, BRACE3032538, BRACE3032631, BRACE3032980, BRACE3033525, BRACE3034183, BRACE3034389, BRACE3034964, BRACE3034993, BRACE3035168, BRACE3036156, BRACE3036271, BRACE3036283, BRACE3037612, BRACE3037637, BRACE3037803, BRACE3038012, BRACE3038030, BRACE3038570, BRACE3038760, BRACE3039288, BRACE3039358, BRACE3039378, BRACE3039454, BRACE3040012, BRACE3040239, BRACE3040504, BRACE3040644, BRACE3040863, BRACE3041059, BRACE3041162, BRACE3041827, BRACE3042046, BRACE3042210, BRACE3042326, BRACE3042409, BRACE3042432, BRACE3042594, BRACE3043597, BRACE3044090, BRACE3044172, BRACE3044247, BRACE3044377, BRACE3044495, BRACE3045078, BRACE3

045145, BRACE3045424, BRACE3045708, BRACE3045981, BRACE3046049,
BRACE3046152, BRACE3046294, BRACE3046466, BRACE3046491, BRACE3046609, BR
ACE3046837, BRACE3046855, BRACE3046966, BRACE3047018, BRACE3047482, BRAC
E3047801, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3004364, BRAMY3
005912, BRAMY3008436, BRAMY3009491, BRAWH2000256, BRAWH2002333,
BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BR
AWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAW
H2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2
016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638,
BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BR
AWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAW
H3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3
010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833,
BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BR
AWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAW
H3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3
014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610,
BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BR
AWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAW
H3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3
019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928,
BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BR
AWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAW
H3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3
023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231,
BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BR
AWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAW
H3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3
028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313,

BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2019953, BRCAN2022126, BRCAN2025093, BRCCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP2029643, BRHIP3001360, BRHIP3001573, BRHIP3002000, BRHIP3002114, BRHIP3003063, BRHIP3003126, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004774, BRHIP3005801, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSSN2011843, BRSSN2013696, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016992, BRTHA2033155, BRTHA2035743, BRTHA3003736, BRTHA3005988, BRTHA3009858, BRTHA3010135, BRTHA3010212, BRTHA3010530, BRTHA3011194, BRTHA3011265, BRTHA3011998, BRTHA3017791, BRTHA3020771, BRTHA3021708, BRTHA3021971, BRTHA3023403, CHONS2002829, CTONG2006235, CTONG2009033, CTONG2020582, CTONG2027959, D90ST2003106, DFNES2001829, KIDNE2010049, KIDNE2017153, LIVER2008465, MESAN2017133, NOVAR2000783, NT2RI2009233, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NT2RP8009119, NTONG2008483, NTONG2009468, OCBBF2003518, OCBBF2014745, OCBBF2018618, OCBBF3001333, OCBBF3004487, PLACE7004103, PLACE7006240, PROST2007444, TBAES2007428, TESTI2005112, TESTI2018867, TESTI2021654, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TESTI4004210, TESTI4005013, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4022158, TESTI4029297, TESTI4032913, TESTI4043223, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3007308, THYMU3021586, TH

YMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3033626, THYMU3034671, THYMU3037827, THYMU3038214, THYMU3044075, TLIVE2007736, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3007995, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3000670, UTERU3010409, UTERU3013167, UTERU3015011

これらの遺伝子は平衡感覚および運動機能に関する遺伝子である。

【 0 2 6 6 】

感覚器からの情報伝達に関与する遺伝子

視床は、大脳と結びつきの強い神経細胞が集まった部分であり、脊髄などから伝わってきた感覚情報を大脳の関係部分に伝えたり、大脳の運動の指令を調節する。例えば視覚では映像を大きさ、形、色に分け、聴覚では音声を音量、耳障りの良し悪しで分け、大脳皮質の感覚野に送る。脳組織全体と視床とを比較した時、発現に差のある遺伝子は感覚器からの情報伝達に関与する遺伝子であり、脳が制御する情報伝達の分子メカニズム解明に有用であると考えられる。視床由来のライブラリー (BRTHA) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 8)、両者で発現変化のある遺伝子は以下の 4 4 0 クローンであった。

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE2002392, BRACE2012528, BRACE2019348, BRACE3004371, BRACE3004767, BRACE3019941, BRACE3022312, BRACE3022340, BRACE3031185, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3036156, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2031516, BRAMY3002329, BRAMY3004126, BRAMY3005912, BRAMY3008436, BRAMY3009556, BRAMY3010654, BRAMY4001863, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BR

AWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH

H3038324, BRCAN2002892, BRCAN2010665, BRCAN2020234, BRCAN2022126, BRCAN2025093, BRCOC2006164, BRCOC2012386, BRHIP2013958, BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3002691, BRHIP3002920, BRHIP3003063, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004774, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3014675, BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSSN2015497, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016992, BRTHA2000969, BRTHA2001304, BRTHA2001953, BRTHA2002091, BRTHA2003759, BRTHA2005448, BRTHA2006720, BRTHA2008502, BRTHA2008598, BRTHA2010672, BRTHA2012189, BRTHA2014647, BRTHA2018304, BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566, BRTHA2020642, BRTHA2020695, BRTHA2020721, BRTHA2020781, BRTHA2020910, BRTHA2021212, BRTHA2021440, BRTHA2021450, BRTHA2022074, BRTHA2022914, BRTHA2022968, BRTHA2023402, BRTHA2023437, BRTHA2024177, BRTHA2024354, BRTHA2024712, BRTHA2025869, BRTHA2026071, BRTHA2026290, BRTHA2026311, BRTHA2027227, BRTHA2027229, BRTHA2027250, BRTHA2028297, BRTHA2029969, BRTHA2030036, BRTHA2030213, BRTHA2031517, BRTHA2031917, BRTHA2032763, BRTHA2033122, BRTHA2033155, BRTHA2033320, BRTHA2033469, BRTHA2033683, BRTHA2034281, BRTHA2034576, BRTHA2035743, BRTHA2036055, BRTHA2036295, BRTHA2037247, BRTHA2038279, BRTHA2038345, BRTHA2038353, BRTHA3000456, BRTHA3002411, BRTHA3003225, BRTHA3003417, BRTHA3003736, BRTHA3005988, BRTHA3006593, BRTHA3007469, BRTHA3007662, BRTHA3009858, BRTHA3010135, BRTHA3010212, BRTHA3010469, BRTHA3010530, BRTHA3010540, BRTHA3010717, BRTHA3011187, BRTHA3011194, BRTHA3011229, BRTHA3011265, BRTHA3011306, BRTHA3011361, BRTHA3011510, BRTHA3011892, BRTHA3011998, BRTHA3012265, BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3014105, BRTHA3014507, BRTHA3014547, BRTHA3014835, BRTHA3014854, BRTHA3014920, BRTHA3016616, BRTHA3017791, BRTHA3018409, BRTHA3018623, BRTHA3019183, BRTHA3020369, BRTHA3020771, BRTHA3021569, BRTHA3021708, BRTHA3021786, BRTHA3021971, BRTHA3022641, BRTHA3023403, BRTHA3023590, BRTHA3

023929, BRTHA3024600, BRTHA3025073, BRTHA3026161, BRTHA3026180, BRTHA3026556, BRTHA3026916, BRTHA3027171, BRTHA3027318, BRTHA3027638, BRTHA3027820, BRTHA3027879, BRTHA3027957, BRTHA3028339, BRTHA3028505, CHONS2002829, CTONG2006235, CTONG2009033, CTONG2011801, CTONG2020582, D90ST2003106, DFNES2001829, KIDNE2010049, LIVER2008465, MESAN2017133, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT2RP8007920, NTONG2008483, OCBBF2003518, OCBBF2009536, OCBBF2018618, OCBBF3001333, OCBBF3004487, OCBBF3008835, PLACE6003004, PLACE7004103, PLACE7006240, PROST2007444, SMINT2009292, TBAES2007428, TESTI2005112, TESTI2021654, TESTI2039342, TESTI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TESTI4004210, TESTI4004695, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4007965, TESTI4010979, TESTI4013474, TESTI4014908, TESTI4022158, TESTI4029297, TESTI4032913, THYMU3000776, THYMU3002887, THYMU3003350, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3008508, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3010409, UTERU3012414, UTERU3013167, UTERU3017995, UTERU3018172

これらの遺伝子は感覚器からの情報伝達に関する遺伝子である。

【 0 2 6 7 】

情動反応に関する遺伝子

扁桃は脳の感情中枢である。扁桃を通過した情報は感情反応、例えばパニックや恐怖反応などを引き起こす。刺激が扁桃で情動評価されて強い恐怖を生じたとき、扁桃は脳の各部に警戒信号を出す。その結果、手の平の発汗、心悸亢進、血圧上昇、アドレナリンの急激分泌等の反応が起きる。いわば扁桃体は身体に警戒信号を送り、その結果として体を警戒態勢に入らせる一種の防衛本能を司ってい

る組織とも言える。脳組織全体と扁桃とを比較した時、発現に差のある遺伝子は情動反応に関与する遺伝子であり、感情反応や恐怖反応、パニックなどの分子メカニズム解明に有用であると考えられる。扁桃由来のライブラリー (BRAMY) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果 (表 9)、両者で発現変化のある遺伝子は以下の 3 5 7 クローンであった。

ASTR02016114, BRACE2002392, BRACE2012528, BRACE2017397, BRACE2017844, BRACE3004371, BRACE3004767, BRACE3022340, BRACE3031185, BRACE3031315, BRACE3031743, BRACE3032385, BRACE3032631, BRACE3039358, BRACE3040863, BRACE3042432, BRACE3045981, BRAMY2015516, BRAMY2021098, BRAMY2022320, BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895, BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609, BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384, BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537, BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508, BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184, BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449, BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491, BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603, BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234, BRAMY4001652, BRAMY4001863, BRAMY4001913, BRAMY4002575, BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049,

BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2010665, BRCAN2022126, BRCAN2025093, BRCOC2012386, BRHIP2015153, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3002691, BRHIP3003063, BRHIP3003984, BRHIP3004215, BRHIP3004774, BRHIP3005673, BRHIP3007223, BRHIP3007409, BRHIP3008320, BRHIP3012736, BRHIP3014675, BRHIP3017146, BRHIP3017855, BRHIP3018784, BRHIP3020046, BRHIP3021019, BRHIP3028246, BRHIP3028570, BRSTN2010089, BRSTN2012069, BRSTN2016992, BRTHA2026071, BRTHA2033155, BRTHA3003736, BRTHA3005988, BRTHA3010135, BRTHA3010212, BRTHA3011194, BRTHA3011265, BR

THA3017791, BRTHA3020771, BRTHA3021971, BRTHA3023403, BRTHA3026916, CHON
S2002829, CTONG2006235, CTONG2009033, CTONG2020582, D90ST2003106, DFNES2
001829, KIDNE2010049, MESAN2017133, NT2RI2009233, NT2RI2010795,
NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001605, NT
2RP8007920, NTONG2008483, OCBBF2000831, OCBBF2003518, OCBBF2018618, OCBB
F2030927, OCBBF3001333, OCBBF3004487, OCBBF3009244, PLACE6008315, PLACE6
010936, PLACE7004103, PLACE7006240, PROST2007444, SPLEN2012571,
SYNOV4004210, SYNOV4009575, TBAES2007428, TESTI2005112, TESTI2021654, TE
STI4002072, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TEST
I4004210, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4014908, TESTI4
022158, TESTI4029297, TESTI4032913, TESTI4043223, TESTI4046073,
THYMU3000776, THYMU3002887, THYMU3003350, THYMU3008105, THYMU3019476, TH
YMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYM
U3032867, THYMU3037827, THYMU3038214, THYMU3044075, TRACH2013585, TRACH3
002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717,
TRACH3007625, TRACH3007689, TRACH3008632, TRACH3009008, TRACH3010079, TR
ACH3016805, TRACH3016885, TRACH3024342, TRACH3024671, TRACH3026303, TRAC
H3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, UTERU3
010409, UTERU3013167

これらの遺伝子は情動反応に関する遺伝子である。

【 0 2 6 8 】

癌関連遺伝子

癌の組織では、正常組織とは異なる遺伝子のセットが発現して組織・細胞の癌化に寄与していると考えられている。したがって、正常組織とは異なる発現をする遺伝子は癌関連遺伝子である。正常な組織と比較して癌組織で発現変化する遺伝子を探索した。

【 0 2 6 9 】

乳がん由来のライブラリー (TBAES) と、正常な乳房由来のライブラリー (BEAST) のcDNAを解析して比較した結果 (表 10)、両者で発現変化のある遺伝子は

以下の 1 0 クローンであった。

BRSTN2011961, BRSTN2012069, TBAES2003917, TBAES2005361, TBAES2007428, TBAES2007548, TBAES2007862, TESTI2005564, TESTI4017854, TRACH3016805

【 0 2 7 0 】

子宮頸癌由来のライブラリー (TCERX) と、正常な子宮頸管由来のライブラリー (CERVX) のcDNAを解析して比較した結果 (表 1 1)、両者で発現変化のある遺伝子は以下の 6 クローンであった。

BRACE2017397, BRHIP2027077, BRSTN2011961, BRSTN2012069, CERVX2000812, CERVX2000968

【 0 2 7 1 】

結腸がん由来のライブラリー (TCOLN) と、正常な結腸由来のライブラリー (COLON) のcDNAを解析して比較した結果 (表 1 2)、両者で発現変化のある遺伝子は以下の 1 0 クローンであった。

BRSTN2011961, BRSTN2012069, COLON2001829, COLON2001866, COLON2004351, COLON2004911, COLON2005623, COLON2005735, OCBBF3001333, SMINT2017964

【 0 2 7 2 】

食道がん由来のライブラリー (TESOP) と、正常な食道由来のライブラリー (NESOP) のcDNAを解析して比較した結果 (表 1 3)、両者で発現変化のある遺伝子は以下の 1 4 クローンであった。

BRAMY3004364, BRAWH3027533, BRHIP3007223, BRSTN2011961, BRSTN2012069, CTONG2011801, CTONG3002518, SMINT2009292, TESOP2002005, TESOP2003308, TESOP2004110, TESOP2008556, UTERU3015011, UTERU3017995

【 0 2 7 3 】

腎臓がん由来のライブラリー (TKIDN) と、正常な腎臓由来のライブラリー (KIDNE) のcDNAを解析して比較した結果 (表 1 4)、両者で発現変化のある遺伝子は以下の 4 3 クローンであった。

BRACE2002392, BRACE2012528, BRACE3004371, BRAMY2039630, BRAMY3004364, BRAMY3008436, BRAWH2004078, BRAWH3012662, BRAWH3021574, BRAWH3022651, BRAWH3037428, BRCAN2019953, BRCAN2022126, BRHIP3002000, BRHIP3002691, BRHIP3

012997, BRHIP3020046, BRSTN2012069, BRSTN2016992, BRTHA3010212, CTONG2006235, KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RI2015533, NT2RP7007387, OCBBF3004487, PLACE6008315, SYNOV4004210, TESTI2005112, THYMU3001776, THYMU3002887, THYMU3029795, THYMU3032867, TKIDN2000319, TKIDN2003396, TKIDN2010602, TKIDN2011051, TKIDN2011160

【 0 2 7 4 】

肝臓がん由来のライブラリー (TLIVE) と、正常な肝臓由来のライブラリー (LIVER) のcDNAを解析して比較した結果 (表 1 5)、両者で発現変化のある遺伝子は以下の 1 4 クローンであった。

BRAWH3022651, BRCAN2020412, BRSTN2012069, BRTHA3003736, CTONG2006235, LIVER2008465, TESTI4013474, THYMU3002887, THYMU3038158, TLIVE2000142, TLIVE2001616, TLIVE2007736, TLIVE2008797, TRACH3027229

【 0 2 7 5 】

肺がん由来のライブラリー (TLUNG) と、正常な肺由来のライブラリー (HLUNG) のcDNAを解析して比較した結果 (表 1 6)、両者で発現変化のある遺伝子は以下の 1 7 クローンであった。

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069, HLUNG2012600, MESAN2009156, NTONG2008483, PROST2007444, TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297, THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428, TRACH3022198

【 0 2 7 6 】

卵巣がん由来のライブラリー (TOVER) と、正常な卵巣由来のライブラリー (NOVER) のcDNAを解析して比較した結果 (表 1 7)、両者で発現変化のある遺伝子は以下の 3 クローンであった。

BRSTN2012069, NOVAR2000783, THYMU3002887

【 0 2 7 7 】

胃がん由来のライブラリー (TSTOM) と、正常な胃由来のライブラリー (STOMA) のcDNAを解析して比較した結果 (表 1 8)、両者で発現変化のある遺伝子は以

下の 9 クローンであった。

BRSTN2012069, CHONS2002829, STOMA2003894, STOMA2004663, THYMU3001776, TS
TOM2000235, TSTOM2001571, TSTOM2002611, TSTOM2002682

【 0 2 7 8 】

子宮がん由来のライブラリー (TUTER) と、正常な子宮由来のライブラリー (U
TERU) の cDNA を解析して比較した結果 (表 1 9)、両者で発現変化のある遺伝子
は以下の 1 2 8 クローンであった。

BRACE2012528, BRACE2017397, BRACE3004371, BRACE3036283, BRACE3040863, BR
AMY2031516, BRAMY3005184, BRAWH2004078, BRAWH3004350, BRAWH3022651, BRAW
H3024186, BRAWH3029806, BRAWH3031342, BRCAN2022126, BRHIP3001076, BRHIP3
002000, BRHIP3002141, BRHIP3005307, BRHIP3007223, BRHIP3017855,
BRHIP3020046, BRSTN2010089, BRSTN2011961, BRSTN2012069, BRSTN2016892, BR
THA3003736, BRTHA3011265, BRTHA3023403, BRTHA3027879, CHONS2002829, CTON
G2001932, CTONG2003517, CTONG2006235, CTONG2011801, CTONG3002518, DFNES2
001829, KIDNE2010049, LIVER2008465, NT2RI3005923, OCBBF3001333,
OCBBF3004487, PLACE6008315, PLACE7006240, PROST2007444, SPLEN2012571, SY
NOV4000598, SYNOV4009575, T1ESE2000904, TESTI4002072, TESTI4002195, TEST
I4002774, TESTI4002799, TESTI4003703, TESTI4003944, TESTI4005399, TESTI4
005653, TESTI4024245, TESTI4029297, THYMU3002887, THYMU3021586,
THYMU3026350, THYMU3032798, THYMU3034616, THYMU3034671, TRACH3003872, TR
ACH3005699, TRACH3006800, TRACH3008632, TRACH3009008, TUTER1000014, TUTE
R2001433, UTERU2000300, UTERU2014998, UTERU2016464, UTERU2016669, UTERU2
020226, UTERU2022955, UTERU2023941, UTERU2024042, UTERU2027369,
UTERU2028377, UTERU2029660, UTERU2035926, UTERU2037423, UTERU3000670, UT
ERU3001029, UTERU3001394, UTERU3001946, UTERU3004635, UTERU3005264, UTER
U3005422, UTERU3006538, UTERU3006720, UTERU3007108, UTERU3009775, UTERU3
010029, UTERU3010409, UTERU3010604, UTERU3010892, UTERU3010919,
UTERU3011092, UTERU3011398, UTERU3011558, UTERU3011579, UTERU3011837, UT
ERU3012293, UTERU3012414, UTERU3012476, UTERU3012599, UTERU3012999, UTER

U3013167, UTERU3013302, UTERU3014274, UTERU3014647, UTERU3014906, UTERU3015011, UTERU3015299, UTERU3015647, UTERU3015844, UTERU3016070, UTERU3016273, UTERU3016274, UTERU3016308, UTERU3017441, UTERU3017626, UTERU3017995, UTERU3018172, UTERU3018255

【 0 2 7 9 】

舌がん由来のライブラリー (CTONG) と、正常な舌由来のライブラリー (NTONG) のcDNAを解析して比較した結果 (表 2 0)、両者で発現変化のある遺伝子は以下の 6 7 クローンであった。

BRACE2012528, BRAMY4001863, BRAWH3021574, BRAWH3022651, BRAWH3024186, BRHIP2027077, BRHIP3001573, BRHIP3002000, BRHIP3007223, BRHIP3012997, BRHIP3020046, BRSSN2013696, BRSTN2011961, BRSTN2012069, BRTHA2027229, BRTHA2033155, BRTHA3011194, BRTHA3022641, CTONG2001932, CTONG2003517, CTONG2006235, CTONG2008989, CTONG2009033, CTONG2009570, CTONG2010330, CTONG2011801, CTONG2012123, CTONG2014206, CTONG2014959, CTONG2020582, CTONG2026987, CTONG2027150, CTONG2027591, CTONG2027783, CTONG2027959, CTONG3001605, CTONG3002518, CTONG3002588, CTONG3003669, CTONG3008223, NT2RI2009233, NTONG2002278, NTONG2003805, NTONG2004829, NTONG2008483, NTONG2009468, OCBBF3004487, PLACE6008315, PLACE7004103, SKNMC2003639, SPLEN2012571, SPLEN2019092, SYNOV4009575, T1ESE2000904, TESTI2005564, TESTI2018867, TESTI4002799, TESTI4005653, TESTI4032913, THYMU3021586, THYMU3047115, TRACH3006717, TRACH3007625, TRACH3016805, TRACH3036932, TRACH3038399, UTERU2000300

これらの遺伝子は、癌に関する遺伝子である。

【 0 2 8 0 】

また、発生や分化に関連する遺伝子を調べる方法として、発生・分化途中の組織・細胞と、成体の組織細胞において遺伝子発現量の違いを調べる発現頻度解析がある。組織の発生・分化に関する遺伝子は、その組織の構築と機能発現に関する遺伝子であり、傷害のある組織を任意に再生せしめる再生医学に利用可能な有用な遺伝子である。

【 0 2 8 1 】

先に記した1,402,070個のクローンの塩基配列のデータベースを基にして得た遺伝子発現頻度情報を用いて、発生・分化途中の組織・細胞と成体の組織・細胞とを比較して遺伝子発現頻度に変化のある遺伝子を解析した。

【 0 2 8 2 】

胎児の脳由来のライブラリー（FCBBF, FEBRAまたはOCBBF）と成体の脳由来のライブラリー（BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTNまたはBRTHA）のcDNAを解析し、胎児と成体で比較した結果（表 2 1）、両者で発現変化のある遺伝子は以下の 9 1 6 クローンであった。

ASTRO2008972, ASTRO2016114, BLADE2004849, BRACE1000475, BRACE2002392, BRACE2003628, BRACE2005991, BRACE2010336, BRACE2012528, BRACE2012625, BRACE2012833, BRACE2012838, BRACE2012936, BRACE2012947, BRACE2013009, BRACE2013126, BRACE2013132, BRACE2016896, BRACE2017359, BRACE2017397, BRACE2017580, BRACE2017844, BRACE2017872, BRACE2017992, BRACE2019348, BRACE2023633, BRACE2023744, BRACE2025452, BRACE2026404, BRACE2027312, BRACE2027382, BRACE2028956, BRACE2030039, BRACE2032584, BRACE2033128, BRACE2034434, BRACE2035120, BRACE2035191, BRACE2039362, BRACE2039607, BRACE2042541, BRACE2046976, BRACE2047232, BRACE2047975, BRACE3001403, BRACE3001973, BRACE3002344, BRACE3002541, BRACE3002756, BRACE3003866, BRACE3004046, BRACE3004371, BRACE3004767, BRACE3004887, BRACE3004981, BRACE3005870, BRACE3005903, BRACE3006553, BRACE3007649, BRACE3007869, BRACE3009075, BRACE3009265, BRACE3009392, BRACE3009416, BRACE3009539, BRACE3010702, BRACE3011447, BRACE3011774, BRACE3013418, BRACE3013874, BRACE3013986, BRACE3014523, BRACE3014714, BRACE3015090, BRACE3015898, BRACE3016020, BRACE3016167, BRACE3016580, BRACE3016788, BRACE3016810, BRACE3016862, BRACE3017253, BRACE3018083, BRACE3019570, BRACE3019611, BRACE3019817, BRACE3019941, BRACE3020356, BRACE3020669, BRACE3021430, BRACE3021517, BRACE3021805, BRACE3022051, BRACE3022303, BRACE3022312, BRACE3022340, BRACE3022847, BRACE3023604, BRACE3024379, BRACE3024444,

BRACE3024497, BRACE3024537, BRACE3024879, BRACE3025627, BRACE3025719, BRACE3026161, BRACE3026290, BRACE3026345, BRACE3026456, BRACE3026802, BRACE3026844, BRACE3026947, BRACE3027256, BRACE3027931, BRACE3028360, BRACE3028895, BRACE3028998, BRACE3029005, BRACE3029021, BRACE3029205, BRACE3029447, BRACE3030538, BRACE3031161, BRACE3031184, BRACE3031185, BRACE3031315, BRACE3031372, BRACE3031579, BRACE3031728, BRACE3031743, BRACE3031843, BRACE3032385, BRACE3032537, BRACE3032538, BRACE3032631, BRACE3032980, BRACE3033525, BRACE3034183, BRACE3034389, BRACE3034964, BRACE3034993, BRACE3035168, BRACE3036156, BRACE3036271, BRACE3036283, BRACE3037612, BRACE3037637, BRACE3037803, BRACE3038012, BRACE3038030, BRACE3038570, BRACE3038760, BRACE3039288, BRACE3039358, BRACE3039378, BRACE3039454, BRACE3040012, BRACE3040239, BRACE3040504, BRACE3040644, BRACE3040863, BRACE3041059, BRACE3041162, BRACE3041827, BRACE3042046, BRACE3042210, BRACE3042326, BRACE3042409, BRACE3042432, BRACE3042594, BRACE3043597, BRACE3044090, BRACE3044172, BRACE3044247, BRACE3044377, BRACE3044495, BRACE3045078, BRACE3045145, BRACE3045424, BRACE3045708, BRACE3045981, BRACE3046049, BRACE3046152, BRACE3046294, BRACE3046466, BRACE3046491, BRACE3046609, BRACE3046837, BRACE3046855, BRACE3046966, BRACE3047018, BRACE3047482, BRACE3047801, BRALZ2003119, BRALZ2007661, BRALZ2008930, BRALZ2010842, BRALZ2011337, BRALZ2013621, BRALZ2013690, BRALZ2014054, BRAMY2015516, BRAMY2021098, BRAMY2022320, BRAMY2023939, BRAMY2025495, BRAMY2031516, BRAMY2033895, BRAMY2035801, BRAMY2036254, BRAMY2036266, BRAMY2037609, BRAMY2039630, BRAMY2040915, BRAMY2041347, BRAMY2041384, BRAMY2041507, BRAMY2044686, BRAMY2046489, BRAMY2046537, BRAMY3000692, BRAMY3001409, BRAMY3002329, BRAMY3002508, BRAMY3002886, BRAMY3004126, BRAMY3004364, BRAMY3005184, BRAMY3005656, BRAMY3005912, BRAMY3007078, BRAMY3007449, BRAMY3007471, BRAMY3008436, BRAMY3009158, BRAMY3009491, BRAMY3009556, BRAMY3009904, BRAMY3010321, BRAMY3010603, BRAMY3010654, BRAMY4000915, BRAMY4000962, BRAMY4001234, BRAMY4001652, BR

AMY4001863, BRAMY4001913, BRAMY4002575, BRAMY4002628, BRAWH2000256, BRAWH2002333, BRAWH2004078, BRAWH2010364, BRAWH2010619, BRAWH2011796, BRAWH2011812, BRAWH2011958, BRAWH2012054, BRAWH2012866, BRAWH2013955, BRAWH2014053, BRAWH2016209, BRAWH2016223, BRAWH2016305, BRAWH2016514, BRAWH2016562, BRAWH2016785, BRAWH3000446, BRAWH3000884, BRAWH3001053, BRAWH3001638, BRAWH3001783, BRAWH3001833, BRAWH3003244, BRAWH3003573, BRAWH3003975, BRAWH3004335, BRAWH3004350, BRAWH3005037, BRAWH3005886, BRAWH3005892, BRAWH3005896, BRAWH3008167, BRAWH3008559, BRAWH3008867, BRAWH3009961, BRAWH3010461, BRAWH3010602, BRAWH3010657, BRAWH3010726, BRAWH3010833, BRAWH3011101, BRAWH3011331, BRAWH3011402, BRAWH3011577, BRAWH3011623, BRAWH3011685, BRAWH3011907, BRAWH3011929, BRAWH3012005, BRAWH3012662, BRAWH3012779, BRAWH3013009, BRAWH3013049, BRAWH3013264, BRAWH3013508, BRAWH3014609, BRAWH3014639, BRAWH3015017, BRAWH3015175, BRAWH3015610, BRAWH3015825, BRAWH3016123, BRAWH3016715, BRAWH3017180, BRAWH3017259, BRAWH3017260, BRAWH3017477, BRAWH3017980, BRAWH3018063, BRAWH3018369, BRAWH3018548, BRAWH3018969, BRAWH3019026, BRAWH3019529, BRAWH3019594, BRAWH3019820, BRAWH3020200, BRAWH3020318, BRAWH3020884, BRAWH3020928, BRAWH3021012, BRAWH3021574, BRAWH3021580, BRAWH3021641, BRAWH3021643, BRAWH3021724, BRAWH3022347, BRAWH3022431, BRAWH3022459, BRAWH3022542, BRAWH3022651, BRAWH3022719, BRAWH3022900, BRAWH3023156, BRAWH3023168, BRAWH3023172, BRAWH3023274, BRAWH3023421, BRAWH3024186, BRAWH3024231, BRAWH3024242, BRAWH3024506, BRAWH3024989, BRAWH3026349, BRAWH3026938, BRAWH3027420, BRAWH3027440, BRAWH3027533, BRAWH3027574, BRAWH3027607, BRAWH3027616, BRAWH3027675, BRAWH3027806, BRAWH3027880, BRAWH3028202, BRAWH3028223, BRAWH3028461, BRAWH3028754, BRAWH3028796, BRAWH3029313, BRAWH3029385, BRAWH3029538, BRAWH3029806, BRAWH3030772, BRAWH3030810, BRAWH3030910, BRAWH3031054, BRAWH3031342, BRAWH3031710, BRAWH3032298, BRAWH3032340, BRAWH3032571, BRAWH3033117, BRAWH3033293, BRAWH3033448, BRAWH3033513, BRAWH3034097, BRAWH3034114, BRAWH3034134, BRAWH

H3034668, BRAWH3034743, BRAWH3034775, BRAWH3034890, BRAWH3035403, BRAWH3035904, BRAWH3035914, BRAWH3035936, BRAWH3036077, BRAWH3036247, BRAWH3036270, BRAWH3036334, BRAWH3036561, BRAWH3037265, BRAWH3037394, BRAWH3037428, BRAWH3037533, BRAWH3037979, BRAWH3038055, BRAWH3038230, BRAWH3038252, BRAWH3038324, BRCAN2000923, BRCAN2002662, BRCAN2002892, BRCAN2003269, BRCAN2003814, BRCAN2006051, BRCAN2006955, BRCAN2007525, BRCAN2008701, BRCAN2009168, BRCAN2010547, BRCAN2010581, BRCAN2010665, BRCAN2015402, BRCAN2015757, BRCAN2018269, BRCAN2018667, BRCAN2019653, BRCAN2019907, BRCAN2019953, BRCAN2020234, BRCAN2020331, BRCAN2020412, BRCAN2020467, BRCAN2020880, BRCAN2021325, BRCAN2021452, BRCAN2021718, BRCAN2022126, BRCAN2025093, BRCAN2027593, BRCAN2028702, BRCOC2001355, BRCOC2002777, BRCOC2006164, BRCOC2006639, BRCOC2006942, BRCOC2009638, BRCOC2010115, BRCOC2012386, BRHIP2006819, BRHIP2006921, BRHIP2008756, BRHIP2009177, BRHIP2011199, BRHIP2013958, BRHIP2015153, BRHIP2016125, BRHIP2017714, BRHIP2020930, BRHIP2021929, BRHIP2023735, BRHIP2024941, BRHIP2026346, BRHIP2027077, BRHIP2027563, BRHIP2029529, BRHIP2029643, BRHIP2029663, BRHIP3000626, BRHIP3000859, BRHIP3001076, BRHIP3001141, BRHIP3001338, BRHIP3001360, BRHIP3001481, BRHIP3001573, BRHIP3001878, BRHIP3002000, BRHIP3002114, BRHIP3002124, BRHIP3002141, BRHIP3002363, BRHIP3002691, BRHIP3002920, BRHIP3002931, BRHIP3003063, BRHIP3003126, BRHIP3003306, BRHIP3003340, BRHIP3003395, BRHIP3003688, BRHIP3003795, BRHIP3003845, BRHIP3003961, BRHIP3003984, BRHIP3004215, BRHIP3004710, BRHIP3004725, BRHIP3004774, BRHIP3004786, BRHIP3005037, BRHIP3005142, BRHIP3005231, BRHIP3005307, BRHIP3005673, BRHIP3005801, BRHIP3005944, BRHIP3006279, BRHIP3006294, BRHIP3006449, BRHIP3006786, BRHIP3006950, BRHIP3007172, BRHIP3007195, BRHIP3007223, BRHIP3007291, BRHIP3007409, BRHIP3007424, BRHIP3007609, BRHIP3007960, BRHIP3008082, BRHIP3008320, BRHIP3008714, BRHIP3009672, BRHIP3009753, BRHIP3010289, BRHIP3010916, BRHIP3011082, BRHIP3011269, BRHIP3011460, BRHIP3011567, BRHIP3011831, BRHIP3

012185, BRHIP3012289, BRHIP3012357, BRHIP3012736, BRHIP3012997,
BRHIP3013078, BRHIP3013588, BRHIP3013698, BRHIP3014675, BRHIP3015854, BR
HIP3016032, BRHIP3016421, BRHIP3017109, BRHIP3017146, BRHIP3017256, BRHI
P3017558, BRHIP3017855, BRHIP3018784, BRHIP3019643, BRHIP3019824, BRHIP3
019880, BRHIP3019956, BRHIP3020046, BRHIP3020155, BRHIP3020733,
BRHIP3021019, BRHIP3021499, BRHIP3021987, BRHIP3022656, BRHIP3023922, BR
HIP3024703, BRHIP3024820, BRHIP3025795, BRHIP3025844, BRHIP3026231, BRHI
P3026651, BRHIP3027160, BRHIP3027191, BRHIP3027651, BRHIP3027947, BRHIP3
028246, BRHIP3028570, BRHIP3028742, BRSSN2004303, BRSSN2004710,
BRSSN2008464, BRSSN2011843, BRSSN2012157, BRSSN2012198, BRSSN2013696, BR
SSN2015497, BRSSN2018218, BRSTN2000312, BRSTN2006466, BRSTN2006638, BRST
N2008475, BRSTN2009247, BRSTN2010089, BRSTN2010416, BRSTN2011688, BRSTN2
011961, BRSTN2012069, BRSTN2016892, BRSTN2016918, BRSTN2016992,
BRSTN2017104, BRSTN2017151, BRSTN2018712, BRTHA2000969, BRTHA2001304, BR
THA2001953, BRTHA2002091, BRTHA2003759, BRTHA2005448, BRTHA2006720, BRTH
A2008502, BRTHA2008598, BRTHA2010672, BRTHA2012189, BRTHA2014647, BRTHA2
018304, BRTHA2019726, BRTHA2019743, BRTHA2020400, BRTHA2020566,
BRTHA2020642, BRTHA2020695, BRTHA2020721, BRTHA2020781, BRTHA2020910, BR
THA2021212, BRTHA2021440, BRTHA2021450, BRTHA2022074, BRTHA2022914, BRTH
A2022968, BRTHA2023402, BRTHA2023437, BRTHA2024177, BRTHA2024354, BRTHA2
024712, BRTHA2025869, BRTHA2026071, BRTHA2026290, BRTHA2026311,
BRTHA2027227, BRTHA2027229, BRTHA2027250, BRTHA2028297, BRTHA2029969, BR
THA2030036, BRTHA2030213, BRTHA2031517, BRTHA2031917, BRTHA2032763, BRTH
A2033122, BRTHA2033155, BRTHA2033320, BRTHA2033469, BRTHA2033683, BRTHA2
034281, BRTHA2034576, BRTHA2035743, BRTHA2036055, BRTHA2036295,
BRTHA2037247, BRTHA2038279, BRTHA2038345, BRTHA2038353, BRTHA3000456, BR
THA3002411, BRTHA3003225, BRTHA3003417, BRTHA3003736, BRTHA3005988, BRTH
A3006593, BRTHA3007469, BRTHA3007662, BRTHA3009858, BRTHA3010135, BRTHA3
010212, BRTHA3010469, BRTHA3010530, BRTHA3010540, BRTHA3010717,

BRTHA3011187, BRTHA3011194, BRTHA3011229, BRTHA3011265, BRTHA3011306, BRTHA3011361, BRTHA3011510, BRTHA3011892, BRTHA3011998, BRTHA3012265, BRTHA3013860, BRTHA3013882, BRTHA3014000, BRTHA3014105, BRTHA3014507, BRTHA3014547, BRTHA3014835, BRTHA3014854, BRTHA3014920, BRTHA3016616, BRTHA3017791, BRTHA3018409, BRTHA3018623, BRTHA3019183, BRTHA3020369, BRTHA3020771, BRTHA3021569, BRTHA3021708, BRTHA3021786, BRTHA3021971, BRTHA3022641, BRTHA3023403, BRTHA3023590, BRTHA3023929, BRTHA3024600, BRTHA3025073, BRTHA3026161, BRTHA3026180, BRTHA3026556, BRTHA3026916, BRTHA3027171, BRTHA3027318, BRTHA3027638, BRTHA3027820, BRTHA3027879, BRTHA3027957, BRTHA3028339, BRTHA3028505, CHONS2002829, CTONG2001932, CTONG2006235, CTONG2009033, CTONG2011801, CTONG2020582, CTONG2027959, D90ST2003106, DFNES2001829, FCBBF3001018, FCBBF3002188, FCBBF3005160, FCBBF3012443, FCBBF3020030, FCBBF3021191, FCBBF3024911, FCBBF5000384, FEBRA2000805, FEBRA2002260, FEBRA2012625, FEBRA2013069, FEBRA2013570, FEBRA2017736, FEBRA2017811, FEBRA2023498, FEBRA2026582, FEBRA2026977, FEBRA2028222, FEBRA2028457, JCMLC2000273, KIDNE2010049, KIDNE2017153, LIVER2008465, MESAN2017133, NOVAR2000783, NT2NE2011107, NT2RI2009233, NT2RI2010795, NT2RI2015533, NT2RI3005923, NT2RI3009524, NT2RP7007387, NT2RP8001604, NT2RP8001605, NT2RP8007920, NT2RP8009119, NTONG2008483, NTONG2009468, OCBBF2000831, OCBBF2003518, OCBBF2004478, OCBBF2007039, OCBBF2009536, OCBBF2014745, OCBBF2016928, OCBBF2018229, OCBBF2018618, OCBBF2019761, OCBBF2024589, OCBBF2024779, OCBBF2025631, OCBBF2030927, OCBBF2036019, OCBBF3000743, OCBBF3000830, OCBBF3001076, OCBBF3001202, OCBBF3001333, OCBBF3001616, OCBBF3003745, OCBBF3004487, OCBBF3004908, OCBBF3005330, OCBBF3005843, OCBBF3006986, OCBBF3007078, OCBBF3007704, OCBBF3008392, OCBBF3008835, OCBBF3009244, PLACE5000492, PLACE6003004, PLACE6008315, PLACE6010936, PLACE7004103, PLACE7006240, PROST2007444, PROST2017910, SMINT2009292, SMINT2012179, SPLEN2012571, SYNOV4004210, SYNOV4009575, T1ESE2000609, T1ESE2000904, TBAES2007428, TESTI2005112, TE

STI2005564, TESTI2009497, TESTI2018867, TESTI2021654, TESTI2039342, TESTI4001569, TESTI4002072, TESTI4002195, TESTI4002774, TESTI4002799, TESTI4003602, TESTI4003703, TESTI4003944, TESTI4004210, TESTI4004695, TESTI4005013, TESTI4005399, TESTI4005653, TESTI4006441, TESTI4007965, TESTI4010979, TESTI4012960, TESTI4013474, TESTI4014908, TESTI4020596, TESTI4022158, TESTI4029297, TESTI4032913, TESTI4035770, TESTI4043223, TESTI4046073, THYMU3000776, THYMU3002887, THYMU3003007, THYMU3003350, THYMU3007308, THYMU3008105, THYMU3019476, THYMU3021586, THYMU3026000, THYMU3026306, THYMU3026350, THYMU3032798, THYMU3032867, THYMU3033626, THYMU3034671, THYMU3037827, THYMU3038214, THYMU3041428, THYMU3044075, TKIDN2000319, TLIVE2007736, TRACH2013585, TRACH3002752, TRACH3003037, TRACH3003872, TRACH3004424, TRACH3006717, TRACH3007625, TRACH3007689, TRACH3007995, TRACH3008508, TRACH3008632, TRACH3009008, TRACH3010079, TRACH3016805, TRACH3016885, TRACH3021544, TRACH3022109, TRACH3022198, TRACH3024342, TRACH3024671, TRACH3025316, TRACH3026303, TRACH3026676, TRACH3028855, TRACH3032570, TRACH3036932, TRACH3038399, TSTOM2000235, UTERU2000300, UTERU2027369, UTERU3000670, UTERU3005422, UTERU3010409, UTERU3012414, UTERU3013167, UTERU3015011, UTERU3016273, UTERU3017995, UTERU3018172

【 0 2 8 3 】

胎児の心臓由来のライブラリー (FEHRT) 成体の心臓由来のライブラリー (HEART) のcDNAを解析し、胎児と成体で比較した結果 (表 2 2)、両者で発現変化のある遺伝子は以下の 1 0 クローンであった。

BRACE2012528, BRACE3004371, BRCAN2003814, BRSTN2011961, BRSTN2012069, BRSTN2016992, HEART2002531, NTONG2008483, PROST2002078, TIESE2000609

胎児の腎臓由来のライブラリー (FEKID) 成体の腎臓由来のライブラリー (KIDNEY) のcDNAを解析し、胎児と成体で比較した結果 (表 2 3)、両者で発現変化のある遺伝子は以下の 2 1 クローンであった。

BRACE3004371, BRAMY2039630, BRAMY3004364, BRAWH2004078, BRHIP3002000, BRSTN2011961, BRSTN2012069, BRTHA2027229, KIDNE2004531, KIDNE2010049, KIDNE2014496, KIDNE2015987, KIDNE2016464, KIDNE2017153, KIDNE2018268, NT2RP7007387, TESTI2005112, TESTI4002799, THYMU3001776, THYMU3029795, THYMU3032867

【 0 2 8 4 】

胎児の肺由来のライブラリー (FELNG) 成体の肺由来のライブラリー (HLUNG) のcDNAを解析し、胎児と成体で比較した結果 (表 2 4)、両者で発現変化のある遺伝子は以下の 1 8 クローンであった。

BRACE3036283, BRAMY2031516, BRSTN2011961, BRSTN2012069, HLUNG2012600, ME SAN2009156, NTONG2008483, PROST2007444, TESTI4003703, TESTI4005653, TESTI4013474, TESTI4029297, THYMU3001776, THYMU3033626, THYMU3034671, THYMU3041428, THYMU3044188, TRACH3022198

これらの遺伝子は組織・細胞の再生に関する遺伝子である

【 0 2 8 5 】

【表 2】

単球／マクロファージ系の前駆細胞 (糖タンパク質CD34を発現している細胞：CD34+細胞) での発現頻度と比較して、CD34+細胞を破骨細胞分化因子 (Molecular Medicine 38. 642-648. (2001)) で処理した細胞で増加または減少する遺伝子を、塩基配列情報にしたがって解析し、探索した。CD34+細胞のRNAから作製したライブラリー (CD34C)、CD34+細胞を破骨細胞分化因子で処理した細胞のRNAから作製したライブラリー (D30ST, D60STまたはD90ST) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	CD34C	D30ST	D60ST	D90ST
BRAWH3018063	0.000	30.813	0.000	0.000
BRHIP3020046	0.000	0.000	68.001	0.000
BRSSN2013696	0.000	41.698	0.000	0.000

BRSTN2012069	2.383	0.442	0.000	0.128
BRTHA2027229	0.000	0.000	61.446	0.000
D90ST2003106	0.000	0.000	0.000	93.096
D90ST2003989	0.000	0.000	0.000	100.000
D90ST2004417	0.000	0.000	0.000	100.000
OCBBF2016928	0.000	31.972	0.000	0.000
TESTI4005653	0.000	0.000	0.000	6.704
TESTI4013474	43.396	0.000	0.000	0.000
THYMU3032798	0.000	0.000	0.000	26.074

【 0 2 8 6 】

【表 3】

神経系の培養細胞NT2を分化誘導（レチノイン酸(RA)刺激またはRA刺激後さらに増殖阻害剤処理）して発現変化する遺伝子を探索した。未分化なNT2細胞由来のライブラリー（NT2RM）と分化誘導処理した細胞のライブラリー（NT2RP, NT2RI またはNT2NE）のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	NT2RM	NT2RP	NT2RI	NT2NE
BLADE2004849	0.000	0.000	0.000	26.862
BRACE2003628	0.000	16.442	0.000	0.000
BRACE2012528	0.000	1.143	0.862	0.000
BRAMY2023939	0.000	0.000	11.107	22.151
BRAMY2031516	0.000	17.802	0.000	0.000
BRAMY4002628	0.000	17.119	12.908	0.000
BRAWH3010461	0.000	0.000	3.733	0.000
BRAWH3017259	0.000	0.000	0.000	50.722
BRAWH3018063	0.000	0.000	14.389	0.000
BRAWH3022651	0.000	3.948	0.000	0.000

BRAWH3024186	0.000	0.000	18.135	0.000
BRCAN2019653	0.000	15.031	0.000	0.000
BRCAN2022126	0.000	0.000	8.824	0.000
BRCOC2012386	0.000	27.482	20.721	0.000
BRHIP3002000	0.000	3.615	0.000	0.000
BRHIP3007223	0.000	4.859	3.664	0.000
BRHIP3021019	0.000	0.000	14.074	0.000
BRSTN2011961	8.334	0.000	0.526	3.149
BRSTN2012069	0.000	0.479	0.052	0.788
BRTHA2033155	0.000	0.000	7.729	0.000
BRTHA3010212	0.000	13.315	0.000	0.000
BRTHA3011194	0.000	0.000	0.000	12.809
BRTHA3011265	0.000	20.563	0.000	0.000
BRTHA3017791	0.000	5.698	0.000	0.000
BRTHA3021971	55.855	0.000	0.000	0.000
CHONS2002829	0.000	0.000	2.969	0.000
CTONG2006235	0.000	3.948	0.000	0.000
FCBBF3012443	0.000	0.000	49.588	0.000
FEBRA2026582	0.000	0.000	42.162	0.000
LIVER2008465	0.000	15.950	0.000	0.000
NT2NE2011107	0.000	0.000	0.000	43.585
NT2NE2016041	0.000	0.000	0.000	100.000
NT2RI2004818	0.000	0.000	100.000	0.000
NT2RI2009233	0.000	5.436	4.099	0.000
NT2RI2010795	0.000	0.000	29.973	0.000
NT2RI2015533	0.000	0.000	2.824	0.000
NT2RI2023671	0.000	0.000	100.000	0.000
NT2RI2028537	0.000	0.000	100.000	0.000
NT2RI3001573	0.000	0.000	100.000	0.000

NT2RI3001967	0.000	0.000	100.000	0.000
NT2RI3005861	0.000	0.000	100.000	0.000
NT2RI3005923	0.000	0.000	35.423	0.000
NT2RI3007095	0.000	0.000	100.000	0.000
NT2RI3008179	0.000	0.000	100.000	0.000
NT2RI3009480	0.000	0.000	68.547	0.000
NT2RI3009524	0.000	0.000	64.504	0.000
NT2RP7003439	0.000	100.000	0.000	0.000
NT2RP7007387	0.000	9.894	3.730	0.000
NT2RP7014178	0.000	100.000	0.000	0.000
NT2RP7014778	0.000	100.000	0.000	0.000
NT2RP7016508	0.000	100.000	0.000	0.000
NT2RP7017139	0.000	100.000	0.000	0.000
NT2RP7019682	0.000	100.000	0.000	0.000
NT2RP7020343	0.000	100.000	0.000	0.000
NT2RP8000633	0.000	100.000	0.000	0.000
NT2RP8001363	0.000	100.000	0.000	0.000
NT2RP8001407	0.000	100.000	0.000	0.000
NT2RP8001584	0.000	100.000	0.000	0.000
NT2RP8001604	0.000	33.445	25.218	0.000
NT2RP8001605	0.000	70.676	0.000	0.000
NT2RP8003490	0.000	100.000	0.000	0.000
NT2RP8003657	0.000	100.000	0.000	0.000
NT2RP8003787	0.000	100.000	0.000	0.000
NT2RP8005546	0.000	59.103	0.000	0.000
NT2RP8006452	0.000	100.000	0.000	0.000
NT2RP8006521	0.000	100.000	0.000	0.000
NT2RP8007416	0.000	100.000	0.000	0.000
NT2RP8007503	0.000	100.000	0.000	0.000

NT2RP8007920	0.000	9.535	0.000	0.000
NT2RP8008057	0.000	68.270	0.000	0.000
NT2RP8009119	0.000	11.123	0.000	0.000
NT2RP8009248	0.000	100.000	0.000	0.000
NTONG2008483	0.000	0.000	4.356	0.000
OCBBF2003518	0.000	0.000	1.873	0.000
OCBBF3001333	0.000	7.743	5.839	0.000
OCBBF3004908	0.000	23.051	17.381	0.000
PLACE7004103	0.000	6.234	9.400	0.000
PROST2017910	0.000	25.185	0.000	0.000
SMINT2009292	0.000	0.000	6.446	0.000
SPLEN2012571	0.000	15.323	5.777	0.000
T1ESE2000904	0.000	11.128	0.000	0.000
TESTI4002072	0.000	8.048	6.068	0.000
TESTI4002774	0.000	0.000	7.456	0.000
TESTI4002799	0.000	4.258	1.605	0.000
TESTI4005653	0.000	1.198	7.228	1.802
TESTI4007965	0.000	0.000	32.797	0.000
TESTI4012960	0.000	71.770	0.000	0.000
TESTI4018436	0.000	0.000	9.457	0.000
THYMU3001776	0.000	7.637	0.000	0.000
THYMU3002887	0.000	1.880	0.000	14.135
THYMU3029795	0.000	0.000	19.335	0.000
THYMU3041428	0.000	0.614	0.463	0.000
THYMU3047115	0.000	0.000	0.747	0.000
TRACH3003872	0.000	13.230	0.000	0.000
TRACH3004424	0.000	0.000	30.905	0.000
TRACH3006717	0.000	0.000	6.668	0.000
TRACH3007625	0.000	2.833	2.136	4.260

TRACH3009008	0.000	11.807	0.000	0.000
TRACH3016805	0.000	10.851	0.000	0.000
TRACH3016885	0.000	0.000	14.459	0.000
TRACH3026303	0.000	27.016	0.000	0.000
UTERU2016669	0.000	0.000	0.000	29.924

【 0 2 8 7 】

【表 4】

アルツハイマー患者の脳皮質由来のライブラリー (BRALZ、BRASW) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRALZ	BRASW
ASTRO2016114	14.497	0.000	0.000
BRACE2002392	0.000	18.684	0.000
BRACE2012528	3.794	1.714	0.000
BRACE3004371	11.270	0.000	0.000
BRACE3004767	58.488	0.000	0.000
BRACE3022340	58.488	0.000	0.000
BRACE3031185	58.488	0.000	0.000
BRACE3031743	5.455	0.000	0.000
BRACE3032385	13.674	0.000	0.000
BRACE3032631	12.612	0.000	0.000
BRACE3039358	41.331	0.000	0.000
BRACE3040863	17.888	0.000	0.000
BRACE3042432	58.488	0.000	0.000
BRACE3045981	26.434	0.000	0.000
BRALZ2003119	0.000	100.000	0.000

BRALZ2007661	0.000	100.000	0.000
BRALZ2008930	0.000	100.000	0.000
BRALZ2010842	0.000	100.000	0.000
BRALZ2011337	0.000	100.000	0.000
BRALZ2013621	0.000	100.000	0.000
BRALZ2013690	0.000	100.000	0.000
BRALZ2014054	0.000	38.408	0.000
BRAMY2031516	14.772	0.000	0.000
BRAMY3002329	20.323	0.000	0.000
BRAMY3004126	49.811	0.000	0.000
BRAMY3005912	21.416	0.000	0.000
BRAMY3008436	5.603	5.061	0.000
BRAWH2000256	100.000	0.000	0.000
BRAWH2002333	100.000	0.000	0.000
BRAWH2004078	10.539	0.000	0.000
BRAWH2010364	34.464	0.000	0.000
BRAWH2010619	100.000	0.000	0.000
BRAWH2011796	100.000	0.000	0.000
BRAWH2011812	13.544	0.000	0.000
BRAWH2011958	100.000	0.000	0.000
BRAWH2012054	100.000	0.000	0.000
BRAWH2012866	8.503	0.000	0.000
BRAWH2013955	100.000	0.000	0.000
BRAWH2014053	23.222	0.000	0.000
BRAWH2016209	8.306	0.000	0.000
BRAWH2016223	100.000	0.000	0.000
BRAWH2016305	4.308	0.000	0.000
BRAWH2016514	35.037	0.000	0.000
BRAWH2016562	49.499	0.000	0.000

BRAWH2016785	100.000	0.000	0.000
BRAWH3000446	100.000	0.000	0.000
BRAWH3000884	100.000	0.000	0.000
BRAWH3001053	100.000	0.000	0.000
BRAWH3001638	100.000	0.000	0.000
BRAWH3001783	100.000	0.000	0.000
BRAWH3001833	100.000	0.000	0.000
BRAWH3003244	100.000	0.000	0.000
BRAWH3003573	20.162	0.000	0.000
BRAWH3003975	100.000	0.000	0.000
BRAWH3004335	100.000	0.000	0.000
BRAWH3004350	16.580	0.000	0.000
BRAWH3005037	100.000	0.000	0.000
BRAWH3005886	100.000	0.000	0.000
BRAWH3005892	100.000	0.000	0.000
BRAWH3005896	100.000	0.000	0.000
BRAWH3008167	100.000	0.000	0.000
BRAWH3008559	100.000	0.000	0.000
BRAWH3008867	100.000	0.000	0.000
BRAWH3009961	47.417	0.000	0.000
BRAWH3010461	16.435	0.000	0.000
BRAWH3010602	100.000	0.000	0.000
BRAWH3010657	100.000	0.000	0.000
BRAWH3010726	100.000	0.000	0.000
BRAWH3010833	100.000	0.000	0.000
BRAWH3011101	100.000	0.000	0.000
BRAWH3011331	100.000	0.000	0.000
BRAWH3011402	100.000	0.000	0.000
BRAWH3011577	100.000	0.000	0.000

BRAWH3011623	100.000	0.000	0.000
BRAWH3011685	100.000	0.000	0.000
BRAWH3011907	47.417	0.000	0.000
BRAWH3011929	100.000	0.000	0.000
BRAWH3012005	100.000	0.000	0.000
BRAWH3012662	33.972	0.000	0.000
BRAWH3012779	100.000	0.000	0.000
BRAWH3013009	100.000	0.000	0.000
BRAWH3013049	100.000	0.000	0.000
BRAWH3013264	100.000	0.000	0.000
BRAWH3013508	100.000	0.000	0.000
BRAWH3014609	44.597	0.000	0.000
BRAWH3014639	100.000	0.000	0.000
BRAWH3015017	100.000	0.000	0.000
BRAWH3015175	100.000	0.000	0.000
BRAWH3015610	100.000	0.000	0.000
BRAWH3015825	100.000	0.000	0.000
BRAWH3016123	100.000	0.000	0.000
BRAWH3016715	100.000	0.000	0.000
BRAWH3017180	28.251	0.000	0.000
BRAWH3017259	13.996	0.000	0.000
BRAWH3017260	100.000	0.000	0.000
BRAWH3017477	100.000	0.000	0.000
BRAWH3017980	49.811	0.000	0.000
BRAWH3018063	15.836	0.000	0.000
BRAWH3018369	100.000	0.000	0.000
BRAWH3018548	100.000	0.000	0.000
BRAWH3018969	100.000	0.000	0.000
BRAWH3019026	100.000	0.000	0.000

BRAWH3019529	100.000	0.000	0.000
BRAWH3019594	100.000	0.000	0.000
BRAWH3019820	100.000	0.000	0.000
BRAWH3020200	100.000	0.000	0.000
BRAWH3020318	100.000	0.000	0.000
BRAWH3020884	100.000	0.000	0.000
BRAWH3020928	49.499	0.000	0.000
BRAWH3021012	100.000	0.000	0.000
BRAWH3021574	9.400	0.000	0.000
BRAWH3021580	100.000	0.000	0.000
BRAWH3021641	100.000	0.000	0.000
BRAWH3021643	100.000	0.000	0.000
BRAWH3021724	100.000	0.000	0.000
BRAWH3022347	100.000	0.000	0.000
BRAWH3022431	100.000	0.000	0.000
BRAWH3022459	100.000	0.000	0.000
BRAWH3022542	100.000	0.000	0.000
BRAWH3022651	9.828	5.919	0.000
BRAWH3022719	100.000	0.000	0.000
BRAWH3022900	100.000	0.000	0.000
BRAWH3023156	100.000	0.000	0.000
BRAWH3023168	100.000	0.000	0.000
BRAWH3023172	0.916	0.000	0.000
BRAWH3023274	100.000	0.000	0.000
BRAWH3023421	100.000	0.000	0.000
BRAWH3024186	19.959	0.000	0.000
BRAWH3024231	100.000	0.000	0.000
BRAWH3024242	31.843	0.000	0.000
BRAWH3024506	100.000	0.000	0.000

BRAWH3024989	2.369	0.000	0.000
BRAWH3026349	100.000	0.000	0.000
BRAWH3026938	6.894	8.303	0.000
BRAWH3027420	100.000	0.000	0.000
BRAWH3027440	58.488	0.000	0.000
BRAWH3027533	11.008	0.000	0.000
BRAWH3027574	47.417	0.000	0.000
BRAWH3027607	100.000	0.000	0.000
BRAWH3027616	100.000	0.000	0.000
BRAWH3027675	100.000	0.000	0.000
BRAWH3027806	100.000	0.000	0.000
BRAWH3027880	100.000	0.000	0.000
BRAWH3028202	100.000	0.000	0.000
BRAWH3028223	100.000	0.000	0.000
BRAWH3028461	100.000	0.000	0.000
BRAWH3028754	100.000	0.000	0.000
BRAWH3028796	100.000	0.000	0.000
BRAWH3029313	100.000	0.000	0.000
BRAWH3029385	35.187	0.000	0.000
BRAWH3029538	100.000	0.000	0.000
BRAWH3029806	26.735	0.000	0.000
BRAWH3030772	100.000	0.000	0.000
BRAWH3030810	21.287	0.000	0.000
BRAWH3030910	100.000	0.000	0.000
BRAWH3031054	100.000	0.000	0.000
BRAWH3031342	10.856	0.000	0.000
BRAWH3031710	100.000	0.000	0.000
BRAWH3032298	100.000	0.000	0.000
BRAWH3032340	100.000	0.000	0.000

BRAWH3032571	100.000	0.000	0.000
BRAWH3033117	100.000	0.000	0.000
BRAWH3033293	100.000	0.000	0.000
BRAWH3033448	100.000	0.000	0.000
BRAWH3033513	100.000	0.000	0.000
BRAWH3034097	100.000	0.000	0.000
BRAWH3034114	100.000	0.000	0.000
BRAWH3034134	100.000	0.000	0.000
BRAWH3034668	100.000	0.000	0.000
BRAWH3034743	16.662	0.000	0.000
BRAWH3034775	100.000	0.000	0.000
BRAWH3034890	100.000	0.000	0.000
BRAWH3035403	35.337	0.000	0.000
BRAWH3035904	100.000	0.000	0.000
BRAWH3035914	100.000	0.000	0.000
BRAWH3035936	70.575	0.000	0.000
BRAWH3036077	100.000	0.000	0.000
BRAWH3036247	54.530	0.000	0.000
BRAWH3036270	100.000	0.000	0.000
BRAWH3036334	6.241	0.000	0.000
BRAWH3036561	100.000	0.000	0.000
BRAWH3037265	44.597	0.000	0.000
BRAWH3037394	100.000	0.000	0.000
BRAWH3037428	5.877	0.000	0.000
BRAWH3037533	100.000	0.000	0.000
BRAWH3037979	100.000	0.000	0.000
BRAWH3038055	100.000	0.000	0.000
BRAWH3038230	100.000	0.000	0.000
BRAWH3038252	100.000	0.000	0.000

BRAWH3038324	100.000	0.000	0.000
BRCAN2010665	19.610	0.000	0.000
BRCAN2019653	0.000	22.535	0.000
BRCAN2022126	4.855	0.000	0.000
BRCAN2025093	21.732	0.000	0.000
BRCOC2012386	11.403	0.000	0.000
BRHIP2015153	20.038	0.000	0.000
BRHIP2027077	2.020	0.000	0.000
BRHIP3001573	24.474	0.000	0.000
BRHIP3002000	4.500	2.710	0.000
BRHIP3003063	10.960	0.000	0.000
BRHIP3003984	27.477	0.000	0.000
BRHIP3004774	39.520	0.000	0.000
BRHIP3007223	2.016	0.000	0.000
BRHIP3007409	31.957	0.000	0.000
BRHIP3008320	23.349	0.000	0.000
BRHIP3014675	37.925	0.000	0.000
BRHIP3017855	15.316	0.000	0.000
BRHIP3018784	6.930	0.000	0.000
BRHIP3021019	7.745	0.000	0.000
BRHIP3028246	22.147	0.000	0.000
BRHIP3028570	31.957	0.000	0.000
BRSTN2010089	6.598	0.000	0.000
BRSTN2012069	0.047	0.718	7.145
BRSTN2016992	1.476	40.898	0.000
BRTHA2033155	4.253	0.000	0.000
BRTHA3003736	4.302	0.000	0.000
BRTHA3005988	31.076	0.000	0.000
BRTHA3010135	20.010	0.000	0.000

BRTHA3010212	5.525	0.000	0.000
BRTHA3011194	3.534	0.000	0.000
BRTHA3011265	25.596	0.000	0.000
BRTHA3017791	11.821	4.271	0.000
BRTHA3020771	31.957	0.000	0.000
BRTHA3021971	1.941	0.000	0.000
BRTHA3023403	14.857	0.000	0.000
CTONG2006235	9.828	5.919	0.000
CTONG2009033	25.755	0.000	0.000
CTONG2020582	9.594	0.000	0.000
D90ST2003106	6.904	0.000	0.000
DFNES2001829	9.228	0.000	0.000
KIDNE2010049	3.438	0.000	0.000
MESAN2017133	17.548	31.703	0.000
NT2RI2009233	6.767	0.000	0.000
NT2RI2015533	6.216	5.616	0.000
NT2RI3005923	19.493	0.000	0.000
NT2RI3009524	35.496	0.000	0.000
NT2RP7007387	6.158	0.000	0.000
NT2RP8001605	29.324	0.000	0.000
NT2RP8007920	1.978	0.000	0.000
NTONG2008483	2.397	0.000	0.000
OCBBF2003518	2.062	0.000	0.000
OCBBF2018618	16.218	0.000	0.000
OCBBF3001333	9.639	0.000	0.000
OCBBF3004487	4.531	0.000	0.000
PLACE7004103	3.880	0.000	0.000
PLACE7006240	25.174	0.000	0.000
PROST2007444	4.374	0.000	0.000

PROST2017910	0.000	37.758	0.000
TBAES2007428	5.371	0.000	0.000
TESTI2005112	19.455	0.000	0.000
TESTI2021654	9.773	0.000	0.000
TESTI4002072	16.696	0.000	0.000
TESTI4002774	4.103	0.000	0.000
TESTI4002799	1.767	0.000	0.000
TESTI4003602	25.967	0.000	0.000
TESTI4004210	36.051	0.000	0.000
TESTI4005399	7.797	0.000	0.000
TESTI4005653	1.989	0.000	0.000
TESTI4006441	60.471	0.000	0.000
TESTI4013474	0.000	3.733	0.000
TESTI4014908	36.051	0.000	0.000
TESTI4022158	53.386	0.000	0.000
THYMU3000776	15.604	0.000	0.000
THYMU3002887	4.680	0.000	0.000
THYMU3003350	54.530	0.000	0.000
THYMU3021586	20.651	0.000	0.000
THYMU3026000	49.066	0.000	0.000
THYMU3026306	46.281	0.000	0.000
THYMU3026350	14.291	0.000	0.000
THYMU3032798	9.668	0.000	0.000
THYMU3032867	12.871	0.000	0.000
THYMU3037827	54.530	0.000	0.000
THYMU3038214	39.314	0.000	0.000
THYMU3041428	0.000	0.000	96.263
THYMU3044075	37.925	0.000	0.000
TRACH2013585	23.471	0.000	0.000

TRACH3002752	10.215	0.000	0.000
TRACH3003037	64.100	0.000	0.000
TRACH3003872	2.745	0.000	0.000
TRACH3004424	17.006	0.000	0.000
TRACH3006717	18.347	0.000	0.000
TRACH3007625	1.175	0.000	0.000
TRACH3007689	47.167	0.000	0.000
TRACH3008632	25.351	0.000	0.000
TRACH3009008	24.495	0.000	0.000
TRACH3010079	48.305	0.000	0.000
TRACH3016805	4.502	0.000	0.000
TRACH3016885	3.978	0.000	0.000
TRACH3024342	47.167	0.000	0.000
TRACH3024671	47.167	0.000	0.000
TRACH3026303	5.605	0.000	0.000
TRACH3026676	11.631	0.000	0.000
TRACH3028855	22.309	0.000	0.000
TRACH3032570	47.167	0.000	0.000
TRACH3036932	14.659	0.000	0.000
TRACH3038399	12.435	0.000	0.000
UTERU3010409	3.461	0.000	0.000
UTERU3013167	45.606	0.000	0.000

【 0 2 8 8 】

【表 5】

黒質由来のライブラリー (BRSSN) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRSSN
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ASTRO2016114	14.497	0.000
BRACE2012528	3.794	0.000
BRACE2017844	0.000	38.254
BRACE3004371	11.270	0.000
BRACE3004767	58.488	0.000
BRACE3022340	58.488	0.000
BRACE3025719	0.000	67.040
BRACE3026802	0.000	63.610
BRACE3031185	58.488	0.000
BRACE3031743	5.455	0.000
BRACE3032385	13.674	0.000
BRACE3032631	12.612	0.000
BRACE3039358	41.331	0.000
BRACE3040863	17.888	0.000
BRACE3042432	58.488	0.000
BRACE3045981	26.434	0.000
BRAMY2031516	14.772	0.000
BRAMY3002329	20.323	0.000
BRAMY3004126	49.811	0.000
BRAMY3005912	21.416	0.000
BRAMY3008436	5.603	10.427
BRAWH2000256	100.000	0.000
BRAWH2002333	100.000	0.000
BRAWH2004078	10.539	0.000
BRAWH2010364	34.464	0.000
BRAWH2010619	100.000	0.000
BRAWH2011796	100.000	0.000
BRAWH2011812	13.544	0.000

BRAWH2011958	100.000	0.000
BRAWH2012054	100.000	0.000
BRAWH2012866	8.503	0.000
BRAWH2013955	100.000	0.000
BRAWH2014053	23.222	0.000
BRAWH2016209	8.306	0.000
BRAWH2016223	100.000	0.000
BRAWH2016305	4.308	0.000
BRAWH2016514	35.037	0.000
BRAWH2016562	49.499	0.000
BRAWH2016785	100.000	0.000
BRAWH3000446	100.000	0.000
BRAWH3000884	100.000	0.000
BRAWH3001053	100.000	0.000
BRAWH3001638	100.000	0.000
BRAWH3001783	100.000	0.000
BRAWH3001833	100.000	0.000
BRAWH3003244	100.000	0.000
BRAWH3003573	20.162	0.000
BRAWH3003975	100.000	0.000
BRAWH3004335	100.000	0.000
BRAWH3004350	16.580	0.000
BRAWH3005037	100.000	0.000
BRAWH3005886	100.000	0.000
BRAWH3005892	100.000	0.000
BRAWH3005896	100.000	0.000
BRAWH3008167	100.000	0.000
BRAWH3008559	100.000	0.000
BRAWH3008867	100.000	0.000

BRAWH3009961	47.417	0.000
BRAWH3010461	16.435	7.646
BRAWH3010602	100.000	0.000
BRAWH3010657	100.000	0.000
BRAWH3010726	100.000	0.000
BRAWH3010833	100.000	0.000
BRAWH3011101	100.000	0.000
BRAWH3011331	100.000	0.000
BRAWH3011402	100.000	0.000
BRAWH3011577	100.000	0.000
BRAWH3011623	100.000	0.000
BRAWH3011685	100.000	0.000
BRAWH3011907	47.417	0.000
BRAWH3011929	100.000	0.000
BRAWH3012005	100.000	0.000
BRAWH3012662	33.972	0.000
BRAWH3012779	100.000	0.000
BRAWH3013009	100.000	0.000
BRAWH3013049	100.000	0.000
BRAWH3013264	100.000	0.000
BRAWH3013508	100.000	0.000
BRAWH3014609	44.597	0.000
BRAWH3014639	100.000	0.000
BRAWH3015017	100.000	0.000
BRAWH3015175	100.000	0.000
BRAWH3015610	100.000	0.000
BRAWH3015825	100.000	0.000
BRAWH3016123	100.000	0.000
BRAWH3016715	100.000	0.000

BRAWH3017180	28.251	0.000
BRAWH3017259	13.996	0.000
BRAWH3017260	100.000	0.000
BRAWH3017477	100.000	0.000
BRAWH3017980	49.811	0.000
BRAWH3018063	15.836	0.000
BRAWH3018369	100.000	0.000
BRAWH3018548	100.000	0.000
BRAWH3018969	100.000	0.000
BRAWH3019026	100.000	0.000
BRAWH3019529	100.000	0.000
BRAWH3019594	100.000	0.000
BRAWH3019820	100.000	0.000
BRAWH3020200	100.000	0.000
BRAWH3020318	100.000	0.000
BRAWH3020884	100.000	0.000
BRAWH3020928	49.499	0.000
BRAWH3021012	100.000	0.000
BRAWH3021574	9.400	17.492
BRAWH3021580	100.000	0.000
BRAWH3021641	100.000	0.000
BRAWH3021643	100.000	0.000
BRAWH3021724	100.000	0.000
BRAWH3022347	100.000	0.000
BRAWH3022431	100.000	0.000
BRAWH3022459	100.000	0.000
BRAWH3022542	100.000	0.000
BRAWH3022651	9.828	6.097
BRAWH3022719	100.000	0.000

BRAWH3022900	100.000	0.000
BRAWH3023156	100.000	0.000
BRAWH3023168	100.000	0.000
BRAWH3023172	0.916	0.000
BRAWH3023274	100.000	0.000
BRAWH3023421	100.000	0.000
BRAWH3024186	19.959	0.000
BRAWH3024231	100.000	0.000
BRAWH3024242	31.843	0.000
BRAWH3024506	100.000	0.000
BRAWH3024989	2.369	0.000
BRAWH3026349	100.000	0.000
BRAWH3026938	6.894	0.000
BRAWH3027420	100.000	0.000
BRAWH3027440	58.488	0.000
BRAWH3027533	11.008	0.000
BRAWH3027574	47.417	0.000
BRAWH3027607	100.000	0.000
BRAWH3027616	100.000	0.000
BRAWH3027675	100.000	0.000
BRAWH3027806	100.000	0.000
BRAWH3027880	100.000	0.000
BRAWH3028202	100.000	0.000
BRAWH3028223	100.000	0.000
BRAWH3028461	100.000	0.000
BRAWH3028754	100.000	0.000
BRAWH3028796	100.000	0.000
BRAWH3029313	100.000	0.000
BRAWH3029385	35.187	0.000

BRAWH3029538	100.000	0.000
BRAWH3029806	26.735	0.000
BRAWH3030772	100.000	0.000
BRAWH3030810	21.287	0.000
BRAWH3030910	100.000	0.000
BRAWH3031054	100.000	0.000
BRAWH3031342	10.856	0.000
BRAWH3031710	100.000	0.000
BRAWH3032298	100.000	0.000
BRAWH3032340	100.000	0.000
BRAWH3032571	100.000	0.000
BRAWH3033117	100.000	0.000
BRAWH3033293	100.000	0.000
BRAWH3033448	100.000	0.000
BRAWH3033513	100.000	0.000
BRAWH3034097	100.000	0.000
BRAWH3034114	100.000	0.000
BRAWH3034134	100.000	0.000
BRAWH3034668	100.000	0.000
BRAWH3034743	16.662	0.000
BRAWH3034775	100.000	0.000
BRAWH3034890	100.000	0.000
BRAWH3035403	35.337	0.000
BRAWH3035904	100.000	0.000
BRAWH3035914	100.000	0.000
BRAWH3035936	70.575	0.000
BRAWH3036077	100.000	0.000
BRAWH3036247	54.530	0.000
BRAWH3036270	100.000	0.000

BRAWH3036334	6.241	0.000
BRAWH3036561	100.000	0.000
BRAWH3037265	44.597	0.000
BRAWH3037394	100.000	0.000
BRAWH3037428	5.877	21.873
BRAWH3037533	100.000	0.000
BRAWH3037979	100.000	0.000
BRAWH3038055	100.000	0.000
BRAWH3038230	100.000	0.000
BRAWH3038252	100.000	0.000
BRAWH3038324	100.000	0.000
BRCAN2010665	19.610	0.000
BRCAN2022126	4.855	0.000
BRCAN2025093	21.732	0.000
BRCOC2012386	11.403	0.000
BRHIP2015153	20.038	0.000
BRHIP2027077	2.020	0.000
BRHIP2029643	0.000	55.599
BRHIP3001573	24.474	0.000
BRHIP3002000	4.500	5.583
BRHIP3003063	10.960	0.000
BRHIP3003984	27.477	0.000
BRHIP3004774	39.520	0.000
BRHIP3007223	2.016	0.000
BRHIP3007409	31.957	0.000
BRHIP3008320	23.349	0.000
BRHIP3014675	37.925	0.000
BRHIP3017855	15.316	0.000
BRHIP3018784	6.930	0.000

BRHIP3020046	0.000	3.770
BRHIP3021019	7.745	0.000 -
BRHIP3028246	22.147	0.000
BRHIP3028570	31.957	0.000
BRSSN2004303	0.000	100.000
BRSSN2004710	0.000	100.000
BRSSN2008464	0.000	100.000
BRSSN2011843	0.000	44.546
BRSSN2012157	0.000	100.000
BRSSN2012198	0.000	100.000
BRSSN2013696	0.000	13.293
BRSSN2015497	0.000	26.619
BRSSN2018218	0.000	100.000
BRSTN2010089	6.598	0.000
BRSTN2011961	0.000	1.078
BRSTN2012069	0.047	0.000
BRSTN2016992	1.476	5.495
BRSTN2017104	0.000	7.257
BRTHA2033155	4.253	15.830
BRTHA3003736	4.302	0.000
BRTHA3005988	31.076	0.000
BRTHA3010135	20.010	0.000
BRTHA3010212	5.525	0.000
BRTHA3011194	3.534	0.000
BRTHA3011265	25.596	0.000
BRTHA3017791	11.821	0.000
BRTHA3020771	31.957	0.000
BRTHA3021971	1.941	0.000
BRTHA3023403	14.857	0.000

CTONG2006235	9.828	6.097
CTONG2009033	25.755	0.000
CTONG2011801	0.000	11.021
CTONG2020582	9.594	0.000
D90ST2003106	6.904	0.000
DFNES2001829	9.228	0.000
KIDNE2010049	3.438	0.000
MESAN2017133	17.548	0.000
NT2RI2009233	6.767	0.000
NT2RI2015533	6.216	0.000
NT2RI3005923	19.493	0.000
NT2RI3009524	35.496	0.000
NT2RP7007387	6.158	0.000
NT2RP8001605	29.324	0.000
NT2RP8007920	1.978	7.363
NTONG2008483	2.397	0.000
OCBBF2003518	2.062	0.000
OCBBF2018618	16.218	0.000
OCBBF3001333	9.639	0.000
OCBBF3004487	4.531	0.000
PLACE7004103	3.880	0.000
PLACE7006240	25.174	0.000
PROST2007444	4.374	8.140
SMINT2009292	0.000	13.202
T1ESE2000904	0.000	8.593
TBAES2007428	5.371	0.000
TESTI2005112	19.455	0.000
TESTI2021654	9.773	0.000
TESTI4002072	16.696	0.000

TESTI4002774	4.103	0.000
TESTI4002799	1.767	0.000
TESTI4003602	25.967	0.000
TESTI4004210	36.051	0.000
TESTI4005399	7.797	0.000
TESTI4005653	1.989	0.000
TESTI4006441	60.471	0.000
TESTI4014908	36.051	0.000
TESTI4022158	53.386	0.000
THYMU3000776	15.604	0.000
THYMU3002887	4.680	2.903
THYMU3003350	54.530	0.000
THYMU3021586	20.651	0.000
THYMU3026000	49.066	0.000
THYMU3026306	46.281	0.000
THYMU3026350	14.291	0.000
THYMU3032798	9.668	0.000
THYMU3032867	12.871	0.000
THYMU3037827	54.530	0.000
THYMU3038214	39.314	0.000
THYMU3044075	37.925	0.000
TRACH2013585	23.471	0.000
TRACH3002752	10.215	19.010
TRACH3003037	64.100	0.000
TRACH3003872	2.745	10.216
TRACH3004424	17.006	0.000
TRACH3006717	18.347	0.000
TRACH3007625	1.175	0.000
TRACH3007689	47.167	0.000

TRACH3008632	25.351	0.000
TRACH3009008	24.495	0.000
TRACH3010079	48.305	0.000
TRACH3016805	4.502	0.000
TRACH3016885	3.978	0.000
TRACH3022198	0.000	30.935
TRACH3024342	47.167	0.000
TRACH3024671	47.167	0.000
TRACH3026303	5.605	0.000
TRACH3026676	11.631	0.000
TRACH3028855	22.309	0.000
TRACH3032570	47.167	0.000
TRACH3036932	14.659	0.000
TRACH3038399	12.435	0.000
UTERU3010409	3.461	0.000
UTERU3013167	45.606	0.000

【 0 2 8 9 】

【表 6】

海馬由来のライブラリー (BRHIP) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRHIP

ASTRO2016114	14.497	0.000
BRACE2002392	0.000	5.275
BRACE2012528	3.794	4.354
BRACE2017359	0.000	41.817
BRACE2017397	0.000	4.813

BRACE2017844	0.000	5.243
BRACE3004046	0.000	58.973
BRACE3004371	11.270	7.666
BRACE3004767	58.488	0.000
BRACE3009416	0.000	29.118
BRACE3022340	58.488	0.000
BRACE3027931	0.000	34.325
BRACE3029021	0.000	74.193
BRACE3031185	58.488	0.000
BRACE3031743	5.455	5.566
BRACE3032385	13.674	20.927
BRACE3032631	12.612	0.000
BRACE3036156	0.000	44.660
BRACE3039358	41.331	21.084
BRACE3040863	17.888	18.250
BRACE3042326	0.000	35.796
BRACE3042432	58.488	0.000
BRACE3045078	0.000	41.817
BRACE3045981	26.434	0.000
BRAMY2031516	14.772	7.536
BRAMY3002329	20.323	34.558
BRAMY3004126	49.811	0.000
BRAMY3005184	0.000	22.861
BRAMY3005912	21.416	0.000
BRAMY3007078	0.000	50.312
BRAMY3008436	5.603	27.152
BRAMY4000915	0.000	50.312
BRAWH2000256	100.000	0.000
BRAWH2002333	100.000	0.000

BRAWH2004078	10.539	0.000
BRAWH2010364	34.464	17.581
BRAWH2010619	100.000	0.000
BRAWH2011796	100.000	0.000
BRAWH2011812	13.544	0.000
BRAWH2011958	100.000	0.000
BRAWH2012054	100.000	0.000
BRAWH2012866	8.503	4.337
BRAWH2013955	100.000	0.000
BRAWH2014053	23.222	0.000
BRAWH2016209	8.306	0.000
BRAWH2016223	100.000	0.000
BRAWH2016305	4.308	0.000
BRAWH2016514	35.037	35.747
BRAWH2016562	49.499	50.501
BRAWH2016785	100.000	0.000
BRAWH3000446	100.000	0.000
BRAWH3000884	100.000	0.000
BRAWH3001053	100.000	0.000
BRAWH3001638	100.000	0.000
BRAWH3001783	100.000	0.000
BRAWH3001833	100.000	0.000
BRAWH3003244	100.000	0.000
BRAWH3003573	20.162	0.000
BRAWH3003975	100.000	0.000
BRAWH3004335	100.000	0.000
BRAWH3004350	16.580	0.000
BRAWH3005037	100.000	0.000
BRAWH3005886	100.000	0.000

BRAWH3005892	100.000	0.000
BRAWH3005896	100.000	0.000
BRAWH3008167	100.000	0.000
BRAWH3008559	100.000	0.000
BRAWH3008867	100.000	0.000
BRAWH3009961	47.417	0.000
BRAWH3010461	16.435	8.384
BRAWH3010602	100.000	0.000
BRAWH3010657	100.000	0.000
BRAWH3010726	100.000	0.000
BRAWH3010833	100.000	0.000
BRAWH3011101	100.000	0.000
BRAWH3011331	100.000	0.000
BRAWH3011402	100.000	0.000
BRAWH3011577	100.000	0.000
BRAWH3011623	100.000	0.000
BRAWH3011685	100.000	0.000
BRAWH3011907	47.417	0.000
BRAWH3011929	100.000	0.000
BRAWH3012005	100.000	0.000
BRAWH3012662	33.972	11.553
BRAWH3012779	100.000	0.000
BRAWH3013009	100.000	0.000
BRAWH3013049	100.000	0.000
BRAWH3013264	100.000	0.000
BRAWH3013508	100.000	0.000
BRAWH3014609	44.597	0.000
BRAWH3014639	100.000	0.000
BRAWH3015017	100.000	0.000

BRAWH3015175	100.000	0.000
BRAWH3015610	100.000	0.000
BRAWH3015825	100.000	0.000
BRAWH3016123	100.000	0.000
BRAWH3016715	100.000	0.000
BRAWH3017180	28.251	0.000
BRAWH3017259	13.996	0.000
BRAWH3017260	100.000	0.000
BRAWH3017477	100.000	0.000
BRAWH3017980	49.811	0.000
BRAWH3018063	15.836	0.000
BRAWH3018369	100.000	0.000
BRAWH3018548	100.000	0.000
BRAWH3018969	100.000	0.000
BRAWH3019026	100.000	0.000
BRAWH3019529	100.000	0.000
BRAWH3019594	100.000	0.000
BRAWH3019820	100.000	0.000
BRAWH3020200	100.000	0.000
BRAWH3020318	100.000	0.000
BRAWH3020884	100.000	0.000
BRAWH3020928	49.499	50.501
BRAWH3021012	100.000	0.000
BRAWH3021574	9.400	0.000
BRAWH3021580	100.000	0.000
BRAWH3021641	100.000	0.000
BRAWH3021643	100.000	0.000
BRAWH3021724	100.000	0.000
BRAWH3022347	100.000	0.000

BRAWH3022431	100.000	0.000
BRAWH3022459	100.000	0.000
BRAWH3022542	100.000	0.000
BRAWH3022651	9.828	5.014
BRAWH3022719	100.000	0.000
BRAWH3022900	100.000	0.000
BRAWH3023156	100.000	0.000
BRAWH3023168	100.000	0.000
BRAWH3023172	0.916	1.869
BRAWH3023274	100.000	0.000
BRAWH3023421	100.000	0.000
BRAWH3024186	19.959	10.182
BRAWH3024231	100.000	0.000
BRAWH3024242	31.843	32.488
BRAWH3024506	100.000	0.000
BRAWH3024989	2.369	4.834
BRAWH3026349	100.000	0.000
BRAWH3026938	6.894	2.344
BRAWH3027420	100.000	0.000
BRAWH3027440	58.488	0.000
BRAWH3027533	11.008	0.000
BRAWH3027574	47.417	0.000
BRAWH3027607	100.000	0.000
BRAWH3027616	100.000	0.000
BRAWH3027675	100.000	0.000
BRAWH3027806	100.000	0.000
BRAWH3027880	100.000	0.000
BRAWH3028202	100.000	0.000
BRAWH3028223	100.000	0.000

BRAWH3028461	100.000	0.000
BRAWH3028754	100.000	0.000
BRAWH3028796	100.000	0.000
BRAWH3029313	100.000	0.000
BRAWH3029385	35.187	17.949
BRAWH3029538	100.000	0.000
BRAWH3029806	26.735	0.000
BRAWH3030772	100.000	0.000
BRAWH3030810	21.287	0.000
BRAWH3030910	100.000	0.000
BRAWH3031054	100.000	0.000
BRAWH3031342	10.856	0.000
BRAWH3031710	100.000	0.000
BRAWH3032298	100.000	0.000
BRAWH3032340	100.000	0.000
BRAWH3032571	100.000	0.000
BRAWH3033117	100.000	0.000
BRAWH3033293	100.000	0.000
BRAWH3033448	100.000	0.000
BRAWH3033513	100.000	0.000
BRAWH3034097	100.000	0.000
BRAWH3034114	100.000	0.000
BRAWH3034134	100.000	0.000
BRAWH3034668	100.000	0.000
BRAWH3034743	16.662	21.249
BRAWH3034775	100.000	0.000
BRAWH3034890	100.000	0.000
BRAWH3035403	35.337	0.000
BRAWH3035904	100.000	0.000

BRAWH3035914	100.000	0.000
BRAWH3035936	70.575	0.000
BRAWH3036077	100.000	0.000
BRAWH3036247	54.530	0.000
BRAWH3036270	100.000	0.000
BRAWH3036334	6.241	19.102
BRAWH3036561	100.000	0.000
BRAWH3037265	44.597	0.000
BRAWH3037394	100.000	0.000
BRAWH3037428	5.877	0.000
BRAWH3037533	100.000	0.000
BRAWH3037979	100.000	0.000
BRAWH3038055	100.000	0.000
BRAWH3038230	100.000	0.000
BRAWH3038252	100.000	0.000
BRAWH3038324	100.000	0.000
BRCAN2010665	19.610	13.338
BRCAN2019953	0.000	9.704
BRCAN2022126	4.855	4.954
BRCAN2025093	21.732	0.000
BRCOC2012386	11.403	0.000
BRHIP2006819	0.000	100.000
BRHIP2006921	0.000	100.000
BRHIP2008756	0.000	100.000
BRHIP2009177	0.000	100.000
BRHIP2011199	0.000	55.026
BRHIP2013958	0.000	36.661
BRHIP2015153	20.038	20.443
BRHIP2016125	0.000	100.000

BRHIP2017714	0.000	100.000
BRHIP2020930	0.000	100.000
BRHIP2021929	0.000	100.000
BRHIP2023735	0.000	100.000
BRHIP2024941	0.000	100.000
BRHIP2026346	0.000	100.000
BRHIP2027077	2.020	2.061
BRHIP2027563	0.000	100.000
BRHIP2029529	0.000	100.000
BRHIP2029643	0.000	15.240
BRHIP2029663	0.000	45.093
BRHIP3000626	0.000	100.000
BRHIP3000859	0.000	100.000
BRHIP3001076	0.000	46.104
BRHIP3001141	0.000	100.000
BRHIP3001338	0.000	100.000
BRHIP3001360	0.000	58.973
BRHIP3001481	0.000	38.435
BRHIP3001573	24.474	24.970
BRHIP3001878	0.000	100.000
BRHIP3002000	4.500	3.826
BRHIP3002114	0.000	39.793
BRHIP3002124	0.000	100.000
BRHIP3002141	0.000	16.008
BRHIP3002363	0.000	100.000
BRHIP3002691	0.000	16.923
BRHIP3002920	0.000	64.789
BRHIP3002931	0.000	100.000
BRHIP3003063	10.960	55.910

BRHIP3003126	0.000	74.193
BRHIP3003306	0.000	60.949
BRHIP3003340	0.000	100.000
BRHIP3003395	0.000	100.000
BRHIP3003688	0.000	100.000
BRHIP3003795	0.000	45.093
BRHIP3003845	0.000	10.774
BRHIP3003961	0.000	19.351
BRHIP3003984	27.477	28.033
BRHIP3004215	0.000	13.851
BRHIP3004710	0.000	100.000
BRHIP3004725	0.000	100.000
BRHIP3004774	39.520	60.480
BRHIP3004786	0.000	100.000
BRHIP3005037	0.000	82.401
BRHIP3005142	0.000	60.949
BRHIP3005231	0.000	100.000
BRHIP3005307	0.000	46.104
BRHIP3005673	0.000	52.564
BRHIP3005801	0.000	19.121
BRHIP3005944	0.000	100.000
BRHIP3006279	0.000	100.000
BRHIP3006294	0.000	40.683
BRHIP3006449	0.000	100.000
BRHIP3006786	0.000	100.000
BRHIP3006950	0.000	100.000
BRHIP3007172	0.000	100.000
BRHIP3007195	0.000	75.737
BRHIP3007223	2.016	2.057

BRHIP3007291	0.000	100.000
BRHIP3007409	31.957	32.604
BRHIP3007424	0.000	100.000
BRHIP3007609	0.000	100.000
BRHIP3007960	0.000	100.000
BRHIP3008082	0.000	45.093
BRHIP3008320	23.349	47.644
BRHIP3008714	0.000	100.000
BRHIP3009672	0.000	100.000
BRHIP3009753	0.000	1.187
BRHIP3010289	0.000	100.000
BRHIP3010916	0.000	45.093
BRHIP3011082	0.000	100.000
BRHIP3011269	0.000	100.000
BRHIP3011460	0.000	100.000
BRHIP3011567	0.000	100.000
BRHIP3011831	0.000	100.000
BRHIP3012185	0.000	100.000
BRHIP3012289	0.000	100.000
BRHIP3012357	0.000	100.000
BRHIP3012736	0.000	33.611
BRHIP3012997	0.000	2.837
BRHIP3013078	0.000	100.000
BRHIP3013588	0.000	60.949
BRHIP3013698	0.000	100.000
BRHIP3014675	37.925	19.346
BRHIP3015854	0.000	100.000
BRHIP3016032	0.000	100.000
BRHIP3016421	0.000	100.000

BRHIP3017109	0.000	100.000
BRHIP3017146	0.000	66.943
BRHIP3017256	0.000	100.000
BRHIP3017558	0.000	100.000
BRHIP3017855	15.316	11.720
BRHIP3018784	6.930	3.535
BRHIP3019643	0.000	100.000
BRHIP3019824	0.000	100.000
BRHIP3019880	0.000	100.000
BRHIP3019956	0.000	100.000
BRHIP3020046	0.000	2.067
BRHIP3020155	0.000	100.000
BRHIP3020733	0.000	55.026
BRHIP3021019	7.745	7.901
BRHIP3021499	0.000	100.000
BRHIP3021987	0.000	36.438
BRHIP3022656	0.000	100.000
BRHIP3023922	0.000	100.000
BRHIP3024703	0.000	100.000
BRHIP3024820	0.000	100.000
BRHIP3025795	0.000	100.000
BRHIP3025844	0.000	100.000
BRHIP3026231	0.000	100.000
BRHIP3026651	0.000	100.000
BRHIP3027160	0.000	100.000
BRHIP3027191	0.000	100.000
BRHIP3027651	0.000	100.000
BRHIP3027947	0.000	100.000
BRHIP3028246	22.147	22.595

BRHIP3028570	31.957	32.604
BRHIP3028742	0.000	100.000
BRSTN2010089	6.598	0.000
BRSTN2012069	0.047	0.000
BRSTN2016992	1.476	2.510
BRTHA2001953	0.000	9.766
BRTHA2008502	0.000	22.073
BRTHA2031517	0.000	47.917
BRTHA2033155	4.253	0.000
BRTHA2035743	0.000	34.617
BRTHA3003417	0.000	31.398
BRTHA3003736	4.302	6.584
BRTHA3005988	31.076	0.000
BRTHA3007662	0.000	64.789
BRTHA3010135	20.010	0.000
BRTHA3010212	5.525	0.000
BRTHA3011194	3.534	10.818
BRTHA3011265	25.596	0.000
BRTHA3012265	0.000	64.789
BRTHA3017791	11.821	4.824
BRTHA3020771	31.957	32.604
BRTHA3021971	1.941	1.980
BRTHA3023403	14.857	15.157
CHONS2002829	0.000	11.668
CTONG2006235	9.828	5.014
CTONG2009033	25.755	26.276
CTONG2020582	9.594	1.958
D9OST2003106	6.904	0.000
DFNES2001829	9.228	18.830

KIDNE2010049	3.438	0.000
LIVER2008465	0.000	6.752
MESAN2017133	17.548	0.000
NT2RI2009233	6.767	0.000
NT2RI2010795	0.000	16.827
NT2RI2015533	6.216	1.586
NT2RI3005923	19.493	0.000
NT2RI3009524	35.496	0.000
NT2RP7007387	6.158	2.094
NT2RP8001605	29.324	0.000
NT2RP8007920	1.978	0.000
NTONG2008483	2.397	0.815
OCBBF2000831	0.000	9.824
OCBBF2003518	2.062	0.000
OCBBF2018618	16.218	16.546
OCBBF3001333	9.639	0.000
OCBBF3004487	4.531	4.622
PLACE7004103	3.880	5.278
PLACE7006240	25.174	0.000
PROST2007444	4.374	5.578
SMINT2012179	0.000	18.954
SYNOV4004210	0.000	1.927
TBAES2007428	5.371	0.000
TESTI2005112	19.455	0.000
TESTI2005564	0.000	3.736
TESTI2021654	9.773	0.000
TESTI4001569	0.000	43.832
TESTI4002072	16.696	20.440
TESTI4002774	4.103	4.186

TESTI4002799	1.767	2.703
TESTI4003602	25.967	0.000
TESTI4003703	0.000	4.514
TESTI4003944	0.000	35.590
TESTI4004210	36.051	0.000
TESTI4005399	7.797	15.910
TESTI4005653	1.989	3.551
TESTI4006441	60.471	0.000
TESTI4014908	36.051	0.000
TESTI4022158	53.386	13.617
TESTI4029297	0.000	4.514
THYMU3000776	15.604	0.000
THYMU3002887	4.680	6.367
THYMU3003007	0.000	19.391
THYMU3003350	54.530	0.000
THYMU3007308	0.000	39.793
THYMU3008105	0.000	20.662
THYMU3021586	20.651	16.855
THYMU3026000	49.066	0.000
THYMU3026306	46.281	0.000
THYMU3026350	14.291	14.581
THYMU3032798	9.668	0.000
THYMU3032867	12.871	0.000
THYMU3034671	0.000	4.866
THYMU3037827	54.530	0.000
THYMU3038214	39.314	0.000
THYMU3044075	37.925	19.346
TKIDN2000319	0.000	21.607
TRACH2013585	23.471	23.946

TRACH3002752	10.215	10.422
TRACH3003037	64.100	0.000
TRACH3003872	2.745	5.600
TRACH3004424	17.006	0.000
TRACH3006717	18.347	11.231
TRACH3007625	1.175	10.794
TRACH3007689	47.167	0.000
TRACH3008632	25.351	8.621
TRACH3009008	24.495	0.000
TRACH3010079	48.305	24.641
TRACH3016805	4.502	0.000
TRACH3016885	3.978	4.059
TRACH3022198	0.000	8.480
TRACH3024342	47.167	0.000
TRACH3024671	47.167	0.000
TRACH3025316	0.000	31.291
TRACH3026303	5.605	11.436
TRACH3026676	11.631	0.000
TRACH3028855	22.309	0.000
TRACH3032570	47.167	0.000
TRACH3036932	14.659	14.956
TRACH3038399	12.435	0.000
TSTOM2000235	0.000	4.535
UTERU3005422	0.000	21.641
UTERU3010409	3.461	7.062
UTERU3013167	45.606	0.000
UTERU3016273	0.000	46.104

【 0 2 9 0 】

【表 7】

小脳由来のライブラリー (BRACE) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRACE
ASTR02016114	14.497	0.000
BRACE1000475	0.000	100.000
BRACE2002392	0.000	3.670
BRACE2003628	0.000	9.684
BRACE2005991	0.000	100.000
BRACE2010336	0.000	9.658
BRACE2012528	3.794	15.820
BRACE2012625	0.000	100.000
BRACE2012833	0.000	100.000
BRACE2012838	0.000	100.000
BRACE2012936	0.000	100.000
BRACE2012947	0.000	100.000
BRACE2013009	0.000	100.000
BRACE2013126	0.000	100.000
BRACE2013132	0.000	100.000
BRACE2016896	0.000	100.000
BRACE2017359	0.000	58.183
BRACE2017397	0.000	3.348
BRACE2017580	0.000	100.000
BRACE2017844	0.000	29.179
BRACE2017872	0.000	100.000
BRACE2017992	0.000	100.000
BRACE2019348	0.000	74.228

BRACE2023633	0.000	100.000
BRACE2023744	0.000	100.000
BRACE2025452	0.000	100.000
BRACE2026404	0.000	100.000
BRACE2027312	0.000	100.000
BRACE2027382	0.000	100.000
BRACE2028956	0.000	100.000
BRACE2030039	0.000	100.000
BRACE2032584	0.000	100.000
BRACE2033128	0.000	100.000
BRACE2034434	0.000	100.000
BRACE2035120	0.000	100.000
BRACE2035191	0.000	100.000
BRACE2039362	0.000	100.000
BRACE2039607	0.000	100.000
BRACE2042541	0.000	100.000
BRACE2046976	0.000	100.000
BRACE2047232	0.000	100.000
BRACE2047975	0.000	100.000
BRACE3001403	0.000	100.000
BRACE3001973	0.000	36.360
BRACE3002344	0.000	100.000
BRACE3002541	0.000	100.000
BRACE3002756	0.000	100.000
BRACE3003866	0.000	100.000
BRACE3004046	0.000	41.027
BRACE3004371	11.270	10.666
BRACE3004767	58.488	41.512
BRACE3004887	0.000	100.000

BRACE3004981	0.000	100.000
BRACE3005870	0.000	100.000
BRACE3005903	0.000	100.000
BRACE3006553	0.000	18.271
BRACE3007649	0.000	100.000
BRACE3007869	0.000	100.000
BRACE3009075	0.000	100.000
BRACE3009265	0.000	100.000
BRACE3009392	0.000	100.000
BRACE3009416	0.000	20.257
BRACE3009539	0.000	100.000
BRACE3010702	0.000	100.000
BRACE3011447	0.000	100.000
BRACE3011774	0.000	100.000
BRACE3013418	0.000	100.000
BRACE3013874	0.000	100.000
BRACE3013986	0.000	100.000
BRACE3014523	0.000	100.000
BRACE3014714	0.000	100.000
BRACE3015090	0.000	100.000
BRACE3015898	0.000	100.000
BRACE3016020	0.000	100.000
BRACE3016167	0.000	100.000
BRACE3016580	0.000	100.000
BRACE3016788	0.000	100.000
BRACE3016810	0.000	100.000
BRACE3016862	0.000	100.000
BRACE3017253	0.000	55.894
BRACE3018083	0.000	100.000

BRACE3019570	0.000	100.000
BRACE3019611	0.000	100.000
BRACE3019817	0.000	100.000
BRACE3019941	0.000	2.074
BRACE3020356	0.000	100.000
BRACE3020669	0.000	38.787
BRACE3021430	0.000	8.467
BRACE3021517	0.000	100.000
BRACE3021805	0.000	100.000
BRACE3022051	0.000	100.000
BRACE3022303	0.000	100.000
BRACE3022312	0.000	24.151
BRACE3022340	58.488	41.512
BRACE3022847	0.000	100.000
BRACE3023604	0.000	100.000
BRACE3024379	0.000	100.000
BRACE3024444	0.000	100.000
BRACE3024497	0.000	100.000
BRACE3024537	0.000	100.000
BRACE3024879	0.000	100.000
BRACE3025627	0.000	100.000
BRACE3025719	0.000	12.784
BRACE3026161	0.000	100.000
BRACE3026290	0.000	100.000
BRACE3026345	0.000	100.000
BRACE3026456	0.000	100.000
BRACE3026802	0.000	36.390
BRACE3026844	0.000	100.000
BRACE3026947	0.000	100.000

BRACE3027256	0.000	100.000
BRACE3027931	0.000	23.879
BRACE3028360	0.000	100.000
BRACE3028895	0.000	32.302
BRACE3028998	0.000	100.000
BRACE3029005	0.000	100.000
BRACE3029021	0.000	25.807
BRACE3029205	0.000	100.000
BRACE3029447	0.000	100.000
BRACE3030538	0.000	36.360
BRACE3031161	0.000	100.000
BRACE3031184	0.000	100.000
BRACE3031185	58.488	41.512
BRACE3031315	0.000	41.329
BRACE3031372	0.000	100.000
BRACE3031579	0.000	100.000
BRACE3031728	0.000	100.000
BRACE3031743	5.455	15.488
BRACE3031843	0.000	100.000
BRACE3032385	13.674	19.411
BRACE3032537	0.000	100.000
BRACE3032538	0.000	100.000
BRACE3032631	12.612	8.951
BRACE3032980	0.000	100.000
BRACE3033525	0.000	100.000
BRACE3034183	0.000	100.000
BRACE3034389	0.000	100.000
BRACE3034964	0.000	100.000
BRACE3034993	0.000	100.000

BRACE3035168	0.000	29.854
BRACE3036156	0.000	31.069
BRACE3036271	0.000	100.000
BRACE3036283	0.000	5.298
BRACE3037612	0.000	100.000
BRACE3037637	0.000	100.000
BRACE3037803	0.000	100.000
BRACE3038012	0.000	100.000
BRACE3038030	0.000	100.000
BRACE3038570	0.000	100.000
BRACE3038760	0.000	100.000
BRACE3039288	0.000	100.000
BRACE3039358	41.331	14.668
BRACE3039378	0.000	100.000
BRACE3039454	0.000	100.000
BRACE3040012	0.000	100.000
BRACE3040239	0.000	100.000
BRACE3040504	0.000	100.000
BRACE3040644	0.000	100.000
BRACE3040863	17.888	12.696
BRACE3041059	0.000	100.000
BRACE3041162	0.000	100.000
BRACE3041827	0.000	100.000
BRACE3042046	0.000	100.000
BRACE3042210	0.000	100.000
BRACE3042326	0.000	24.903
BRACE3042409	0.000	100.000
BRACE3042432	58.488	41.512
BRACE3042594	0.000	100.000

BRACE3043597	0.000	100.000
BRACE3044090	0.000	100.000
BRACE3044172	0.000	100.000
BRACE3044247	0.000	100.000
BRACE3044377	0.000	100.000
BRACE3044495	0.000	100.000
BRACE3045078	0.000	58.183
BRACE3045145	0.000	100.000
BRACE3045424	0.000	100.000
BRACE3045708	0.000	100.000
BRACE3045981	26.434	56.286
BRACE3046049	0.000	100.000
BRACE3046152	0.000	100.000
BRACE3046294	0.000	100.000
BRACE3046466	0.000	100.000
BRACE3046491	0.000	100.000
BRACE3046609	0.000	100.000
BRACE3046837	0.000	100.000
BRACE3046855	0.000	100.000
BRACE3046966	0.000	100.000
BRACE3047018	0.000	100.000
BRACE3047482	0.000	100.000
BRACE3047801	0.000	100.000
BRAMY2031516	14.772	0.000
BRAMY3002329	20.323	9.616
BRAMY3004126	49.811	0.000
BRAMY3004364	0.000	4.821
BRAMY3005912	21.416	30.401
BRAMY3008436	5.603	5.965

BRAMY3009491	0.000	22.146
BRAWH2000256	100.000	0.000
BRAWH2002333	100.000	0.000
BRAWH2004078	10.539	3.740
BRAWH2010364	34.464	36.692
BRAWH2010619	100.000	0.000
BRAWH2011796	100.000	0.000
BRAWH2011812	13.544	0.000
BRAWH2011958	100.000	0.000
BRAWH2012054	100.000	0.000
BRAWH2012866	8.503	3.017
BRAWH2013955	100.000	0.000
BRAWH2014053	23.222	16.482
BRAWH2016209	8.306	11.791
BRAWH2016223	100.000	0.000
BRAWH2016305	4.308	0.000
BRAWH2016514	35.037	0.000
BRAWH2016562	49.499	0.000
BRAWH2016785	100.000	0.000
BRAWH3000446	100.000	0.000
BRAWH3000884	100.000	0.000
BRAWH3001053	100.000	0.000
BRAWH3001638	100.000	0.000
BRAWH3001783	100.000	0.000
BRAWH3001833	100.000	0.000
BRAWH3003244	100.000	0.000
BRAWH3003573	20.162	14.310
BRAWH3003975	100.000	0.000
BRAWH3004335	100.000	0.000

BRAWH3004350	16.580	0.000
BRAWH3005037	100.000	0.000
BRAWH3005886	100.000	0.000
BRAWH3005892	100.000	0.000
BRAWH3005896	100.000	0.000
BRAWH3008167	100.000	0.000
BRAWH3008559	100.000	0.000
BRAWH3008867	100.000	0.000
BRAWH3009961	47.417	0.000
BRAWH3010461	16.435	10.207
BRAWH3010602	100.000	0.000
BRAWH3010657	100.000	0.000
BRAWH3010726	100.000	0.000
BRAWH3010833	100.000	0.000
BRAWH3011101	100.000	0.000
BRAWH3011331	100.000	0.000
BRAWH3011402	100.000	0.000
BRAWH3011577	100.000	0.000
BRAWH3011623	100.000	0.000
BRAWH3011685	100.000	0.000
BRAWH3011907	47.417	0.000
BRAWH3011929	100.000	0.000
BRAWH3012005	100.000	0.000
BRAWH3012662	33.972	0.000
BRAWH3012779	100.000	0.000
BRAWH3013009	100.000	0.000
BRAWH3013049	100.000	0.000
BRAWH3013264	100.000	0.000
BRAWH3013508	100.000	0.000

BRAWH3014609	44.597	0.000
BRAWH3014639	100.000	0.000
BRAWH3015017	100.000	0.000
BRAWH3015175	100.000	0.000
BRAWH3015610	100.000	0.000
BRAWH3015825	100.000	0.000
BRAWH3016123	100.000	0.000
BRAWH3016715	100.000	0.000
BRAWH3017180	28.251	40.103
BRAWH3017259	13.996	4.967
BRAWH3017260	100.000	0.000
BRAWH3017477	100.000	0.000
BRAWH3017980	49.811	0.000
BRAWH3018063	15.836	0.000
BRAWH3018369	100.000	0.000
BRAWH3018548	100.000	0.000
BRAWH3018969	100.000	0.000
BRAWH3019026	100.000	0.000
BRAWH3019529	100.000	0.000
BRAWH3019594	100.000	0.000
BRAWH3019820	100.000	0.000
BRAWH3020200	100.000	0.000
BRAWH3020318	100.000	0.000
BRAWH3020884	100.000	0.000
BRAWH3020928	49.499	0.000
BRAWH3021012	100.000	0.000
BRAWH3021574	9.400	3.336
BRAWH3021580	100.000	0.000
BRAWH3021641	100.000	0.000

BRAWH3021643	100.000	0.000
BRAWH3021724	100.000	0.000
BRAWH3022347	100.000	0.000
BRAWH3022431	100.000	0.000
BRAWH3022459	100.000	0.000
BRAWH3022542	100.000	0.000
BRAWH3022651	9.828	1.163
BRAWH3022719	100.000	0.000
BRAWH3022900	100.000	0.000
BRAWH3023156	100.000	0.000
BRAWH3023168	100.000	0.000
BRAWH3023172	0.916	0.000
BRAWH3023274	100.000	0.000
BRAWH3023421	100.000	0.000
BRAWH3024186	19.959	0.000
BRAWH3024231	100.000	0.000
BRAWH3024242	31.843	0.000
BRAWH3024506	100.000	0.000
BRAWH3024989	2.369	0.000
BRAWH3026349	100.000	0.000
BRAWH3026938	6.894	4.893
BRAWH3027420	100.000	0.000
BRAWH3027440	58.488	41.512
BRAWH3027533	11.008	0.000
BRAWH3027574	47.417	0.000
BRAWH3027607	100.000	0.000
BRAWH3027616	100.000	0.000
BRAWH3027675	100.000	0.000
BRAWH3027806	100.000	0.000

BRAWH3027880	100.000	0.000
BRAWH3028202	100.000	0.000
BRAWH3028223	100.000	0.000
BRAWH3028461	100.000	0.000
BRAWH3028754	100.000	0.000
BRAWH3028796	100.000	0.000
BRAWH3029313	100.000	0.000
BRAWH3029385	35.187	12.487
BRAWH3029538	100.000	0.000
BRAWH3029806	26.735	0.000
BRAWH3030772	100.000	0.000
BRAWH3030810	21.287	67.989
BRAWH3030910	100.000	0.000
BRAWH3031054	100.000	0.000
BRAWH3031342	10.856	7.705
BRAWH3031710	100.000	0.000
BRAWH3032298	100.000	0.000
BRAWH3032340	100.000	0.000
BRAWH3032571	100.000	0.000
BRAWH3033117	100.000	0.000
BRAWH3033293	100.000	0.000
BRAWH3033448	100.000	0.000
BRAWH3033513	100.000	0.000
BRAWH3034097	100.000	0.000
BRAWH3034114	100.000	0.000
BRAWH3034134	100.000	0.000
BRAWH3034668	100.000	0.000
BRAWH3034743	16.662	5.913
BRAWH3034775	100.000	0.000

BRAWH3034890	100.000	0.000
BRAWH3035403	35.337	25.081
BRAWH3035904	100.000	0.000
BRAWH3035914	100.000	0.000
BRAWH3035936	70.575	0.000
BRAWH3036077	100.000	0.000
BRAWH3036247	54.530	0.000
BRAWH3036270	100.000	0.000
BRAWH3036334	6.241	4.430
BRAWH3036561	100.000	0.000
BRAWH3037265	44.597	0.000
BRAWH3037394	100.000	0.000
BRAWH3037428	5.877	25.026
BRAWH3037533	100.000	0.000
BRAWH3037979	100.000	0.000
BRAWH3038055	100.000	0.000
BRAWH3038230	100.000	0.000
BRAWH3038252	100.000	0.000
BRAWH3038324	100.000	0.000
BRCAN2010665	19.610	0.000
BRCAN2019953	0.000	6.751
BRCAN2022126	4.855	3.446
BRCAN2025093	21.732	0.000
BRCOC2012386	11.403	0.000
BRHIP2015153	20.038	14.222
BRHIP2027077	2.020	0.000
BRHIP2029643	0.000	10.603
BRHIP3001360	0.000	41.027
BRHIP3001573	24.474	0.000

BRHIP3002000	4.500	0.532
BRHIP3002114	0.000	27.684
BRHIP3003063	10.960	0.000
BRHIP3003126	0.000	25.807
BRHIP3003961	0.000	13.462
BRHIP3003984	27.477	29.254
BRHIP3004215	0.000	9.636
BRHIP3004774	39.520	0.000
BRHIP3005801	0.000	13.302
BRHIP3007223	2.016	1.431
BRHIP3007409	31.957	0.000
BRHIP3008320	23.349	0.000
BRHIP3014675	37.925	26.918
BRHIP3017855	15.316	13.588
BRHIP3018784	6.930	0.000
BRHIP3021019	7.745	0.000
BRHIP3028246	22.147	0.000
BRHIP3028570	31.957	0.000
BRSSN2011843	0.000	8.495
BRSSN2013696	0.000	12.675
BRSTN2010089	6.598	4.683
BRSTN2011961	0.000	3.083
BRSTN2012069	0.047	0.517
BRSTN2016992	1.476	5.588
BRTHA2033155	4.253	9.056
BRTHA2035743	0.000	4.816
BRTHA3003736	4.302	1.527
BRTHA3005988	31.076	0.000
BRTHA3009858	0.000	16.462

BRTHA3010135	20.010	0.000
BRTHA3010212	5.525	0.000
BRTHA3010530	0.000	19.846
BRTHA3011194	3.534	0.000
BRTHA3011265	25.596	0.000
BRTHA3011998	0.000	56.141
BRTHA3017791	11.821	9.229
BRTHA3020771	31.957	0.000
BRTHA3021708	0.000	39.025
BRTHA3021971	1.941	0.000
BRTHA3023403	14.857	0.000
CHONS2002829	0.000	1.160
CTONG2006235	9.828	1.163
CTONG2009033	25.755	0.000
CTONG2020582	9.594	1.362
CTONG2027959	0.000	27.592
D90ST2003106	6.904	0.000
DFNES2001829	9.228	6.550
KIDNE2010049	3.438	0.000
KIDNE2017153	0.000	16.915
LIVER2008465	0.000	4.697
MESAN2017133	17.548	0.000
NOVAR2000783	0.000	2.684
NT2RI2009233	6.767	1.601
NT2RI2015533	6.216	3.309
NT2RI3005923	19.493	0.000
NT2RI3009524	35.496	0.000
NT2RP7007387	6.158	0.000
NT2RP8001605	29.324	0.000

NT2RP8007920	1.978	1.404
NT2RP8009119	0.000	3.276
NTONG2008483	2.397	0.000
NTONG2009468	0.000	13.482
OCBBF2003518	2.062	0.000
OCBBF2014745	0.000	36.360
OCBBF2018618	16.218	0.000
OCBBF3001333	9.639	4.561
OCBBF3004487	4.531	6.432
PLACE7004103	3.880	0.918
PLACE7006240	25.174	0.000
PROST2007444	4.374	5.433
TBAES2007428	5.371	0.000
TESTI2005112	19.455	0.000
TESTI2018867	0.000	4.042
TESTI2021654	9.773	0.000
TESTI4002072	16.696	11.850
TESTI4002774	4.103	0.000
TESTI4002799	1.767	0.627
TESTI4003602	25.967	18.431
TESTI4003703	0.000	6.281
TESTI4004210	36.051	0.000
TESTI4005013	0.000	11.599
TESTI4005399	7.797	11.068
TESTI4005653	1.989	1.059
TESTI4006441	60.471	0.000
TESTI4014908	36.051	0.000
TESTI4022158	53.386	9.473
TESTI4029297	0.000	6.281

TESTI4032913	0.000	5.753
TESTI4043223	0.000	19.643
THYMU3000776	15.604	22.150
THYMU3002887	4.680	7.197
THYMU3003350	54.530	0.000
THYMU3007308	0.000	27.684
THYMU3021586	20.651	0.000
THYMU3026000	49.066	0.000
THYMU3026306	46.281	0.000
THYMU3026350	14.291	0.000
THYMU3032798	9.668	10.979
THYMU3032867	12.871	9.135
THYMU3033626	0.000	7.979
THYMU3034671	0.000	5.078
THYMU3037827	54.530	0.000
THYMU3038214	39.314	27.904
THYMU3044075	37.925	26.918
TLIVE2007736	0.000	9.358
TRACH2013585	23.471	0.000
TRACH3002752	10.215	3.625
TRACH3003037	64.100	0.000
TRACH3003872	2.745	0.000
TRACH3004424	17.006	0.000
TRACH3006717	18.347	10.418
TRACH3007625	1.175	2.503
TRACH3007689	47.167	0.000
TRACH3007995	0.000	38.787
TRACH3008632	25.351	11.995
TRACH3009008	24.495	0.000

TRACH3010079	48.305	0.000
TRACH3016805	4.502	3.196
TRACH3016885	3.978	5.647
TRACH3024342	47.167	0.000
TRACH3024671	47.167	0.000
TRACH3026303	5.605	0.000
TRACH3026676	11.631	0.000
TRACH3028855	22.309	0.000
TRACH3032570	47.167	0.000
TRACH3036932	14.659	10.405
TRACH3038399	12.435	8.826
UTERU3000670	0.000	16.553
UTERU3010409	3.461	17.196
UTERU3013167	45.606	0.000
UTERU3015011	0.000	5.009

【 0 2 9 1 】

【表 8】

視床由来のライブラリー (BRTHA) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRTHA

ASTR02008972	0.000	17.271
ASTR02016114	14.497	0.000
BLADE2004849	0.000	8.220
BRACE2002392	0.000	1.911
BRACE2012528	3.794	13.673
BRACE2019348	0.000	25.772

BRACE3004371	11.270	4.166
BRACE3004767	58.488	0.000
BRACE3019941	0.000	6.480
BRACE3022312	0.000	37.734
BRACE3022340	58.488	0.000
BRACE3031185	58.488	0.000
BRACE3031743	5.455	0.000
BRACE3032385	13.674	15.164
BRACE3032631	12.612	0.000
BRACE3036156	0.000	24.272
BRACE3039358	41.331	22.917
BRACE3040863	17.888	0.000
BRACE3042432	58.488	0.000
BRACE3045981	26.434	0.000
BRAMY2031516	14.772	0.000
BRAMY3002329	20.323	15.025
BRAMY3004126	49.811	0.000
BRAMY3005912	21.416	0.000
BRAMY3008436	5.603	12.427
BRAMY3009556	0.000	52.395
BRAMY3010654	0.000	52.395
BRAMY4001863	0.000	16.612
BRAWH2000256	100.000	0.000
BRAWH2002333	100.000	0.000
BRAWH2004078	10.539	0.000
BRAWH2010364	34.464	0.000
BRAWH2010619	100.000	0.000
BRAWH2011796	100.000	0.000
BRAWH2011812	13.544	0.000

BRAWH2011958	100.000	0.000
BRAWH2012054	100.000	0.000
BRAWH2012866	8.503	11.786
BRAWH2013955	100.000	0.000
BRAWH2014053	23.222	25.752
BRAWH2016209	8.306	0.000
BRAWH2016223	100.000	0.000
BRAWH2016305	4.308	0.000
BRAWH2016514	35.037	0.000
BRAWH2016562	49.499	0.000
BRAWH2016785	100.000	0.000
BRAWH3000446	100.000	0.000
BRAWH3000884	100.000	0.000
BRAWH3001053	100.000	0.000
BRAWH3001638	100.000	0.000
BRAWH3001783	100.000	0.000
BRAWH3001833	100.000	0.000
BRAWH3003244	100.000	0.000
BRAWH3003573	20.162	22.358
BRAWH3003975	100.000	0.000
BRAWH3004335	100.000	0.000
BRAWH3004350	16.580	18.386
BRAWH3005037	100.000	0.000
BRAWH3005886	100.000	0.000
BRAWH3005892	100.000	0.000
BRAWH3005896	100.000	0.000
BRAWH3008167	100.000	0.000
BRAWH3008559	100.000	0.000
BRAWH3008867	100.000	0.000

BRAWH3009961	47.417	52.583
BRAWH3010461	16.435	11.391
BRAWH3010602	100.000	0.000
BRAWH3010657	100.000	0.000
BRAWH3010726	100.000	0.000
BRAWH3010833	100.000	0.000
BRAWH3011101	100.000	0.000
BRAWH3011331	100.000	0.000
BRAWH3011402	100.000	0.000
BRAWH3011577	100.000	0.000
BRAWH3011623	100.000	0.000
BRAWH3011685	100.000	0.000
BRAWH3011907	47.417	52.583
BRAWH3011929	100.000	0.000
BRAWH3012005	100.000	0.000
BRAWH3012662	33.972	12.558
BRAWH3012779	100.000	0.000
BRAWH3013009	100.000	0.000
BRAWH3013049	100.000	0.000
BRAWH3013264	100.000	0.000
BRAWH3013508	100.000	0.000
BRAWH3014609	44.597	0.000
BRAWH3014639	100.000	0.000
BRAWH3015017	100.000	0.000
BRAWH3015175	100.000	0.000
BRAWH3015610	100.000	0.000
BRAWH3015825	100.000	0.000
BRAWH3016123	100.000	0.000
BRAWH3016715	100.000	0.000

BRAWH3017180	28.251	0.000
BRAWH3017259	13.996	0.000
BRAWH3017260	100.000	0.000
BRAWH3017477	100.000	0.000
BRAWH3017980	49.811	0.000
BRAWH3018063	15.836	0.000
BRAWH3018369	100.000	0.000
BRAWH3018548	100.000	0.000
BRAWH3018969	100.000	0.000
BRAWH3019026	100.000	0.000
BRAWH3019529	100.000	0.000
BRAWH3019594	100.000	0.000
BRAWH3019820	100.000	0.000
BRAWH3020200	100.000	0.000
BRAWH3020318	100.000	0.000
BRAWH3020884	100.000	0.000
BRAWH3020928	49.499	0.000
BRAWH3021012	100.000	0.000
BRAWH3021574	9.400	0.000
BRAWH3021580	100.000	0.000
BRAWH3021641	100.000	0.000
BRAWH3021643	100.000	0.000
BRAWH3021724	100.000	0.000
BRAWH3022347	100.000	0.000
BRAWH3022431	100.000	0.000
BRAWH3022459	100.000	0.000
BRAWH3022542	100.000	0.000
BRAWH3022651	9.828	5.450
BRAWH3022719	100.000	0.000

BRAWH3022900	100.000	0.000
BRAWH3023156	100.000	0.000
BRAWH3023168	100.000	0.000
BRAWH3023172	0.916	2.031
BRAWH3023274	100.000	0.000
BRAWH3023421	100.000	0.000
BRAWH3024186	19.959	0.000
BRAWH3024231	100.000	0.000
BRAWH3024242	31.843	0.000
BRAWH3024506	100.000	0.000
BRAWH3024989	2.369	0.000
BRAWH3026349	100.000	0.000
BRAWH3026938	6.894	0.000
BRAWH3027420	100.000	0.000
BRAWH3027440	58.488	0.000
BRAWH3027533	11.008	0.000
BRAWH3027574	47.417	52.583
BRAWH3027607	100.000	0.000
BRAWH3027616	100.000	0.000
BRAWH3027675	100.000	0.000
BRAWH3027806	100.000	0.000
BRAWH3027880	100.000	0.000
BRAWH3028202	100.000	0.000
BRAWH3028223	100.000	0.000
BRAWH3028461	100.000	0.000
BRAWH3028754	100.000	0.000
BRAWH3028796	100.000	0.000
BRAWH3029313	100.000	0.000
BRAWH3029385	35.187	0.000

BRAWH3029538	100.000	0.000
BRAWH3029806	26.735	9.883
BRAWH3030772	100.000	0.000
BRAWH3030810	21.287	0.000
BRAWH3030910	100.000	0.000
BRAWH3031054	100.000	0.000
BRAWH3031342	10.856	0.000
BRAWH3031710	100.000	0.000
BRAWH3032298	100.000	0.000
BRAWH3032340	100.000	0.000
BRAWH3032571	100.000	0.000
BRAWH3033117	100.000	0.000
BRAWH3033293	100.000	0.000
BRAWH3033448	100.000	0.000
BRAWH3033513	100.000	0.000
BRAWH3034097	100.000	0.000
BRAWH3034114	100.000	0.000
BRAWH3034134	100.000	0.000
BRAWH3034668	100.000	0.000
BRAWH3034743	16.662	18.478
BRAWH3034775	100.000	0.000
BRAWH3034890	100.000	0.000
BRAWH3035403	35.337	0.000
BRAWH3035904	100.000	0.000
BRAWH3035914	100.000	0.000
BRAWH3035936	70.575	0.000
BRAWH3036077	100.000	0.000
BRAWH3036247	54.530	0.000
BRAWH3036270	100.000	0.000

BRAWH3036334	6.241	6.921
BRAWH3036561	100.000	0.000
BRAWH3037265	44.597	0.000
BRAWH3037394	100.000	0.000
BRAWH3037428	5.877	19.551
BRAWH3037533	100.000	0.000
BRAWH3037979	100.000	0.000
BRAWH3038055	100.000	0.000
BRAWH3038230	100.000	0.000
BRAWH3038252	100.000	0.000
BRAWH3038324	100.000	0.000
BRCAN2002892	0.000	32.586
BRCAN2010665	19.610	7.249
BRCAN2020234	0.000	27.335
BRCAN2022126	4.855	0.000
BRCAN2025093	21.732	0.000
BRCOC2006164	0.000	32.234
BRCOC2012386	11.403	0.000
BRHIP2013958	0.000	39.849
BRHIP2015153	20.038	0.000
BRHIP2027077	2.020	0.000
BRHIP3001573	24.474	27.141
BRHIP3002000	4.500	0.832
BRHIP3002691	0.000	18.395
BRHIP3002920	0.000	35.211
BRHIP3003063	10.960	0.000
BRHIP3003961	0.000	21.034
BRHIP3003984	27.477	15.236
BRHIP3004215	0.000	15.055

BRHIP3004774	39.520	0.000
BRHIP3007223	2.016	4.472
BRHIP3007409	31.957	35.439
BRHIP3008320	23.349	0.000
BRHIP3014675	37.925	0.000
BRHIP3017855	15.316	4.246
BRHIP3018784	6.930	0.000
BRHIP3020046	0.000	1.123
BRHIP3021019	7.745	0.000
BRHIP3028246	22.147	0.000
BRHIP3028570	31.957	35.439
BRSSN2015497	0.000	7.931
BRSTN2010089	6.598	0.000
BRSTN2011961	0.000	1.285
BRSTN2012069	0.047	0.000
BRSTN2016992	1.476	1.091
BRTHA2000969	0.000	100.000
BRTHA2001304	0.000	100.000
BRTHA2001953	0.000	10.615
BRTHA2002091	0.000	100.000
BRTHA2003759	0.000	100.000
BRTHA2005448	0.000	100.000
BRTHA2006720	0.000	100.000
BRTHA2008502	0.000	23.993
BRTHA2008598	0.000	100.000
BRTHA2010672	0.000	100.000
BRTHA2012189	0.000	100.000
BRTHA2014647	0.000	100.000
BRTHA2018304	0.000	100.000

BRTHA2019726	0.000	100.000
BRTHA2019743	0.000	100.000
BRTHA2020400	0.000	100.000
BRTHA2020566	0.000	100.000
BRTHA2020642	0.000	100.000
BRTHA2020695	0.000	100.000
BRTHA2020721	0.000	100.000
BRTHA2020781	0.000	100.000
BRTHA2020910	0.000	100.000
BRTHA2021212	0.000	100.000
BRTHA2021440	0.000	57.080
BRTHA2021450	0.000	100.000
BRTHA2022074	0.000	100.000
BRTHA2022914	0.000	100.000
BRTHA2022968	0.000	100.000
BRTHA2023402	0.000	100.000
BRTHA2023437	0.000	100.000
BRTHA2024177	0.000	100.000
BRTHA2024354	0.000	100.000
BRTHA2024712	0.000	100.000
BRTHA2025869	0.000	100.000
BRTHA2026071	0.000	13.612
BRTHA2026290	0.000	100.000
BRTHA2026311	0.000	100.000
BRTHA2027227	0.000	100.000
BRTHA2027229	0.000	2.030
BRTHA2027250	0.000	100.000
BRTHA2028297	0.000	100.000
BRTHA2029969	0.000	100.000

BRTHA2030036	0.000	100.000
BRTHA2030213	0.000	100.000
BRTHA2031517	0.000	52.083
BRTHA2031917	0.000	100.000
BRTHA2032763	0.000	100.000
BRTHA2033122	0.000	100.000
BRTHA2033155	4.253	9.433
BRTHA2033320	0.000	100.000
BRTHA2033469	0.000	38.930
BRTHA2033683	0.000	100.000
BRTHA2034281	0.000	100.000
BRTHA2034576	0.000	100.000
BRTHA2035743	0.000	22.576
BRTHA2036055	0.000	100.000
BRTHA2036295	0.000	100.000
BRTHA2037247	0.000	100.000
BRTHA2038279	0.000	100.000
BRTHA2038345	0.000	100.000
BRTHA2038353	0.000	100.000
BRTHA3000456	0.000	62.915
BRTHA3002411	0.000	100.000
BRTHA3003225	0.000	47.165
BRTHA3003417	0.000	34.129
BRTHA3003736	4.302	2.385
BRTHA3005988	31.076	68.924
BRTHA3006593	0.000	100.000
BRTHA3007469	0.000	100.000
BRTHA3007662	0.000	35.211
BRTHA3009858	0.000	25.720

BRTHA3010135	20.010	44.380
BRTHA3010212	5.525	6.127
BRTHA3010469	0.000	100.000
BRTHA3010530	0.000	31.009
BRTHA3010540	0.000	7.466
BRTHA3010717	0.000	100.000
BRTHA3011187	0.000	100.000
BRTHA3011194	3.534	3.920
BRTHA3011229	0.000	100.000
BRTHA3011265	25.596	18.923
BRTHA3011306	0.000	13.657
BRTHA3011361	0.000	62.915
BRTHA3011510	0.000	100.000
BRTHA3011892	0.000	100.000
BRTHA3011998	0.000	43.859
BRTHA3012265	0.000	35.211
BRTHA3013860	0.000	100.000
BRTHA3013882	0.000	100.000
BRTHA3014000	0.000	100.000
BRTHA3014105	0.000	100.000
BRTHA3014507	0.000	100.000
BRTHA3014547	0.000	100.000
BRTHA3014835	0.000	100.000
BRTHA3014854	0.000	100.000
BRTHA3014920	0.000	100.000
BRTHA3016616	0.000	100.000
BRTHA3017791	11.821	5.244
BRTHA3018409	0.000	100.000
BRTHA3018623	0.000	100.000

BRTHA3019183	0.000	100.000
BRTHA3020369	0.000	100.000
BRTHA3020771	31.957	35.439
BRTHA3021569	0.000	100.000
BRTHA3021708	0.000	60.975
BRTHA3021786	0.000	100.000
BRTHA3021971	1.941	4.305
BRTHA3022641	0.000	19.618
BRTHA3023403	14.857	8.238
BRTHA3023590	0.000	100.000
BRTHA3023929	0.000	100.000
BRTHA3024600	0.000	100.000
BRTHA3025073	0.000	100.000
BRTHA3026161	0.000	100.000
BRTHA3026180	0.000	100.000
BRTHA3026556	0.000	100.000
BRTHA3026916	0.000	52.395
BRTHA3027171	0.000	100.000
BRTHA3027318	0.000	100.000
BRTHA3027638	0.000	100.000
BRTHA3027820	0.000	100.000
BRTHA3027879	0.000	48.181
BRTHA3027957	0.000	100.000
BRTHA3028339	0.000	100.000
BRTHA3028505	0.000	100.000
CHONS2002829	0.000	1.812
CTONG2006235	9.828	5.450
CTONG2009033	25.755	0.000
CTONG2011801	0.000	3.284

CTONG2020582	9.594	4.256
D90ST2003106	6.904	0.000
DFNES2001829	9.228	0.000
KIDNE2010049	3.438	0.000
LIVER2008465	0.000	7.339
MESAN2017133	17.548	0.000
NT2RI2009233	6.767	2.501
NT2RI2010795	0.000	36.581
NT2RI2015533	6.216	12.064
NT2RI3005923	19.493	0.000
NT2RI3009524	35.496	0.000
NT2RP7007387	6.158	2.276
NT2RP8001605	29.324	0.000
NT2RP8007920	1.978	0.000
NTONG2008483	2.397	1.772
OCBBF2003518	2.062	0.000
OCBBF2009536	0.000	47.165
OCBBF2018618	16.218	0.000
OCBBF3001333	9.639	0.000
OCBBF3004487	4.531	0.000
OCBBF3008835	0.000	47.165
PLACE6003004	0.000	38.390
PLACE7004103	3.880	4.302
PLACE7006240	25.174	0.000
PROST2007444	4.374	3.638
SMINT2009292	0.000	3.933
TBAES2007428	5.371	0.000
TESTI2005112	19.455	0.000
TESTI2021654	9.773	10.838

TESTI2039342	0.000	77.236
TESTI4002072	16.696	11.109
TESTI4002774	4.103	0.000
TESTI4002799	1.767	1.469
TESTI4003602	25.967	0.000
TESTI4003703	0.000	4.907
TESTI4004210	36.051	0.000
TESTI4004695	0.000	36.122
TESTI4005399	7.797	0.000
TESTI4005653	1.989	0.551
TESTI4006441	60.471	0.000
TESTI4007965	0.000	20.014
TESTI4010979	0.000	21.790
TESTI4013474	0.000	2.292
TESTI4014908	36.051	0.000
TESTI4022158	53.386	14.801
TESTI4029297	0.000	4.907
TESTI4032913	0.000	8.989
THYMU3000776	15.604	0.000
THYMU3002887	4.680	3.460
THYMU3003350	54.530	0.000
THYMU3021586	20.651	4.580
THYMU3026000	49.066	0.000
THYMU3026306	46.281	0.000
THYMU3026350	14.291	15.849
THYMU3032798	9.668	4.289
THYMU3032867	12.871	0.000
THYMU3037827	54.530	0.000
THYMU3038214	39.314	0.000

THYMU3044075	37.925	0.000
TRACH2013585	23.471	0.000
TRACH3002752	10.215	0.000
TRACH3003037	64.100	0.000
TRACH3003872	2.745	0.000
TRACH3004424	17.006	18.859
TRACH3006717	18.347	0.000
TRACH3007625	1.175	3.911
TRACH3007689	47.167	0.000
TRACH3008508	0.000	21.245
TRACH3008632	25.351	9.371
TRACH3009008	24.495	0.000
TRACH3010079	48.305	0.000
TRACH3016805	4.502	0.000
TRACH3016885	3.978	0.000
TRACH3024342	47.167	0.000
TRACH3024671	47.167	0.000
TRACH3026303	5.605	0.000
TRACH3026676	11.631	12.899
TRACH3028855	22.309	0.000
TRACH3032570	47.167	0.000
TRACH3036932	14.659	16.256
TRACH3038399	12.435	13.790
UTERU3010409	3.461	0.000
UTERU3012414	0.000	48.181
UTERU3013167	45.606	0.000
UTERU3017995	0.000	12.128
UTERU3018172	0.000	35.368

【 0 2 9 2 】

【表 9】

扁桃由来のライブラリー (BRAMY) と、正常全脳組織由来のライブラリー (BRAWH) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BRAWH	BRAMY
ASTR02016114	14.497	0.000
BRACE2002392	0.000	5.210
BRACE2012528	3.794	10.512
BRACE2017397	0.000	2.376
BRACE2017844	0.000	15.534
BRACE3004371	11.270	7.571
BRACE3004767	58.488	0.000
BRACE3022340	58.488	0.000
BRACE3031185	58.488	0.000
BRACE3031315	0.000	58.671
BRACE3031743	5.455	5.497
BRACE3032385	13.674	13.778
BRACE3032631	12.612	0.000
BRACE3039358	41.331	0.000
BRACE3040863	17.888	0.000
BRACE3042432	58.488	0.000
BRACE3045981	26.434	0.000
BRAMY2015516	0.000	100.000
BRAMY2021098	0.000	100.000
BRAMY2022320	0.000	100.000
BRAMY2023939	0.000	6.159
BRAMY2025495	0.000	100.000

BRAMY2031516	14.772	7.442
BRAMY2033895	0.000	100.000
BRAMY2035801	0.000	100.000
BRAMY2036254	0.000	100.000
BRAMY2036266	0.000	100.000
BRAMY2037609	0.000	100.000
BRAMY2039630	0.000	8.744
BRAMY2040915	0.000	100.000
BRAMY2041347	0.000	100.000
BRAMY2041384	0.000	100.000
BRAMY2041507	0.000	100.000
BRAMY2044686	0.000	100.000
BRAMY2046489	0.000	100.000
BRAMY2046537	0.000	100.000
BRAMY3000692	0.000	100.000
BRAMY3001409	0.000	100.000
BRAMY3002329	20.323	20.478
BRAMY3002508	0.000	100.000
BRAMY3002886	0.000	100.000
BRAMY3004126	49.811	50.189
BRAMY3004364	0.000	13.689
BRAMY3005184	0.000	22.578
BRAMY3005656	0.000	100.000
BRAMY3005912	21.416	21.579
BRAMY3007078	0.000	49.688
BRAMY3007449	0.000	100.000
BRAMY3007471	0.000	100.000
BRAMY3008436	5.603	4.234
BRAMY3009158	0.000	100.000

BRAMY3009491	0.000	31.439
BRAMY3009556	0.000	47.605
BRAMY3009904	0.000	100.000
BRAMY3010321	0.000	100.000
BRAMY3010603	0.000	100.000
BRAMY3010654	0.000	47.605
BRAMY4000915	0.000	49.688
BRAMY4000962	0.000	100.000
BRAMY4001234	0.000	54.718
BRAMY4001652	0.000	100.000
BRAMY4001863	0.000	15.094
BRAMY4001913	0.000	100.000
BRAMY4002575	0.000	100.000
BRAMY4002628	0.000	7.157
BRAWH2000256	100.000	0.000
BRAWH2002333	100.000	0.000
BRAWH2004078	10.539	0.000
BRAWH2010364	34.464	0.000
BRAWH2010619	100.000	0.000
BRAWH2011796	100.000	0.000
BRAWH2011812	13.544	13.646
BRAWH2011958	100.000	0.000
BRAWH2012054	100.000	0.000
BRAWH2012866	8.503	14.993
BRAWH2013955	100.000	0.000
BRAWH2014053	23.222	0.000
BRAWH2016209	8.306	0.000
BRAWH2016223	100.000	0.000
BRAWH2016305	4.308	0.000

BRAWH2016514	35.037	0.000
BRAWH2016562	49.499	0.000
BRAWH2016785	100.000	0.000
BRAWH3000446	100.000	0.000
BRAWH3000884	100.000	0.000
BRAWH3001053	100.000	0.000
BRAWH3001638	100.000	0.000
BRAWH3001783	100.000	0.000
BRAWH3001833	100.000	0.000
BRAWH3003244	100.000	0.000
BRAWH3003573	20.162	0.000
BRAWH3003975	100.000	0.000
BRAWH3004335	100.000	0.000
BRAWH3004350	16.580	0.000
BRAWH3005037	100.000	0.000
BRAWH3005886	100.000	0.000
BRAWH3005892	100.000	0.000
BRAWH3005896	100.000	0.000
BRAWH3008167	100.000	0.000
BRAWH3008559	100.000	0.000
BRAWH3008867	100.000	0.000
BRAWH3009961	47.417	0.000
BRAWH3010461	16.435	14.490
BRAWH3010602	100.000	0.000
BRAWH3010657	100.000	0.000
BRAWH3010726	100.000	0.000
BRAWH3010833	100.000	0.000
BRAWH3011101	100.000	0.000
BRAWH3011331	100.000	0.000

BRAWH3011402	100.000	0.000
BRAWH3011577	100.000	0.000
BRAWH3011623	100.000	0.000
BRAWH3011685	100.000	0.000
BRAWH3011907	47.417	0.000
BRAWH3011929	100.000	0.000
BRAWH3012005	100.000	0.000
BRAWH3012662	33.972	0.000
BRAWH3012779	100.000	0.000
BRAWH3013009	100.000	0.000
BRAWH3013049	100.000	0.000
BRAWH3013264	100.000	0.000
BRAWH3013508	100.000	0.000
BRAWH3014609	44.597	0.000
BRAWH3014639	100.000	0.000
BRAWH3015017	100.000	0.000
BRAWH3015175	100.000	0.000
BRAWH3015610	100.000	0.000
BRAWH3015825	100.000	0.000
BRAWH3016123	100.000	0.000
BRAWH3016715	100.000	0.000
BRAWH3017180	28.251	0.000
BRAWH3017259	13.996	0.000
BRAWH3017260	100.000	0.000
BRAWH3017477	100.000	0.000
BRAWH3017980	49.811	50.189
BRAWH3018063	15.836	7.978
BRAWH3018369	100.000	0.000
BRAWH3018548	100.000	0.000

BRAWH3018969	100.000	0.000
BRAWH3019026	100.000	0.000
BRAWH3019529	100.000	0.000
BRAWH3019594	100.000	0.000
BRAWH3019820	100.000	0.000
BRAWH3020200	100.000	0.000
BRAWH3020318	100.000	0.000
BRAWH3020884	100.000	0.000
BRAWH3020928	49.499	0.000
BRAWH3021012	100.000	0.000
BRAWH3021574	9.400	0.000
BRAWH3021580	100.000	0.000
BRAWH3021641	100.000	0.000
BRAWH3021643	100.000	0.000
BRAWH3021724	100.000	0.000
BRAWH3022347	100.000	0.000
BRAWH3022431	100.000	0.000
BRAWH3022459	100.000	0.000
BRAWH3022542	100.000	0.000
BRAWH3022651	9.828	4.952
BRAWH3022719	100.000	0.000
BRAWH3022900	100.000	0.000
BRAWH3023156	100.000	0.000
BRAWH3023168	100.000	0.000
BRAWH3023172	0.916	0.000
BRAWH3023274	100.000	0.000
BRAWH3023421	100.000	0.000
BRAWH3024186	19.959	10.055
BRAWH3024231	100.000	0.000

BRAWH3024242	31.843	0.000
BRAWH3024506	100.000	0.000
BRAWH3024989	2.369	0.000
BRAWH3026349	100.000	0.000
BRAWH3026938	6.894	0.000
BRAWH3027420	100.000	0.000
BRAWH3027440	58.488	0.000
BRAWH3027533	11.008	0.000
BRAWH3027574	47.417	0.000
BRAWH3027607	100.000	0.000
BRAWH3027616	100.000	0.000
BRAWH3027675	100.000	0.000
BRAWH3027806	100.000	0.000
BRAWH3027880	100.000	0.000
BRAWH3028202	100.000	0.000
BRAWH3028223	100.000	0.000
BRAWH3028461	100.000	0.000
BRAWH3028754	100.000	0.000
BRAWH3028796	100.000	0.000
BRAWH3029313	100.000	0.000
BRAWH3029385	35.187	0.000
BRAWH3029538	100.000	0.000
BRAWH3029806	26.735	8.979
BRAWH3030772	100.000	0.000
BRAWH3030810	21.287	10.724
BRAWH3030910	100.000	0.000
BRAWH3031054	100.000	0.000
BRAWH3031342	10.856	0.000
BRAWH3031710	100.000	0.000

BRAWH3032298	100.000	0.000
BRAWH3032340	100.000	0.000
BRAWH3032571	100.000	0.000
BRAWH3033117	100.000	0.000
BRAWH3033293	100.000	0.000
BRAWH3033448	100.000	0.000
BRAWH3033513	100.000	0.000
BRAWH3034097	100.000	0.000
BRAWH3034114	100.000	0.000
BRAWH3034134	100.000	0.000
BRAWH3034668	100.000	0.000
BRAWH3034743	16.662	12.592
BRAWH3034775	100.000	0.000
BRAWH3034890	100.000	0.000
BRAWH3035403	35.337	0.000
BRAWH3035904	100.000	0.000
BRAWH3035914	100.000	0.000
BRAWH3035936	70.575	0.000
BRAWH3036077	100.000	0.000
BRAWH3036247	54.530	0.000
BRAWH3036270	100.000	0.000
BRAWH3036334	6.241	0.000
BRAWH3036561	100.000	0.000
BRAWH3037265	44.597	0.000
BRAWH3037394	100.000	0.000
BRAWH3037428	5.877	5.921
BRAWH3037533	100.000	0.000
BRAWH3037979	100.000	0.000
BRAWH3038055	100.000	0.000

BRAWH3038230	100.000	0.000
BRAWH3038252	100.000	0.000
BRAWH3038324	100.000	0.000
BRCAN2010665	19.610	9.879
BRCAN2022126	4.855	14.677
BRCAN2025093	21.732	0.000
BRCOC2012386	11.403	0.000
BRHIP2015153	20.038	10.095
BRHIP2027077	2.020	2.035
BRHIP3001573	24.474	8.220
BRHIP3002000	4.500	0.756
BRHIP3002691	0.000	8.357
BRHIP3003063	10.960	33.130
BRHIP3003984	27.477	0.000
BRHIP3004215	0.000	13.679
BRHIP3004774	39.520	0.000
BRHIP3005673	0.000	25.956
BRHIP3007223	2.016	0.000
BRHIP3007409	31.957	0.000
BRHIP3008320	23.349	0.000
BRHIP3012736	0.000	66.389
BRHIP3014675	37.925	0.000
BRHIP3017146	0.000	33.057
BRHIP3017855	15.316	0.000
BRHIP3018784	6.930	0.000
BRHIP3020046	0.000	1.021
BRHIP3021019	7.745	7.803
BRHIP3028246	22.147	22.315
BRHIP3028570	31.957	0.000

BRSTN2010089	6.598	0.000
BRSTN2012069	0.047	0.029
BRSTN2016992	1.476	4.958
BRTHA2026071	0.000	12.368
BRTHA2033155	4.253	4.285
BRTHA3003736	4.302	0.000
BRTHA3005988	31.076	0.000
BRTHA3010135	20.010	0.000
BRTHA3010212	5.525	5.567
BRTHA3011194	3.534	0.000
BRTHA3011265	25.596	0.000
BRTHA3017791	11.821	5.956
BRTHA3020771	31.957	0.000
BRTHA3021971	1.941	1.956
BRTHA3023403	14.857	7.485
BRTHA3026916	0.000	47.605
CHONS2002829	0.000	1.646
CTONG2006235	9.828	4.952
CTONG2009033	25.755	0.000
CTONG2020582	9.594	3.867
D90ST2003106	6.904	0.000
DFNES2001829	9.228	0.000
KIDNE2010049	3.438	0.000
MESAN2017133	17.548	0.000
NT2RI2009233	6.767	4.545
NT2RI2010795	0.000	16.619
NT2RI2015533	6.216	12.527
NT2RI3005923	19.493	0.000
NT2RI3009524	35.496	0.000

NT2RP7007387	6.158	0.000
NT2RP8001605	29.324	0.000
NT2RP8007920	1.978	0.000
NTONG2008483	2.397	0.000
OCBBF2000831	0.000	9.702
OCBBF2003518	2.062	1.039
OCBBF2018618	16.218	16.341
OCBBF2030927	0.000	44.784
OCBBF3001333	9.639	6.475
OCBBF3004487	4.531	4.565
OCBBF3009244	0.000	34.702
PLACE6008315	0.000	1.403
PLACE6010936	0.000	12.399
PLACE7004103	3.880	1.303
PLACE7006240	25.174	0.000
PROST2007444	4.374	1.102
SPLEN2012571	0.000	3.203
SYNOV4004210	0.000	0.952
SYNOV4009575	0.000	4.828
TBAES2007428	5.371	0.000
TESTI2005112	19.455	0.000
TESTI2021654	9.773	9.847
TESTI4002072	16.696	3.364
TESTI4002774	4.103	0.000
TESTI4002799	1.767	0.000
TESTI4003602	25.967	0.000
TESTI4003703	0.000	4.458
TESTI4004210	36.051	0.000
TESTI4005399	7.797	15.713

TESTI4005653	1.989	3.507
TESTI4006441	60.471	0.000
TESTI4014908	36.051	0.000
TESTI4022158	53.386	0.000
TESTI4029297	0.000	4.458
TESTI4032913	0.000	8.167
TESTI4043223	0.000	27.886
TESTI4046073	0.000	19.130
THYMU3000776	15.604	0.000
THYMU3002887	4.680	3.930
THYMU3003350	54.530	0.000
THYMU3008105	0.000	20.406
THYMU3019476	0.000	54.718
THYMU3021586	20.651	4.162
THYMU3026000	49.066	0.000
THYMU3026306	46.281	0.000
THYMU3026350	14.291	14.400
THYMU3032798	9.668	1.948
THYMU3032867	12.871	0.000
THYMU3037827	54.530	0.000
THYMU3038214	39.314	0.000
THYMU3044075	37.925	0.000
TRACH2013585	23.471	0.000
TRACH3002752	10.215	0.000
TRACH3003037	64.100	0.000
TRACH3003872	2.745	2.765
TRACH3004424	17.006	0.000
TRACH3006717	18.347	3.697
TRACH3007625	1.175	3.553

TRACH3007689	47.167	0.000
TRACH3008632	25.351	0.000
TRACH3009008	24.495	0.000
TRACH3010079	48.305	0.000
TRACH3016805	4.502	0.000
TRACH3016885	3.978	12.025
TRACH3024342	47.167	0.000
TRACH3024671	47.167	0.000
TRACH3026303	5.605	0.000
TRACH3026676	11.631	0.000
TRACH3028855	22.309	0.000
TRACH3032570	47.167	0.000
TRACH3036932	14.659	0.000
TRACH3038399	12.435	0.000
UTERU3010409	3.461	0.000
UTERU3013167	45.606	0.000

【 0 2 9 3 】

【表 1 0】

乳がん由来のライブラリー (TBAES) と、正常な乳房由来のライブラリー (BEAST) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	BEAST	TBAES

BRSTN2011961	6.317	4.075
BRSTN2012069	0.000	0.067
TBAES2003917	0.000	100.000
TBAES2005361	0.000	100.000
TBAES2007428	0.000	37.783

TBAES2007548	0.000	100.000
TBAES2007862	0.000	100.000
TESTI2005564	0.000	25.762
TESTI4017854	0.000	91.498
TRACH3016805	0.000	31.673

【 0 2 9 4 】

【表 1 1】

子宮頸癌由来のライブラリー (TCERX) と、正常な子宮頸管由来のライブラリー (CERVX) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

【 0 2 9 5 】

Clone ID	CERVX	TCERX
BRACE2017397	48.741	0.000
BRHIP2027077	41.741	0.000
BRSTN2011961	5.985	0.000
BRSTN2012069	5.668	7.585
CERVX2000812	100.000	0.000
CERVX2000968	100.000	0.000

【表 1 2】

結腸がん由来のライブラリー (TCOLN) と、正常な結腸由来のライブラリー (COLON) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	COLON	TCOLN
BRSTN2011961	0.000	6.140
BRSTN2012069	1.726	1.805

COLON2001829	100.000	0.000
COLON2001866	100.000	0.000
COLON2004351	100.000	0.000
COLON2004911	100.000	0.000
COLON2005623	100.000	0.000
COLON2005735	100.000	0.000
OCBBF3001333	22.556	0.000
SMINT2017964	34.030	0.000

【 0 2 9 6 】

【表 1 3】

食道がん由来のライブラリー (TESOP) と、正常な食道由来のライブラリー (NESOP) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	NESOP	TESOP
BRAMY3004364	0.000	46.478
BRAWH3027533	0.000	75.317
BRHIP3007223	42.899	0.000
BRSTN2011961	0.000	1.981
BRSTN2012069	1.409	2.071
CTONG2011801	0.000	20.259
CTONG3002518	0.000	57.732
SMINT2009292	0.000	24.268
TESOP2002005	0.000	100.000
TESOP2003308	0.000	100.000
TESOP2004110	0.000	100.000
TESOP2008556	0.000	100.000
UTERU3015011	0.000	48.286

UTERU3017995 0.000 74.828

【 0 2 9 7 】

【表 1 4】

腎臓がん由来のライブラリー (TKIDN) と、正常な腎臓由来のライブラリー (KIDNE) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	KIDNE	TKIDN
BRACE2002392	0.000	6.380
BRACE2012528	0.000	14.044
BRACE3004371	13.097	0.000
BRAMY2039630	60.511	0.000
BRAMY3004364	23.683	0.000
BRAMY3008436	0.000	5.185
BRAWH2004078	18.371	0.000
BRAWH3012662	0.000	41.917
BRAWH3021574	0.000	17.397
BRAWH3022651	0.000	6.064
BRAWH3037428	0.000	21.753
BRCAN2019953	0.000	35.208
BRCAN2022126	0.000	17.973
BRHIP3002000	10.458	0.000
BRHIP3002691	0.000	30.700
BRHIP3012997	0.000	3.431
BRHIP3020046	0.000	3.749
BRSTN2012069	0.429	0.140
BRSTN2016992	0.000	1.822
BRTHA3010212	0.000	20.450

CTONG2006235	0.000	6.064
KIDNE2004531	80.699	0.000
KIDNE2010049	11.987	0.000
KIDNE2014496	100.000	0.000
KIDNE2015987	100.000	0.000
KIDNE2016464	100.000	0.000
KIDNE2017153	83.085	0.000
KIDNE2018268	100.000	0.000
NT2RI2015533	0.000	11.506
NT2RP7007387	7.156	0.000
OCBBF3004487	0.000	16.771
PLACE6008315	0.000	5.154
SYNOV4004210	0.000	3.496
TESTI2005112	67.827	0.000
THYMU3001776	22.094	0.000
THYMU3002887	0.000	2.887
THYMU3029795	37.093	0.000
THYMU3032867	44.871	0.000
TKIDN2000319	0.000	78.393
TKIDN2003396	0.000	100.000
TKIDN2010602	0.000	100.000
TKIDN2011051	0.000	100.000
TKIDN2011160	0.000	100.000

【 0 2 9 8 】

【表 1 5】

肝臓がん由来のライブラリー (TLIVE) と、正常な肝臓由来のライブラリー (LIV
ER) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	LIVER	TLIVE

BRAWH3022651	14.200	0.000
BRCAN2020412	0.000	74.979
BRSTN2012069	0.000	0.390
BRTHA3003736	18.647	0.000
CTONG2006235	14.200	0.000
LIVER2008465	57.368	0.000
TESTI4013474	0.000	7.104
THYMU3002887	6.762	0.000
THYMU3038158	53.382	0.000
TLIVE2000142	0.000	100.000
TLIVE2001616	0.000	100.000
TLIVE2007736	0.000	90.642
TLIVE2008797	0.000	100.000
TRACH3027229	93.931	0.000

【 0 2 9 9 】

【表 1 6】

肺がん由来のライブラリー (TLUNG) と、正常な肺由来のライブラリー (HLUNG) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	HLUNG	TLUNG

BRACE3036283	27.376	0.000
BRAMY2031516	27.091	0.000
BRSTN2011961	2.124	0.000
BRSTN2012069	0.763	0.000
HLUNG2012600	100.000	0.000

MESAN2009156	38.142	0.000
NTONG2008483	2.930	0.000
PROST2007444	4.011	0.000
TESTI4003703	16.229	0.000
TESTI4005653	1.824	0.000
TESTI4013474	3.790	0.000
TESTI4029297	16.229	0.000
THYMU3001776	11.622	0.000
THYMU3033626	20.615	0.000
THYMU3034671	8.747	0.000
THYMU3041428	0.935	0.000
TRACH3022198	30.484	0.000

【 0 3 0 0 】

【表 1 7】

卵巣がん由来のライブラリー (TOVER) と、正常な卵巣由来のライブラリー (NOVER) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	NOVAR	TOVAR
<hr/>		
BRSTN2012069	5.861	6.386
NOVAR2000783	90.145	0.000
THYMU3002887	0.000	16.991

【 0 3 0 1 】

【表 1 8】

胃がん由来のライブラリー (TSTOM) と、正常な胃由来のライブラリー (STOMA) のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	STOMA	TSTOM
BRSTN2012069	1.995	4.062
CHONS2002829	11.118	0.000
STOMA2003894	100.000	0.000
STOMA2004663	47.516	0.000
THYMU3001776	21.564	0.000
TSTOM2000235	0.000	95.465
TSTOM2001571	0.000	100.000
TSTOM2002611	0.000	100.000
TSTOM2002682	0.000	100.000

【 0 3 0 2 】

【表 1 9】

子宮がん由来のライブラリー（TUTER）と、正常な子宮由来のライブラリー（UTERU）のcDNAを解析して比較した結果、両者で発現変化のある遺伝子

Clone ID	UTERU	TUTER
BRACE2012528	0.566	0.000
BRACE2017397	11.252	0.000
BRACE3004371	4.481	0.000
BRACE3036283	8.902	0.000
BRACE3040863	21.335	0.000
BRAMY2031516	8.809	0.000
BRAMY3005184	26.725	0.000
BRAWH2004078	6.285	0.000
BRAWH3004350	19.774	0.000
BRAWH3022651	1.954	0.000

BRAWH3024186	11.902	0.000
BRAWH3029806	10.629	0.000
BRAWH3031342	6.474	0.000
BRCAN2022126	5.791	0.000
BRHIP3001076	53.896	0.000
BRHIP3002000	0.894	0.000
BRHIP3002141	18.713	0.000
BRHIP3005307	53.896	0.000
BRHIP3007223	2.405	0.000
BRHIP3017855	27.401	0.000
BRHIP3020046	1.208	0.000
BRSTN2010089	7.869	0.000
BRSTN2011961	0.345	0.000
BRSTN2012069	0.271	3.583
BRSTN2016892	3.559	0.000
BRTHA3003736	5.131	0.000
BRTHA3011265	10.176	0.000
BRTHA3023403	26.579	0.000
BRTHA3027879	51.819	0.000
CHONS2002829	11.691	0.000
CTONG2001932	12.322	0.000
CTONG2003517	13.371	0.000
CTONG2006235	1.954	0.000
CTONG2011801	3.532	0.000
CTONG3002518	10.064	0.000
DFNES2001829	11.006	0.000
KIDNE2010049	4.101	76.623
LIVER2008465	7.893	0.000
NT2RI3005923	23.249	0.000

OCBBF3001333	3.832	0.000
OCBBF3004487	5.404	0.000
PLACE6008315	1.661	0.000
PLACE7006240	30.024	0.000
PROST2007444	5.217	0.000
SPLEN2012571	3.792	0.000
SYNOV4000598	35.608	0.000
SYNOV4009575	5.715	0.000
TIESE2000904	2.754	0.000
TESTI4002072	3.983	0.000
TESTI4002195	15.959	0.000
TESTI4002774	9.787	0.000
TESTI4002799	1.053	9.842
TESTI4003703	5.277	0.000
TESTI4003944	41.606	0.000
TESTI4005399	9.300	0.000
TESTI4005653	1.779	0.000
TESTI4024245	40.205	0.000
TESTI4029297	5.277	0.000
THYMU3002887	0.930	0.000
THYMU3021586	4.926	0.000
THYMU3026350	17.045	0.000
THYMU3032798	2.306	0.000
THYMU3034616	58.853	0.000
THYMU3034671	19.911	0.000
TRACH3003872	9.820	0.000
TRACH3005699	22.893	0.000
TRACH3006800	34.742	0.000
TRACH3008632	20.157	0.000

TRACH3009008	5.843	0.000
TUTER1000014	0.000	100.000
TUTER2001433	0.000	100.000
UTERU2000300	11.765	0.000
UTERU2014998	100.000	0.000
UTERU2016464	100.000	0.000
UTERU2016669	9.848	0.000
UTERU2020226	78.491	0.000
UTERU2022955	100.000	0.000
UTERU2023941	100.000	0.000
UTERU2024042	100.000	0.000
UTERU2027369	39.231	0.000
UTERU2028377	100.000	0.000
UTERU2029660	100.000	0.000
UTERU2035926	100.000	0.000
UTERU2037423	100.000	0.000
UTERU3000670	83.447	0.000
UTERU3001029	100.000	0.000
UTERU3001394	100.000	0.000
UTERU3001946	34.742	0.000
UTERU3004635	100.000	0.000
UTERU3005264	100.000	0.000
UTERU3005422	25.298	0.000
UTERU3006538	100.000	0.000
UTERU3006720	100.000	0.000
UTERU3007108	100.000	0.000
UTERU3009775	100.000	0.000
UTERU3010029	100.000	0.000
UTERU3010409	53.665	0.000

UTERU3010604	40.126	0.000
UTERU3010892	100.000	0.000
UTERU3010919	100.000	0.000
UTERU3011092	100.000	0.000
UTERU3011398	100.000	0.000
UTERU3011558	100.000	0.000
UTERU3011579	34.742	0.000
UTERU3011837	100.000	0.000
UTERU3012293	100.000	0.000
UTERU3012414	51.819	0.000
UTERU3012476	100.000	0.000
UTERU3012599	100.000	0.000
UTERU3012999	100.000	0.000
UTERU3013167	54.394	0.000
UTERU3013302	58.853	0.000
UTERU3014274	100.000	0.000
UTERU3014647	100.000	0.000
UTERU3014906	100.000	0.000
UTERU3015011	16.834	0.000
UTERU3015299	100.000	0.000
UTERU3015647	100.000	0.000
UTERU3015844	100.000	0.000
UTERU3016070	100.000	0.000
UTERU3016273	53.896	0.000
UTERU3016274	100.000	0.000
UTERU3016308	100.000	0.000
UTERU3017441	100.000	0.000
UTERU3017626	100.000	0.000
UTERU3017995	13.044	0.000

UTERU3018172	38.038	0.000
UTERU3018255	100.000	0.000

【 0 3 0 3 】

【表 2 0】

舌がん由来のライブラリー (CTONG) と、正常な舌由来のライブラリー (NTONG) のcDNAを解析して舌がんと正常舌との間で発現変化のある遺伝子

Clone ID	NTONG	CTONG
BRACE2012528	0.000	0.883
BRAMY4001863	0.000	55.803
BRAWH3021574	0.000	17.507
BRAWH3022651	0.000	3.051
BRAWH3024186	0.000	18.588
BRHIP2027077	0.000	3.762
BRHIP3001573	0.000	15.195
BRHIP3002000	0.000	12.571
BRHIP3007223	14.859	3.755
BRHIP3012997	0.000	1.726
BRHIP3020046	0.000	3.773
BRSSN2013696	0.000	6.652
BRSTN2011961	2.134	0.539
BRSTN2012069	0.000	0.018
BRTHA2027229	0.000	3.410
BRTHA2033155	0.000	7.921
BRTHA3011194	0.000	6.583
BRTHA3022641	0.000	32.949
CTONG2001932	0.000	38.485

CTONG2003517	0.000	20.880
CTONG2006235	0.000	3.051
CTONG2008989	0.000	100.000
CTONG2009033	0.000	47.970
CTONG2009570	0.000	100.000
CTONG2010330	0.000	100.000
CTONG2011801	0.000	5.515
CTONG2012123	0.000	100.000
CTONG2014206	0.000	100.000
CTONG2014959	0.000	100.000
CTONG2020582	0.000	21.442
CTONG2026987	0.000	100.000
CTONG2027150	0.000	100.000
CTONG2027591	0.000	100.000
CTONG2027783	0.000	100.000
CTONG2027959	0.000	72.408
CTONG3001605	0.000	100.000
CTONG3002518	0.000	15.716
CTONG3002588	0.000	100.000
CTONG3003669	0.000	100.000
CTONG3008223	0.000	100.000
NT2RI2009233	0.000	8.402
NTONG2002278	100.000	0.000
NTONG2003805	100.000	0.000
NTONG2004829	100.000	0.000
NTONG2008483	17.664	2.976
NTONG2009468	69.996	0.000
OCBBF3004487	0.000	8.439
PLACE6008315	10.262	0.000

PLACE7004103	9.531	12.044
SKNMC2003639	0.000	19.285
SPLEN2012571	0.000	5.921
SPLEN2019092	0.000	51.706
SYNOV4009575	0.000	8.924
TIESE2000904	0.000	4.300
TESTI2005564	0.000	6.821
TESTI2018867	20.987	0.000
TESTI4002799	0.000	1.645
TESTI4005653	0.000	7.408
TESTI4032913	59.736	0.000
THYMU3021586	0.000	7.693
THYMU3047115	57.541	0.000
TRACH3006717	0.000	13.669
TRACH3007625	0.000	4.379
TRACH3016805	0.000	8.386
TRACH3036932	0.000	27.304
TRACH3038399	0.000	23.161
UTERU2000300	0.000	9.187

 【 0 3 0 4 】

【表 2 1】

胎児の脳由来のライブラリー (FCBBF, FEBRAまたはOCBBF) と成体の脳由来のライブラリー (BRACE, BRALZ, BRAMY, BRAWH, BRCAN, BRCOC, BRHIP, BRSSN, BRSTNまたはBRTHA) のcDNAを解析し、胎児と成体の間で発現変化のある遺伝子

Clone ID	FCBBF	FEBRA	OCBBF	BRACE	BRALZ	BRAWY	BRAWH	BRCAN	BRCCOC	BRHIP	BRSSN	BRSTN	BRTHA
ASTRO2006972	28.772	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	17.271
ASTRO2016114	0.000	0.000	0.000	0.000	0.000	0.000	14.497	0.000	0.000	0.000	0.000	0.000	0.000
BLADE2004849	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	8.220
BRACE1000475	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2002392	0.000	0.000	0.000	3.670	18.684	5.210	0.000	15.817	12.212	5.275	0.000	6.215	1.911
BRACE2003628	0.000	0.000	0.000	9.658	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2005991	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2010336	0.000	0.000	0.000	9.658	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2012528	0.876	5.911	3.535	15.820	1.714	10.512	3.794	7.616	0.000	4.354	0.000	6.840	13.673
BRACE2012625	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2012833	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2012838	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2012936	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2012947	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2013009	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2013126	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2013132	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2016896	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2017359	0.000	0.000	0.000	58.183	0.000	0.000	0.000	0.000	0.000	41.817	0.000	0.000	0.000
BRACE2017397	0.000	0.000	0.000	3.348	0.000	2.376	0.000	0.000	0.000	4.813	0.000	0.000	0.000
BRACE2017580	0.000	0.000	0.000	100.000	0.000	15.534	0.000	11.790	0.000	5.243	38.254	0.000	0.000
BRACE2017844	0.000	0.000	0.000	29.179	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2017872	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2017992	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2019348	0.000	0.000	0.000	74.228	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2023633	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	25.772
BRACE2023744	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2025452	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2026404	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2027312	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2027382	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2028956	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2030039	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2032584	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2033128	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2034434	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2035120	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2035191	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2039362	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2039607	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2042541	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2046976	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2047232	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE2047975	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3001403	0.000	0.000	63.640	36.360	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3001973	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3002344	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3002541	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3002756	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BRACE3003866	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

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BRHI P2015153	0.000	14.222	0.000	10.095	20.038	0.000	0.000	0.000	20.443	0.000	0.000	0.000
BRHI P2016125	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2017714	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2020930	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2021929	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2023735	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2024941	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2026346	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2027077	3.732	0.000	0.000	2.035	2.020	0.000	0.000	0.000	2.061	0.000	0.000	0.000
BRHI P2027563	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2029529	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P2029643	0.000	18.557	10.603	0.000	0.000	0.000	0.000	0.000	15.240	55.599	0.000	0.000
BRHI P2029663	0.000	54.907	0.000	0.000	0.000	0.000	0.000	0.000	45.093	0.000	0.000	0.000
BRHI P3000626	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3000859	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3001076	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	46.104	0.000	0.000	0.000
BRHI P3001141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3001338	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3001360	0.000	0.000	41.027	0.000	0.000	0.000	0.000	0.000	58.973	0.000	0.000	0.000
BRHI P3001481	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	38.435	0.000	0.000	0.000
BRHI P3001573	0.000	0.000	0.000	8.220	24.474	0.000	0.000	0.000	24.970	0.000	0.000	27.141
BRHI P3001878	0.000	0.000	0.000	0.756	4.500	0.000	0.000	0.000	3.826	5.583	0.000	0.832
BRHI P3002000	0.000	1.870	0.532	0.000	0.000	0.000	0.000	0.000	39.793	0.000	0.000	0.000
BRHI P3002114	0.000	0.000	27.684	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3002124	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3002141	0.000	39.113	0.000	0.000	0.000	0.000	0.000	0.000	15.008	0.000	0.000	0.000
BRHI P3002363	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3002691	15.322	0.000	0.000	8.357	0.000	0.000	0.000	0.000	16.923	0.000	0.000	18.395
BRHI P3002920	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	64.789	0.000	0.000	35.211
BRHI P3002931	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3003063	0.000	10.303	0.000	0.000	0.000	0.000	0.000	0.000	55.910	0.000	0.000	0.000
BRHI P3003126	0.000	0.000	0.000	33.130	10.960	0.000	0.000	0.000	74.193	0.000	0.000	0.000
BRHI P3003306	0.000	25.807	0.000	0.000	0.000	0.000	0.000	0.000	60.949	0.000	0.000	0.000
BRHI P3003340	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3003395	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3003688	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3003795	0.000	54.907	0.000	0.000	0.000	0.000	0.000	0.000	45.093	0.000	0.000	0.000
BRHI P3003845	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	10.774	0.000	0.000	0.000
BRHI P3003961	0.000	0.000	13.462	0.000	0.000	0.000	0.000	0.000	19.351	0.000	0.000	21.034
BRHI P3003984	0.000	29.254	0.000	0.000	27.477	0.000	0.000	0.000	28.033	0.000	0.000	15.236
BRHI P3004215	0.000	9.636	0.000	13.679	0.000	0.000	0.000	0.000	13.851	0.000	0.000	15.055
BRHI P3004710	0.000	0.000	0.000	0.000	39.520	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3004725	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3004774	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.480	0.000	0.000	0.000
BRHI P3004786	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3005037	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	82.401	0.000	0.000	0.000
BRHI P3005142	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.949	0.000	0.000	0.000
BRHI P3005231	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	100.000	0.000	0.000	0.000
BRHI P3005307	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	46.104	0.000	0.000	0.000
BRHI P3005673	0.000	0.000	0.000	25.956	0.000	0.000	0.000	0.000	52.564	0.000	0.000	0.000
BRHI P3005801	0.000	13.302	0.000	0.000	0.000	0.000	0.000	0.000	19.121	67.577	0.000	0.000

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NT2R12009233	4.167	0.000	0.000	5.604	1.601	0.000	4.545	6.767	5.175	7.991	0.000	0.000	8.133	2.501
NT2R12010795	0.000	0.000	0.000	0.000	0.000	0.000	16.619	0.000	0.000	0.000	0.000	0.000	0.000	36.581
NT2R12015533	5.742	0.000	0.000	3.861	3.309	5.616	12.527	6.216	7.131	0.000	0.000	5.604	0.000	12.064
NT2R13005923	0.000	0.000	0.000	0.000	0.000	0.000	0.000	19.493	0.000	0.000	0.000	0.000	0.000	0.000
NT2R13009524	0.000	0.000	0.000	0.000	0.000	0.000	0.000	35.496	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP7007387	7.584	5.117	0.000	5.100	0.000	0.000	0.000	6.158	4.709	0.000	0.000	0.000	0.000	2.276
NT2RP8001604	0.000	17.297	0.000	0.000	0.000	0.000	0.000	29.324	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP8001605	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.978	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP8007920	10.963	0.000	0.000	31.946	1.404	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NT2RP8009119	0.000	0.000	0.000	0.000	3.276	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
NTONG2008483	1.476	1.992	0.000	1.985	0.000	0.000	0.000	2.397	1.833	5.661	0.815	5.761	0.000	1.772
NTONG2009468	0.000	0.000	0.000	0.000	13.482	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2000831	17.790	0.000	0.000	47.849	0.000	0.000	9.702	0.000	0.000	0.000	9.824	0.000	0.000	0.000
OCBBF2003518	0.000	2.570	0.000	1.281	0.000	0.000	1.039	2.062	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2004478	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2007039	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2009536	0.000	0.000	0.000	52.835	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2014745	0.000	0.000	0.000	63.640	36.360	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	47.165
OCBBF2016928	5.059	0.000	0.000	13.608	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2018229	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2018618	0.000	0.000	0.000	40.294	0.000	0.000	16.341	16.218	0.000	0.000	16.546	0.000	0.000	0.000
OCBBF2019761	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2024569	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2024779	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2025631	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2030927	0.000	0.000	0.000	55.216	0.000	0.000	44.784	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF2036019	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3000743	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3000830	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001076	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001202	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001333	0.000	0.000	0.000	11.974	4.561	0.000	6.475	9.639	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3001616	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3003745	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3004487	0.000	0.000	0.000	11.257	6.432	0.000	4.565	4.531	0.000	0.000	4.622	0.000	0.000	0.000
OCBBF3004908	0.000	47.686	0.000	11.882	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3005330	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3005843	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3006986	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3007078	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3007704	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3008392	0.000	0.000	0.000	100.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
OCBBF3008835	0.000	0.000	0.000	52.835	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	47.165
OCBBF3009244	0.000	0.000	0.000	42.785	0.000	0.000	34.702	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PLACE5000492	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	55.315	0.000	0.000	0.000	0.000	0.000
PLACE6003004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	38.390
PLACE6008315	0.000	0.000	0.000	1.730	0.000	0.000	1.403	0.000	0.000	4.933	0.000	5.021	0.000	0.000
PLACE6010936	0.000	0.000	0.000	0.000	0.000	0.000	12.399	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PLACE7004103	0.000	0.000	0.000	1.607	0.918	0.000	1.303	3.880	0.000	0.000	5.278	0.000	0.000	4.302
PLACE7006240	0.000	0.000	0.000	0.000	0.000	0.000	0.000	25.174	0.000	0.000	0.000	0.000	0.000	0.000
PRUST2007444	0.000	5.452	0.000	4.075	5.433	0.000	1.102	4.374	0.000	0.000	5.578	0.000	0.000	3.638

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PROST2017910	0.000	0.000	0.000	0.000	0.000	37.758	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SWINT2009292	0.000	0.000	4.406	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SWINT2012179	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SPLLEN2012571	0.000	7.925	0.000	0.000	0.000	0.000	0.000	3.203	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SYNOVA4004210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.952	0.000	2.167	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SYNOVA4009575	0.000	0.000	0.000	0.000	0.000	0.000	0.000	4.828	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TYSEZ2006069	0.000	5.666	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TYSEZ2003904	0.000	5.755	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TBAES2007428	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12005112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12005564	0.000	9.129	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12009497	0.000	0.000	65.522	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12018867	0.000	0.000	0.000	4.042	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12021654	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST12039342	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14001569	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14002072	6.169	0.000	4.148	11.850	0.000	0.000	0.000	3.364	16.696	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14002195	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14002774	0.000	0.000	5.097	0.000	0.000	0.000	0.000	0.000	4.103	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14002799	0.000	0.000	1.846	0.627	0.000	0.000	0.000	0.000	1.767	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST140033602	8.175	22.061	0.000	0.000	0.000	0.000	0.000	0.000	25.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14003703	0.000	0.000	0.000	6.281	0.000	0.000	0.000	4.458	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14003944	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14004210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14004695	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14005013	0.000	0.000	0.000	11.599	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14005399	0.000	0.000	9.686	11.068	0.000	0.000	0.000	15.713	7.797	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14005653	7.348	0.000	9.265	1.059	0.000	0.000	0.000	3.507	1.989	1.141	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14006441	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	60.471	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14007965	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14010979	0.000	48.982	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14012960	0.000	0.000	18.497	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14013474	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14014908	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14020596	0.000	0.000	65.522	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14022158	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14029297	8.175	22.061	0.000	0.000	0.000	0.000	0.000	4.458	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14032913	0.000	0.000	0.000	5.753	0.000	0.000	0.000	8.167	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14035770	0.000	0.000	65.522	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14043223	0.000	0.000	34.381	19.643	0.000	0.000	0.000	27.886	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TEST14046073	0.000	0.000	0.000	0.000	0.000	0.000	0.000	19.130	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3000776	0.000	0.000	0.000	22.150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3002887	0.000	1.945	2.907	7.197	0.000	0.000	0.000	3.930	4.680	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3003007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3003350	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3007308	0.000	0.000	0.000	27.684	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3008105	0.000	0.000	25.159	0.000	0.000	0.000	0.000	20.406	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3019476	0.000	0.000	0.000	0.000	0.000	0.000	0.000	54.718	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3021586	0.000	0.000	0.000	0.000	0.000	0.000	0.000	4.162	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
THYML3026000	0.000	0.000	30.477	0.000	0.000	0.000	0.000	0.000	49.066	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.					

【 0 3 2 1 】

[illegible]

【0 3 2 2】

【表 2 2】

胎児の心臓由来のライブラリー (FEHRT) と成体の心臓由来のライブラリー (HEART) のcDNAを解析し、胎児と成体の間で発現変化のある遺伝子

Clone ID	HEART	FEHRT
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BRACE2012528	6.328	0.000
BRACE3004371	25.063	0.000
BRCAN2003814	0.000	90.076
BRSTN2011961	1.932	0.000
BRSTN2012069	1.641	0.394
BRSTN2016992	6.566	0.000
HEART2002531	100.000	0.000
NTONG2008483	5.330	0.000
PROST2002078	16.213	0.000
TIESE2000609	15.163	0.000

【 0 3 2 3 】

【表 2 3】

胎児の腎臓由来のライブラリー (FEKID) と成体の腎臓由来のライブラリー (KIDNE) のcDNAを解析し、胎児と成体の間で発現変化のある遺伝子

Clone ID	KIDNE	FEKID
<hr/>		
BRACE3004371	13.097	0.000
BRAMY2039630	60.511	0.000
BRAMY3004364	23.683	0.000
BRAWH2004078	18.371	0.000
BRHIP3002000	10.458	0.000
BRSTN2011961	0.000	6.265
BRSTN2012069	0.429	1.841
BRTHA2027229	0.000	19.799
KIDNE2004531	80.699	0.000
KIDNE2010049	11.987	0.000

KIDNE2014496	100.000	0.000
KIDNE2015987	100.000	0.000
KIDNE2016464	100.000	0.000
KIDNE2017153	83.085	0.000
KIDNE2018268	100.000	0.000
NT2RP7007387	7.156	0.000
TESTI2005112	67.827	0.000
TESTI4002799	0.000	9.553
THYMU3001776	22.094	0.000
THYMU3029795	37.093	0.000
THYMU3032867	44.871	0.000

【 0 3 2 4 】

【表 2 4】

胎児の肺由来のライブラリー (FELNG) と成体の肺由来のライブラリー (HLUNG) のcDNAを解析し、胎児と成体の間で発現変化のある遺伝子

Clone ID	HLUNG	FELNG

BRACE3036283	27.376	0.000
BRAMY2031516	27.091	0.000
BRSTN2011961	2.124	0.000
BRSTN2012069	0.763	2.238
HLUNG2012600	100.000	0.000
MESAN2009156	38.142	0.000
NTONG2008483	2.930	0.000
PROST2007444	4.011	0.000
TESTI4003703	16.229	0.000
TESTI4005653	1.824	0.000

TESTI4013474	3.790	0.000
TESTI4029297	16.229	0.000
THYMU3001776	11.622	0.000
THYMU3033626	20.615	0.000
THYMU3034671	8.747	0.000
THYMU3041428	0.935	0.000
THYMU3044188	0.000	96.268
TRACH3022198	30.484	0.000

【 0 3 2 5 】**【発明の効果】**

本発明により、1 9 5 6 にも及ぶポリヌクレオチドが提供された。全長cDNAの分離が進んでいないヒトにおいて、新規な全長cDNAを提供した意義は大きい。分泌蛋白質、膜蛋白質、シグナル伝達関連蛋白質、糖蛋白質関連蛋白質、転写関連蛋白質等は、多くの疾患に関連した蛋白質であることがわかっている。疾患に関連した遺伝子や蛋白質は、診断マーカー、発現や活性を制御する医薬品の開発、あるいは遺伝子治療のターゲットになるなど医薬品の開発等に有効である。

中でも、分泌蛋白質をコードするcDNAは、蛋白質自身に医薬品としての有用性が期待できること、および多くの疾患に関連する遺伝子を含む可能性があることから、本発明によって提供されたこれらのcDNAは、産業上きわめて重要である。さらに、膜蛋白質、シグナル伝達関連蛋白質、転写関連蛋白質、あるいは疾患関連蛋白質といった蛋白質やそれをコードする遺伝子についても、疾患の指標となること等が期待できる。これらのcDNAも、産業上きわめて重要であり、コードする蛋白質の持つ活性の制御や、発現の制御を通じて疾患の治療効果をもたらすこと等が期待される。

なお本明細書において引用された全ての先行技術文献は、参照として本明細書に組み入れられる。

【 0 3 2 6 】

相同性検索結果データ

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データを以下に示す。

各データは配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。相同性検索の結果、既知のどの配列にもヒットしなかったものについてはクローン名のみ記載した。

3NB692004045// Sodium/bile acid cotransporter (Na+)/bile acid cotransporter) (Na+)/taurocholate transport protein) (Sodium/taurocholate cotransporting polypeptide).// 3.00E-50// 99aa// 35%

ADIPS2000069// Ig alpha-1 chain C region.// 0// 325aa// 92%

ADRGL2010315

ADRGL2010594

AHMSC1000138

ASTR02008972// Tubulin--tyrosine ligase (EC 6.3.2.25) (TTL).// 6.00E-57// 108aa// 91%

ASTR02015162// CTL2 gene [Homo sapiens]// 1.00E-124// 222aa// 87%

ASTR02016114// Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).// 1.00E-141// 227aa// 70%

ASTR03000154// Jumonji protein.// 7.00E-56// 105aa// 100%

BEAST2000981// gl-related zinc finger protein [Mus musculus]// 4.00E-55// 118aa// 45%

BLADE2000256// suppression of tumorigenicity 5 [Homo sapiens]// 1.00E-135// 255aa// 65%

BLADE2001031

BLADE2002310// SH3-domain binding protein 1 [Homo sapiens]// 0// 408aa// 85%

BLADE2002744

BLADE2004849

BLADE2006043

BLADE2007735

BLADE2007744

BLADE2007799// Hepatocellular carcinoma-associated antigen 66.// 0// 401
aa// 97%

BLADE2008809

BRACE1000475// Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial pr
ecursor (EC 5.3.3.-).// 2.00E-74// 144aa// 93%

BRACE2002392// differential display and activated by p53; p53-regulated
DDA3 [Mus musculus]// 6.00E-75// 143aa// 72%

BRACE2003628// transmembrane protein induced by tumor necrosis factor al
pha [Homo sapiens]// 1.00E-131// 220aa// 65%

BRACE2005991

BRACE2010336

BRACE2012528// NDRG family, member 4; KIAA1180 protein [Homo sapiens]//
0// 342aa// 92%

BRACE2012625

BRACE2012833

BRACE2012838// Complexin 1 (Synaphin 2).// 1.00E-38// 86aa// 64%

BRACE2012936

BRACE2012947// Heat shock factor protein 1 (HSF 1) (Heat shock transcrip
tion factor 1) (HSTF 1).// 3.00E-26// 57aa// 96%

BRACE2013009// EH-domain containing protein 1 (Testilin) (hPAST1).// 1.0
0E-111// 204aa// 88%

BRACE2013126

BRACE2013132// Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolas
e).// 2.00E-11// 52aa// 23%

BRACE2016896// Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase)
(LysRS).// 0// 337aa// 87%

BRACE2017359// Mus musculus suppressor of Ty 6 homolog (S. cerevisiae) (

Supt6h)// 1.00E-82// 144aa// 100%

BRACE2017397// Cartilage matrix protein precursor (Matrilin-1).// 6.00E-36// 83aa// 40%

BRACE2017580// Glycerol-3-phosphate transporter (G-3-P transporter) (G-3-P permease).// 2.00E-15// 50aa// 40%

BRACE2017844

BRACE2017872// nuclear receptor-binding SET-domain protein 1 [Mus musculus]// 1.00E-154// 268aa// 85%

BRACE2017992

BRACE2019348// Zinc finger protein ZIC4 (Zinc finger protein of the cerebellum 4).// 4.00E-45// 82aa// 78%

BRACE2023633

BRACE2023744// Translationally controlled tumor protein (TCTP) (p23) (Histamine-releasing factor) (HRF).// 7.00E-62// 118aa// 88%

BRACE2025452

BRACE2026404

BRACE2027312

BRACE2027382// Opa-interacting protein OIP2 [Homo sapiens].// 1.00E-61// 101aa// 93%

BRACE2028956

BRACE2030039

BRACE2032584

BRACE2033128

BRACE2034434

BRACE2035120// phosphatidylinositol (4,5) biphosphate 5-phosphatase, A [Homo sapiens].// 0// 582aa// 94%

BRACE2035191

BRACE2039362

BRACE2039607

BRACE2042541

BRACE2046976

BRACE2047232

BRACE2047975

BRACE3001403// Dipeptidyl peptidase IV like protein (Dipeptidyl aminopeptidase-related protein) (Dipeptidylpeptidase VI) (DPPX).// 1.00E-57// 107aa// 97%

BRACE3001973// Cadherin-related tumor suppressor homolog precursor (Fat protein homolog).// 1.00E-157// 344aa// 36%

BRACE3002264// Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 2) (RAT brain class D) (RBD).// 5.00E-55// 193aa// 26%

BRACE3002344// Vegetatible incompatibility protein HET-E-1.// 7.00E-19// 127aa// 24%

BRACE3002541

BRACE3002756// protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 2 [Homo sapiens]// 0// 427aa// 68%

BRACE3003866

BRACE3004046

BRACE3004371

BRACE3004767// Spectrin beta chain, brain (Spectrin, non-erythroid beta chain) (Fodrin beta chain).// 4.00E-43// 86aa// 52%

BRACE3004887

BRACE3004981

BRACE3005870

BRACE3005903

BRACE3006553

BRACE3007649

BRACE3007869

BRACE3009075

BRACE3009265

BRACE3009392// Neutral amino acid transporter A (SATT) (Alanine/serine/cysteine/ threonine transporter) (ASCT1).// 1.00E-143// 258aa// 88%

BRACE3009416// testis specific ankyrin-like protein 1 [Homo sapiens]// 1.00E-119// 209aa// 92%

BRACE3009539

BRACE3010702

BRACE3011447

BRACE3011774

BRACE3013418// ankyrin 1, isoform 2; ankyrin-1, erythrocytic; ankyrin-R [Homo sapiens]// 0// 969aa// 95%

BRACE3013874

BRACE3013986

BRACE3014523

BRACE3014714// 116 kDa U5 small nuclear ribonucleoprotein component (U5 snRNP- specific protein, 116 kDa) (U5-116 kDa).// 1.00E-120// 209aa// 99%

BRACE3015090

BRACE3015898

BRACE3016020// SBBI31 protein [Homo sapiens]// 7.00E-20// 47aa// 49%

BRACE3016167

BRACE3016580

BRACE3016788

BRACE3016810

BRACE3016862

BRACE3017253// LAO/AO transport system kinase (EC 2.7.-.-).// 2.00E-65// 130aa// 45%

BRACE3018083// junctophilin 3; junctophilin type3 [Homo sapiens]// 0// 3
31aa// 91%

BRACE3019570// SNAP-25-interacting protein [Rattus norvegicus]// 0// 785
aa// 81%

BRACE3019611

BRACE3019817

BRACE3019941// Recessive polycystic kidney disease protein Tg737 homolog
./// 0// 685aa// 99%

BRACE3020356

BRACE3020669// Eukaryotic translation initiation factor 3 subunit 9 (eIF
-3 eta) (eIF3 p116) (eIF3 p110).// 5.00E-66// 118aa// 92%

BRACE3021430

BRACE3021517

BRACE3021805// sulfhydryl oxidase [Mus musculus]// 3.00E-51// 102aa// 47
%

BRACE3022051

BRACE3022303// Pax transcription activation domain interacting protein [
Mus musculus]// 1.00E-144// 246aa// 84%

BRACE3022312

BRACE3022340// SNAP-25-interacting protein [Rattus norvegicus]// 0// 745
aa// 80%

BRACE3022847

BRACE3023604

BRACE3024379

BRACE3024444

BRACE3024497

BRACE3024537

BRACE3024879

BRACE3025627

BRACE3025719// ring finger protein 22, isoform alpha; brain expressed ring finger; tripartite motif protein TRIM3 [Homo sapiens]// 0// 430aa// 95%

BRACE3026161

BRACE3026290// Homo sapiens lethal giant larvae homolog 2 [Homo sapiens]// 0// 914aa// 95%

BRACE3026345// Insulin-like growth factor II precursor (IGF-II) (Somatomedin A).// 6.00E-87// 153aa// 85%

BRACE3026456

BRACE3026802// Homo sapiens tweety homolog 1 (Drosophila) (TTYH1), mRNA.// 2.00E-97// 190aa// 66%

BRACE3026844// Zinc finger protein 84 (Zinc finger protein HPF2).// 0// 315aa// 48%

BRACE3026947

BRACE3027256

BRACE3027931

BRACE3028360

BRACE3028895

BRACE3028998// D-beta-hydroxybutyrate dehydrogenase precursor (EC 1.1.1.30) (BDH) (3-hydroxybutyrate dehydrogenase).// 8.00E-30// 62aa// 100%

BRACE3029005

BRACE3029021

BRACE3029205

BRACE3029447

BRACE3030538// putative tumor suppressor [Homo sapiens]// 1.00E-35// 77aa// 45%

BRACE3031161

BRACE3031184

BRACE3031185

BRACE3031315// activated p21cdc42Hs kinase [Homo sapiens]// 0// 328aa//
73%

BRACE3031372

BRACE3031579

BRACE3031728

BRACE3031743// Homo sapiens bruno-like 4, RNA binding protein (Drosophila) (BRUNOL4), mRNA.// 2.00E-42// 91aa// 72%

BRACE3031843

BRACE3032385// Voltage-dependent L-type calcium channel alpha-1D subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 2) (RAT brain class D) (RBD).// 2.00E-31// 124aa// 26%

BRACE3032537

BRACE3032538

BRACE3032631// F-box protein FBX13 [Mus musculus].// 0// 276aa// 94%

BRACE3032980

BRACE3033525

BRACE3034183// Zinc finger protein 84 (Zinc finger protein HPF2).// 1.00E-141// 216aa// 55%

BRACE3034389

BRACE3034964// Brain development-related molecule 1.// 1.00E-151// 259aa// 87%

BRACE3034993

BRACE3035168

BRACE3036156

BRACE3036271

BRACE3036283// Cyclin G-associated kinase (EC 2.7.1.-).// 1.00E-69// 138aa// 71%

BRACE3037612

BRACE3037637

BRACE3037803

BRACE3038012

BRACE3038030

BRACE3038570

BRACE3038760

BRACE3039288

BRACE3039358// integral membrane glycoprotein [Mus musculus]// 0// 581aa
// 78%

BRACE3039378// Metabotropic glutamate receptor 4 precursor.// 0// 569aa/
/ 96%

BRACE3039454

BRACE3040012

BRACE3040239// Deltex3 [Mus musculus]// 1.00E-158// 276aa// 79%

BRACE3040504

BRACE3040644// low density lipoprotein receptor-related protein 3 [Homo
sapiens]// 0// 549aa// 89%

BRACE3040863

BRACE3041059// Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15) (Ub
iquitin thiolesterase 4) (Ubiquitin-specific processing protease 4) (Deu
biquitinating enzyme 4) (Ubiquitous nuclear protein homolog).// 6.00E-39
// 82aa// 39%

BRACE3041162// zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin i
nducible transcription repressor-4 [Homo sapiens]// 1.00E-67// 110aa// 6
0%

BRACE3041827

BRACE3042046// Proto-oncogene DBL precursor [Contains: MCF2].// 9.00E-19
// 190aa// 26%

BRACE3042210

BRACE3042326// Protein dpy-19.// 2.00E-59// 166aa// 28%

BRACE3042409// Putative fatty-acid--CoA ligase fadD26 (EC 6.2.1.-) (Acyl-CoA synthetase).// 5.00E-21// 135aa// 25%

BRACE3042432// Vasoactive intestinal polypeptide receptor 1 precursor (VIP-R-1) (Pituitary adenylate cyclase activating polypeptide type II receptor) (PACAP type II receptor) (PACAP-R-2).// 8.00E-67// 123aa// 98%

BRACE3042594

BRACE3043597// 60S ribosomal protein L26.// 3.00E-68// 128aa// 88%

BRACE3044090

BRACE3044172// FKBP-rapamycin associated protein (FRAP) (Rapamycin target protein).// 0// 709aa// 94%

BRACE3044247

BRACE3044377

BRACE3044495// GROS1-L protein [Homo sapiens]// 3.00E-55// 150aa// 44%

BRACE3045078

BRACE3045145

BRACE3045424

BRACE3045708

BRACE3045981

BRACE3046049

BRACE3046152// putative homeodomain transcription factor; putative homeodomain transcription factor 1 [Homo sapiens]// 0// 375aa// 93%

BRACE3046294

BRACE3046466// Crumbs protein homolog 1 precursor.// 1.00E-126// 284aa// 29%

BRACE3046491// Channel associated protein of synapse-110 (Chapsyn-110) (Synaptic density protein PSD-93) (Discs, large homolog 2).// 0// 686aa// 89%

BRACE3046609// putative BTK-binding protein [Homo sapiens].// 1.00E-30// 195aa// 100%

BRACE3046837

BRACE3046855

BRACE3046966

BRACE3047018

BRACE3047482// tripartite motif-containing 9 [Homo sapiens]// 0// 448aa/
/ 60%

BRACE3047801

BRACE3048483

BRACE3048565

BRACE3048615

BRACE3048677

BRACE3048756

BRACE3048904

BRACE3048905

BRACE3049186

BRACE3049714// NYD-TSPG protein [Homo sapiens]// 4.00E-47// 119aa// 32%

BRACE3050270

BRACE3050504

BRACE3051144

BRACE3051621// Polycystin precursor (Autosomal dominant polycystic kidney disease protein 1).// 0// 387aa// 83%

BRACE3051627

BRACE3051722

BRACE3051819// Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha).// 0// 513aa// 55%

BRACE3051879

BRACE3052321// spectrin SH3 domain binding protein 1; eps8 binding protein; interactor protein AblBP4; Abl-interactor protein 1 long [Homo sapiens]// 0// 388aa// 73%

BRACE3052410// IDN3 protein [Homo sapiens]// 0// 532aa// 94%
BRACE3052486
BRACE3052595// Nim2 [Rattus norvegicus]// 1.00E-80// 145aa// 62%
BRALZ2003119
BRALZ2007661
BRALZ2008930
BRALZ2010842// Mitochondrial carnitine/acylcarnitine carrier protein (Ca
rnitine/acylcarnitine translocase) (CAC).// 4.00E-22// 73aa// 31%
BRALZ2011337
BRALZ2013621// Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (DC-s
tretch binding protein) (CSBP) (Transformation upregulated nuclear prote
in) (TUNP).// 5.00E-37// 87aa// 65%
BRALZ2013690
BRALZ2014054// cenexin 2 [Rattus norvegicus].// 4.00E-50// 96aa// 87%
BRAMY2015516
BRAMY2021098
BRAMY2022320
BRAMY2023939
BRAMY2025495
BRAMY2031516
BRAMY2033895
BRAMY2035801
BRAMY2036254
BRAMY2036266
BRAMY2037609
BRAMY2039630
BRAMY2040915// LISCH protein [Homo sapiens]// 1.00E-121// 234aa// 68%
BRAMY2041347
BRAMY2041384// Annexin VI (Lipocortin VI) (P68) (P70) (Protein III) (Chr

omobindin 20) (67 kDa calelectrin) (Calphobindin-II) (CPB-II).// 0// 471
aa// 96%

BRAMY2041507

BRAMY2044686

BRAMY2046489

BRAMY2046537// lipoma HMGIC fusion partner [Homo sapiens]// 5.00E-14// 5
3aa// 28%

BRAMY3000692// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7)
.// 3.00E-30// 56aa// 72%

BRAMY3001409

BRAMY3002329

BRAMY3002508

BRAMY3002886// ancient conserved domain protein 4 [Homo sapiens]// 1.00E
-125// 252aa// 49%

BRAMY3004126// Putative G protein-coupled receptor GPR17 (R12).// 0// 32
2aa// 94%

BRAMY3004364

BRAMY3005184// ankyrin 3, epithelial [Mus musculus]// 0// 769aa// 82%

BRAMY3005656

BRAMY3005912

BRAMY3007078// Peregrin (Bromodomain and PHD finger-containing protein 1
) (BR140 protein).// 5.00E-29// 62aa// 45%

BRAMY3007449

BRAMY3007471// gene trap locus F3b; transcript expressed during hematopo
iesis 2 [Mus musculus]// 3.00E-56// 104aa// 92%

BRAMY3008436

BRAMY3009158

BRAMY3009491// Phosphatidylinositol 4-kinase alpha (EC 2.7.1.67) (PI4-ki
nase) (PtdIns-4-kinase) (PI4K-alpha).// 1.00E-129// 222aa// 97%

BRAMY3009556// TGFB1-induced anti-apoptotic factor 1 (12 kDa TGF-beta1-induced antiapoptotic factor).// 4.00E-56// 104aa// 90%

BRAMY3009904

BRAMY3010321// MRIP-1 protein [Homo sapiens]// 2.00E-18// 56aa// 31%

BRAMY3010603

BRAMY3010654

BRAMY3010902

BRAMY3011501// Heterogenous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A).// 0// 469aa// 79%

BRAMY3011581// DNA topoisomerase III alpha (EC 5.99.1.2).// 0// 410aa// 90%

BRAMY3011865

BRAMY3014027// Zinc finger protein 44 (Zinc finger protein KOX7) (Gonadotropin inducible transcription repressor-2) (GIOT-2).// 0// 339aa// 56%

BRAMY3014555

BRAMY3014613// SH3-domain binding protein 1 [Homo sapiens]// 0// 420aa// 86%

BRAMY3015086// E4L1_HUMAN Band 4.1-like protein 1.// 0// 477aa// 94%

BRAMY3015547// Rho guanine nucleotide exchange factor 10 [Homo sapiens]// 0// 461aa// 44%

BRAMY3015549// Homo sapiens cell adhesion molecule with homology to L1CAM (close homolog of L1) (CHL1)// 0// 1076aa// 95%

BRAMY3016829

BRAMY3017827

BRAMY3017920// Active breakpoint cluster region-related protein.// 1.00E-161// 279aa// 98%

BRAMY3017965

BRAMY3018121

BRAMY3018248// ATP-binding cassette, sub-family B, member 8, mitochondri

al precursor (Mitochondrial ATP-binding cassette 1) (M-ABC1).// 3.00E-27
// 57aa// 100%

BRAMY3018340

BRAMY3018754// junction-mediating and regulatory protein; p300 transcrip
tional cofactor JMY [Mus musculus]// 7.00E-72// 160aa// 35%

BRAMY4000915// Ankyrin 1 (Erythrocyte ankyrin).// 2.00E-68// 190aa// 27%

BRAMY4000962// putative RNA binding protein [Homo sapiens]// 2.00E-16//
65aa// 29%

BRAMY4001234

BRAMY4001652// Ankyrin 1 (Erythrocyte ankyrin).// 2.00E-58// 197aa// 29%

BRAMY4001863// Mus musculus enabled homolog (Drosophila) (Enah), mRNA//
1.00E-84// 161aa// 81%

BRAMY4001913

BRAMY4002575

BRAMY4002628

BRAWH2000256// prestin [Rattus norvegicus]// 1.00E-121// 223aa// 93%

BRAWH2002333// Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phos
phodiesterase 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).// 1.00E-17
5// 302aa// 90%

BRAWH2004078

BRAWH2010364

BRAWH2010619

BRAWH2011796// S-100 protein, alpha chain.// 6.00E-30// 65aa// 69%

BRAWH2011812// VPS10 domain receptor protein SORCS [Mus musculus]// 0//
966aa// 95%

BRAWH2011958

BRAWH2012054

BRAWH2012866// Synaptotagmin I (SytI) (p65).// 0// 335aa// 79%

BRAWH2013955

BRAWH2014053// AFG3-like protein 2 (EC 3.4.24.-) (Paraplegin-like protein).// 4.00E-18// 42aa// 89%

BRAWH2016209// autocrine motility factor receptor [Mus musculus]// 2.00E-28// 89aa// 28%

BRAWH2016223

BRAWH2016305

BRAWH2016514

BRAWH2016562

BRAWH2016785

BRAWH3000446// Kruppel-like zinc finger protein GLIS2 [Homo sapiens]// 0// 300aa// 84%

BRAWH3000884

BRAWH3001053

BRAWH3001638// SUMO-1-specific protease 1 (EC 3.4.22.-) (Sentrin-specific protease SENP6) (Protease FKSG6).// 0// 1009aa// 90%

BRAWH3001783// protocadherin 15 [Homo sapiens]// 0// 688aa// 92%

BRAWH3001833

BRAWH3003244

BRAWH3003573// 45 kDa calcium-binding protein precursor (Stromal cell-derived factor 4) (SDF-4).// 9.00E-69// 121aa// 93%

BRAWH3003975

BRAWH3004335// heparan sulfate D-glucosaminyl 3-O-sulfotransferase 1 precursor; heparin-glucosamine 3-O-sulfotransferase [Homo sapiens]// 5.00E-72// 118aa// 49%

BRAWH3004350// Spindlin (Ovarian cancer-related protein).// 3.00E-96// 170aa// 77%

BRAWH3005037

BRAWH3005886// Zinc-finger protein cer-d4.// 1.00E-160// 273aa// 78%

BRAWH3005892

BRAWH3005896

BRAWH3008167// CUB and Sushi multiple domains 1 [Homo sapiens]// 0// 727
aa// 96%

BRAWH3008559

BRAWH3008867

BRAWH3009961// Nim2 [Rattus norvegicus]// 2.00E-95// 174aa// 69%

BRAWH3010461// secretory carrier membrane protein 5 [Mus musculus]// 1.0
0E-107// 186aa// 79%

BRAWH3010602// Gamma-soluble NSF attachment protein (SNAP-gamma) (N-ethy
lmaleimide- sensitive factor attachment protein, gamma).// 1.00E-113// 2
03aa// 90%

BRAWH3010657

BRAWH3010726// phosphatidylinositol transfer protein, membrane-associate
d; Drosophila retinal degeneration B [Homo sapiens]// 0// 509aa// 96%

BRAWH3010833

BRAWH3011101

BRAWH3011331// heparan sulfate 6-O-sulfotransferase 3 [Mus musculus]// 1
.00E-130// 219aa// 87%

BRAWH3011402

BRAWH3011577// Zinc finger protein 175 (Zinc finger protein OTK18).// 1.
00E-30// 65aa// 51%

BRAWH3011623// Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1
/ hnRNP C2).// 2.00E-97// 192aa// 74%

BRAWH3011685

BRAWH3011907

BRAWH3011929

BRAWH3012005

BRAWH3012662// Mus musculus tweety homolog 1 (Drosophila) (Ttyh1), mRNA.
// 3.00E-15// 42aa// 37%

BRAWH3012779

BRAWH3013009// zinc finger protein 35 [Mus musculus]// 1.00E-136// 280aa
// 49%

BRAWH3013049

BRAWH3013264// SWI/SNF related, matrix associated, actin dependent regul
ator of chromatin, subfamily a, member 3 [Mus musculus]// 3.00E-20// 75a
a// 27%

BRAWH3013508

BRAWH3014609// Insulin-like growth factor binding protein complex acid l
abile chain precursor (ALS).// 1.00E-25// 79aa// 30%

BRAWH3014639

BRAWH3015017// axonemal dynein light chain p33.// 3.00E-22// 34aa// 84%

BRAWH3015175// Myosin heavy chain, muscle.// 6.00E-08// 68aa// 21%

BRAWH3015610

BRAWH3015825

BRAWH3016123

BRAWH3016715

BRAWH3017180// Diacylglycerol kinase, zeta (EC 2.7.1.107) (Diglyceride k
inase) (DGK- zeta) (DAG kinase zeta).// 0// 837aa// 90%

BRAWH3017259// protein tyrosine phosphatase, receptor type, f polypeptid
e (PTPRF), interacting protein (liprin), alpha 2 [Homo sapiens]// 0// 10
68aa// 86%

BRAWH3017260

BRAWH3017477// AE-binding protein 2 [Mus musculus]// 1.00E-162// 273aa//
92%

BRAWH3017980

BRAWH3018063// tulip 1 [Rattus norvegicus]// 0// 444aa// 86%

BRAWH3018369

BRAWH3018548// Vinculin (Metavinculin).// 0// 877aa// 90%

BRAWH3018969

BRAWH3019026// Echinoderm microtubule-associated protein-like 1 (EMAP-1)

(HuEMAP-1).// 0// 612aa// 95%

BRAWH3019529

BRAWH3019594

BRAWH3019820

BRAWH3020200

BRAWH3020318

BRAWH3020884

BRAWH3020928// mitogen-activated protein kinase phosphatase x [Homo sapiens]// 2.00E-35// 66aa// 100%

BRAWH3021012// AP1 gamma subunit binding protein 1; gamma-synergine [Homo sapiens]// 1.00E-172// 302aa// 92%

BRAWH3021574

BRAWH3021580// Restin (Cytoplasmic linker protein-170 alpha-2) (CLIP-170) (Reed- Sternberg intermediate filament associated protein).// 0// 340aa// 72%

BRAWH3021641

BRAWH3021643

BRAWH3021724// kyphoscoliosis [Mus musculus]// 1.00E-136// 248aa// 68%

BRAWH3022347

BRAWH3022431

BRAWH3022459

BRAWH3022542

BRAWH3022651// ubiquitin-protein ligase e3 component n-recognin [Mus musculus]// 1.00E-24// 82aa// 30%

BRAWH3022719

BRAWH3022900

BRAWH3023156// Gamma-aminobutyric-acid receptor beta-1 subunit precursor

(GABA(A) receptor).// 4.00E-62// 115aa// 100%

BRAWH3023168

BRAWH3023172// Mothers against decapentaplegic homolog interacting protein (Madh-interacting protein) (Smad anchor for receptor activation) (Receptor activation anchor) (hSARA) (Novel serine protease) (NSP).// 1.00E-109// 198aa// 56%

BRAWH3023274

BRAWH3023415// alpha 1,2-mannosidase [Homo sapiens]// 5.00E-57// 105aa// 100%

BRAWH3023421// Protein-arginine deiminase type II (EC 3.5.3.15) (Peptidylarginine deiminase II) (PAD-H19).// 1.00E-106// 180aa// 99%

BRAWH3024186// LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).// 0// 862aa// 90%

BRAWH3024231// Tetratricopeptide repeat protein 4.// 1.00E-151// 261aa// 94%

BRAWH3024242

BRAWH3024506// Probable leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).// 2.00E-61// 128aa// 38%

BRAWH3024989

BRAWH3025157

BRAWH3026349// Sorting nexin 7.// 2.00E-94// 160aa// 49%

BRAWH3026938// semaF cytoplasmic domain associated protein 3; semaphorin cytoplasmic domain-associated protein 3A [Mus musculus]// 0// 354aa// 45%

BRAWH3027420

BRAWH3027440// Probable kinesin light chain 3 (KLC 3).// 1.00E-159// 283aa// 85%

BRAWH3027533// rap2 interacting protein x [Homo sapiens].// 1.00E-117// 390aa// 64%

BRAWH3027574// vascular Rab-GAP/TBC-containing [Homo sapiens]// 0// 427a
a// 45%

BRAWH3027607

BRAWH3027616

BRAWH3027675

BRAWH3027806// Echinoderm microtubule-associated protein-like 2 (EMAP-2)
(HuEMAP-2).// 2.00E-92// 211aa// 34%

BRAWH3027880

BRAWH3028202

BRAWH3028223

BRAWH3028461

BRAWH3028754

BRAWH3028796// makorin, ring finger protein, 1 [Homo sapiens]// 0// 362a
a// 86%

BRAWH3029313

BRAWH3029385// Dynamin 2 (EC 3.6.1.50).// 1.00E-131// 237aa// 88%

BRAWH3029538// myelin-associated oligodendrocyte basic protein [Homo sap
iens]// 5.00E-39// 184aa// 99%

BRAWH3029806// Adenylate cyclase, type II (EC 4.6.1.1) (ATP pyrophosphat
e-lyase) (Adenylyl cyclase).// 0// 758aa// 90%

BRAWH3030772

BRAWH3030810

BRAWH3030910// Sec23-interacting protein p125 [Homo sapiens]// 5.00E-92/
/ 180aa// 51%

BRAWH3031054

BRAWH3031342// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7)
.// 0// 301aa// 59%

BRAWH3031710// serologically defined colon cancer antigen 33 [Homo sapie
ns]// 0// 653aa// 96%

BRAWH3032298// Homo sapiens tenascin R (restrictin, janusin) (TNR), mRNA
// 0// 472aa// 36%

BRAWH3032340// Rho-specific guanine nucleotide exchange factor p114 [Homo sapiens]// 0// 824aa// 81%

BRAWH3032571// Chromodomain helicase-DNA-binding protein 4 (CHD-4) (Mi-2 autoantigen 218 kDa protein) (Mi2-beta).// 0// 714aa// 69%

BRAWH3033117

BRAWH3033293// synaptopodin [Homo sapiens]// 0// 580aa// 85%

BRAWH3033448

BRAWH3033513// 3-ketoacyl-CoA thiolase, peroxisomal precursor (EC 2.3.1.16) (Beta- ketothiolase) (Acetyl-CoA acyltransferase) (Peroxisomal 3-oxo acyl- CoA thiolase).// 1.00E-60// 114aa// 87%

BRAWH3034097

BRAWH3034114

BRAWH3034134

BRAWH3034668// Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15) (Ubiquitin thiolesterase 4) (Ubiquitin-specific processing protease 4) (Deubiquitinating enzyme 4) (Ubiquitous nuclear protein homolog).// 0// 624aa// 90%

BRAWH3034743

BRAWH3034775// E1B-55kDa-associated protein 5 [Homo sapiens]// 1.00E-164// 283aa// 93%

BRAWH3034890// CAGH32 [Homo sapiens].// 9.00E-29// 131aa// 94%

BRAWH3035403

BRAWH3035904

BRAWH3035914

BRAWH3035936// Zinc finger protein 208.// 0// 354aa// 51%

BRAWH3036077

BRAWH3036247// Zinc finger protein 228.// 2.00E-54// 96aa// 39%

BRAWH3036270// Hb2E [Homo sapiens].// 1.00E-109// 233aa// 97%

BRAWH3036334// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7)
./ 0// 436aa// 60%

BRAWH3036561

BRAWH3037265

BRAWH3037394

BRAWH3037428// RAB37, member of RAS oncogene family; GTPase Rab37 [Mus musculus]// 1.00E-76// 140aa// 88%

BRAWH3037533

BRAWH3037979// Ubiquitin carboxyl-terminal hydrolase 24 (EC 3.1.2.15) (Ubiquitin thiolesterase 24) (Ubiquitin-specific processing protease 24) (Deubiquitinating enzyme 24) (Fragment).// 0// 415aa// 97%

BRAWH3038055// synaptic nuclei expressed gene 2 [Homo sapiens]// 0// 551aa// 47%

BRAWH3038230

BRAWH3038252// Formin 1 isoform IV (Limb deformity protein).// 0// 411aa// 89%

BRAWH3038324// Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like protein II) (NSPLII).// 1.00E-101// 189aa// 99%

BRAWH3038827// leucine-zipper-like transcriptional regulator, 1; Leucine-zipper-like regulator-1 [Homo sapiens]// 0// 530aa// 96%

BRAWH3039258

BRAWH3039623

BRAWH3040297

BRAWH3040695// Inner nuclear membrane protein Man1.// 1.00E-33// 66aa// 47%

BRAWH3040711

BRAWH3040900// Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) (CELSR2) mRNA// 1.00E-49// 97aa// 82%

BRAWH3041492// erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked); Erythrocyte surface protein band 4.1 [Homo sapiens]// 1.00E-66// 129aa// 64%

BRAWH3041556// C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methylenetetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)].// 0// 536aa// 58%

BRAWH3041928

BRAWH3042132

BRAWH3042438// Diacylglycerol kinase, alpha (EC 2.7.1.107) (Diglyceride kinase) (DGK- alpha) (DAG kinase alpha) (80 kDa diacylglycerol kinase).// 5.00E-56// 103aa// 100%

BRAWH3042447// p53 inducible protein [Homo sapiens].// 0// 694aa// 86%

BRAWH3042568// ventral anterior homeobox containing gene 1 [Mus musculus]// 5.00E-76// 137aa// 95%

BRAWH3042772// Zinc transporter 3 (ZnT-3).// 3.00E-71// 135aa// 87%

BRAWH3042787

BRAWH3042820

BRAWH3042996

BRAWH3043034// Mus musculus neuregulin 1 (Nrg1)// 0// 924aa// 92%

BRAWH3043295// Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phosphatase) (PPase).// 7.00E-53// 95aa// 98%

BRAWH3043498

BRAWH3043623// Cadherin-related tumor suppressor homolog precursor (Fat protein homolog).// 8.00E-24// 74aa// 36%

BRAWH3043944

BRAWH3044122// Munc13-1 [Rattus norvegicus]// 0// 888aa// 98%

BRAWH3044151// ADAM-TS 9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 9) (ADAMTS-9) (ADAM-TS9).// 7.0

0E-45// 118aa// 31%

BRAWH3044487

BRAWH3044585

BRAWH3044676

BRAWH3044985

BRAWH3045118

BRAWH3045229

BRAWH3045625

BRAWH3046196

BRAWH3046209

BRAWH3046424// Histone deacetylase 6 (HD6).// 0// 530aa// 93%

BRAWH3046802

BRAWH3046959

BRAWH3047063

BRAWH3047539

BRAWH3047565// TOLLIP protein [Homo sapiens]// 1.00E-101// 177aa// 86%

BRAWH3047644// Rho guanine nucleotide exchange factor 4, isoform b; APC-stimulated guanine nucleotide exchange factor [Homo sapiens]// 3.00E-84/
/ 142aa// 100%

BRAWH3047692// Lon protease homolog 1, mitochondrial precursor (EC 3.4.2
1.-).// 1.00E-164// 297aa// 51%

BRAWH3047946

BRAWH3048374// CUB and Sushi multiple domains 1 [Homo sapiens]// 0// 715
aa// 96%

BRAWH3048548

BRAWH3048724

BRAWH3049068

BRAWH3049544// Polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.4
1) (Protein- UDP acetylgalactosaminyltransferase) (UDP-GalNAc:polypeptid

e, N- acetylgalactosaminyltransferase) (GalNAc-T1).// 1.00E-119// 230aa/
/ 43%

BRAWH3049726

BRAWH3049858

BRCAN2000923// Putative ADP-ribosylation factor 2.// 2.00E-29// 180aa//
32%

BRCAN2002662

BRCAN2002892// Ras-related protein Rab-7.// 7.00E-47// 96aa// 50%

BRCAN2003269// Multidrug resistance protein 3 (P-glycoprotein 3).// 4.00
E-93// 171aa// 55%

BRCAN2003814// Variant-surface-glycoprotein phospholipase C (EC 3.1.4.47
) (VSG lipase) (Glycosylphosphatidylinositol-specific phospholipase C) (
GPI-PLC).// 3.00E-18// 78aa// 26%

BRCAN2006051// AFG3-like protein 2 (EC 3.4.24.-) (Paraplegin-like protei
n).// 3.00E-50// 97aa// 66%

BRCAN2006955

BRCAN2007525

BRCAN2008701

BRCAN2009168

BRCAN2010547

BRCAN2010581

BRCAN2010665// Channel associated protein of synapse-110 (Chapsyn-110) (
Discs, large homolog 2).// 0// 422aa// 96%

BRCAN2015402// Cytochrome P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (
Olfactive).// 3.00E-73// 129aa// 88%

BRCAN2015757

BRCAN2018269

BRCAN2018667

BRCAN2019653

BRCAN2019907// vascular Rab-GAP/TBC-containing [Homo sapiens]// 8.00E-18
// 44aa// 57%

BRCAN2019953

BRCAN2020234// Quiescence-specific protein precursor (P20K) (CH21 protein).// 2.00E-06// 70aa// 27%

BRCAN2020331// G-rich sequence factor-1 (GRSF-1).// 0// 360aa// 80%

BRCAN2020412// phosphatidylinositol glycan, class S [Homo sapiens]// 6.00E-89// 195aa// 99%

BRCAN2020467// Nuclear movement protein NUDC.// 5.00E-12// 130aa// 32%

BRCAN2020880

BRCAN2020972

BRCAN2021325// Carboxypeptidase H precursor (EC 3.4.17.10) (CPH) (Carboxypeptidase E) (CPE) (Enkephalin convertase) (Prohormone processing carboxypeptidase).// 0// 389aa// 100%

BRCAN2021452

BRCAN2021718

BRCAN2022126// glutamate receptor delta-1 subunit [Rattus norvegicus]// 0// 949aa// 94%

BRCAN2025093

BRCAN2027593

BRCAN2028702

BRCOC2001355

BRCOC2002777

BRCOC2006164

BRCOC2006639

BRCOC2006942

BRCOC2009638

BRCOC2010115

BRCOC2012386// Zinc finger protein 184.// 2.00E-85// 166aa// 42%

BRHIP2006819

BRHIP2006921

BRHIP2008756// Homo sapiens pescadillo homolog 1, containing BRCT domain
(zebrafish) (PES1), mRNA// 0// 352aa// 78%

BRHIP2009177

BRHIP2011199

BRHIP2013958

BRHIP2015153

BRHIP2016125

BRHIP2017714

BRHIP2020930

BRHIP2021929

BRHIP2023735// Zinc-finger protein neuro-d4.// 3.00E-46// 87aa// 87%

BRHIP2024941

BRHIP2026346// lymphocyte specific formin related protein; formin-related
gene in leukocytes [Mus musculus]// 1.00E-114// 216aa// 47%

BRHIP2027077// Flt3 interacting zinc finger protein 1 [Mus musculus]// 4
.00E-14// 54aa// 56%

BRHIP2027563// host cell factor homolog [Homo sapiens]// 2.00E-95// 166a
a// 47%

BRHIP2029529// TFIIH basal transcription factor complex p62 subunit// 0/
/ 414aa// 95%

BRHIP2029643

BRHIP2029663

BRHIP3000626

BRHIP3000859

BRHIP3001076// murine retrovirus integration site 1 homolog; inositol 1,
4,5-triphosphate-associated cGMP kinase substrate; JAW1-related protein
[Homo sapiens]// 0// 482aa// 80%

BRHIP3001141

BRHIP3001338

BRHIP3001360

BRHIP3001481// Protein-tyrosine phosphatase, non-receptor type 7 (EC 3.1.3.48) (Protein-tyrosine phosphatase LC-PTP) (Hematopoietic protein-tyrosine phosphatase) (HEPTP).// 0// 359aa// 99%

BRHIP3001573

BRHIP3001878// peptide transporter 3 [Homo sapiens]// 7.00E-74// 131aa// 86%

BRHIP3002000

BRHIP3002114// rTS beta protein [Homo sapiens]// 1.00E-148// 248aa// 94%

BRHIP3002124

BRHIP3002141

BRHIP3002363

BRHIP3002691

BRHIP3002920

BRHIP3002931

BRHIP3003063// Alpha-2 catenin (Alpha N-catenin) (Neural alpha-catenin).
// 0// 867aa// 95%

BRHIP3003126// Homo sapiens ubiquitin-protein isopeptide ligase (E3) (K1AA0010), mRNA.// 2.00E-88// 195aa// 37%

BRHIP3003306// tulip 1 [Rattus norvegicus]// 1.00E-148// 272aa// 49%

BRHIP3003340// Actin, alpha skeletal muscle 2.// 3.00E-30// 63aa// 96%

BRHIP3003395

BRHIP3003688

BRHIP3003795// cytochrome P450 retinoid metabolizing protein [Homo sapiens]// 1.00E-28// 97aa// 51%

BRHIP3003845

BRHIP3003961

BRHIP3003984// IkappaB kinase complex-associated protein (IKK complex-associated protein) (p150).// 0// 930aa// 94%

BRHIP3004215// 80 kda MCM3-associated protein (GANP protein).// 0// 792aa// 87%

BRHIP3004710

BRHIP3004725// DNA-binding protein SATB1 (Special AT-rich sequence binding protein 1).// 0// 711aa// 93%

BRHIP3004774

BRHIP3004786

BRHIP3005037// Metastasis-associated protein MTA1.// 0// 339aa// 66%

BRHIP3005142

BRHIP3005231

BRHIP3005307// neuropathy target esterase [Homo sapiens]// 1.00E-176// 308aa// 63%

BRHIP3005673// Glutathione S-transferase Mu 5 (EC 2.5.1.18) (GSTM5-5) (GST class-Mu 5).// 5.00E-58// 111aa// 82%

BRHIP3005801// VAMP (vesicle-associated membrane protein)-associated protein B and C; VAMP-associated protein C; VAMP-associated protein B; VAMP-associated 33 kDa protein [Homo sapiens]// 4.00E-63// 118aa// 99%

BRHIP3005944// Antigen WC1.1 precursor.// 1.00E-50// 100aa// 39%

BRHIP3006279

BRHIP3006294// Cdc42 GTPase-activating protein [Mus musculus]// 5.00E-77// 144aa// 60%

BRHIP3006449// catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein); catenin (cadherin-associated protein), delta 2 [Homo sapiens]// 0// 756aa// 95%

BRHIP3006786// peptidylprolyl isomerase (cyclophilin)-like 2; cyclophilin-like protein CyP-60 [Homo sapiens]// 1.00E-123// 210aa// 99%

BRHIP3006950

BRHIP3007172

BRHIP3007195// Potential phospholipid-transporting ATPase IB (EC 3.6.3.13).// 0// 1049aa// 91%

BRHIP3007223// Ubiquitin carboxyl-terminal hydrolase 64E (EC 3.1.2.15) (Ubiquitin thiolesterase 64E) (Ubiquitin-specific processing protease 64E) (Deubiquitinating enzyme 64E).// 1.00E-139// 272aa// 47%

BRHIP3007291

BRHIP3007409

BRHIP3007424// WNT-14 protein precursor.// 4.00E-83// 143aa// 58%

BRHIP3007609// Homo sapiens Smcy homolog, Y chromosome (mouse) (SMCY)// 0// 571aa// 83%

BRHIP3007960

BRHIP3008082

BRHIP3008320// Rattus norvegicus potassium channel subunit (Slack) (Slack)// 0// 1063aa// 90%

BRHIP3008714

BRHIP3009672

BRHIP3009753

BRHIP3010289// Attractin precursor (Mahogany homolog) (DPPT-L).// 0// 738aa// 58%

BRHIP3010916

BRHIP3011082// Homo sapiens ubiquitin-protein isopeptide ligase (E3) (KIAA0010)// 0// 415aa// 99%

BRHIP3011269// Prenylcysteine lyase precursor (EC 4.4.1.18).// 7.00E-80// 154aa// 39%

BRHIP3011460// Rho guanine exchange factor 16; putative neuroblastoma protein [Homo sapiens]// 1.00E-120// 227aa// 52%

BRHIP3011567// Dihydropyridine-sensitive L-type, channel beta-1-B2 subunit (Beta-1 isoform A).// 1.00E-173// 310aa// 83%

BRHIP3011831

BRHIP3012185

BRHIP3012289

BRHIP3012357// cerebral cell adhesion molecule [Homo sapiens]// 2.00E-61
// 105aa// 55%

BRHIP3012736

BRHIP3012997

BRHIP3013078// BAI1-associated protein 2, isoform 2 [Homo sapiens]// 2.0
0E-40// 77aa// 100%

BRHIP3013588

BRHIP3013698

BRHIP3014675

BRHIP3015854

BRHIP3016032

BRHIP3016421

BRHIP3017109// Socs-5 [Mus musculus]// 1.00E-69// 118aa// 84%

BRHIP3017146// solute carrier family 30 (zinc transporter), member 3// 6
.00E-96// 92aa// 97%

BRHIP3017256

BRHIP3017558// Monocarboxylate transporter 3 (MCT 3) (Retinal epithelial
membrane protein).// 2.00E-60// 137aa// 30%

BRHIP3017855// nuclear pore complex interacting protein [Homo sapiens]//
4.00E-58// 107aa// 82%

BRHIP3018784

BRHIP3019643// Homo sapiens gamma tubulin ring complex protein (76p gene
) (76P), mRNA// 1.00E-104// 187aa// 93%

BRHIP3019824

BRHIP3019880

BRHIP3019956

BRHIP3020046// ubiquitin-protein ligase e3 componen n-recognin [Mus musculus]// 3.00E-96// 167aa// 47%

BRHIP3020155

BRHIP3020733

BRHIP3021019// Protein-tyrosine phosphatase, non-receptor type 5 (EC 3.1.3.48) (Protein-tyrosine phosphatase striatum-enriched) (STEP) (Neural-specific protein-tyrosine phosphatase) (Fragment).// 0// 440aa// 81%

BRHIP3021499

BRHIP3021987

BRHIP3022656

BRHIP3023922// 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) (Methionine synthase, vitamin-B12 dependent) (MS).// 4.00E-72// 134aa// 95%

BRHIP3024703

BRHIP3024820

BRHIP3025795// Monocarboxylate transporter 4 (MCT 4) (MCT 3).// 0// 392aa// 84%

BRHIP3025844// germ cell-specific gene 1 [Mus musculus]// 9.00E-14// 43aa// 47%

BRHIP3026231

BRHIP3026651

BRHIP3027160

BRHIP3027191// 150 kDa oxygen-regulated protein precursor (Orp150).// 0// 904aa// 90%

BRHIP3027651// Bromodomain-containing protein 1 (BR140-like protein).// 2.00E-59// 149aa// 31%

BRHIP3027947

BRHIP3028246// PHD finger protein 2 [Mus musculus]// 2.00E-67// 125aa// 42%

BRHIP3028570

BRHIP3028742// vanilloid receptor subtype 1 [Homo sapiens]// 1.00E-55//
108aa// 50%

BRHIP3029409// secreted frizzled-related protein 1; secreted apoptosis-r
elated protein 2 [Homo sapiens]// 2.00E-43// 87aa// 65%

BRHIP3029530

BRHIP3029670

BRHIP3029866

BRHIP3030230// Neuronal pentraxin I precursor (NP-I) (NP1).// 0// 386aa/
/ 93%

BRHIP3031733

BRHIP3031890

BRHIP3032148// brain-enriched guanylate kinase-associated [Rattus norveg
icus]// 1.00E-16// 49aa// 40%

BRHIP3032311

BRHIP3032374// neuropathy target esterase [Homo sapiens]// 0// 369aa// 6
2%

BRHIP3033481

BRHIP3033557// N-methyl-D-aspartate receptor splice variant NR3A-2// 0//
852aa// 93%

BRHIP3033734

BRHIP3033806

BRHIP3035006// Synthase [Homo sapiens]// 1.00E-161// 276aa// 95%

BRHIP3035222

BRHIP3035754

BRHIP3036371

BRHIP3036715// HLA class I histocompatibility antigen, alpha chain H pre
cursor (HLA-AR) (HLA-12.4).// 2.00E-60// 108aa// 67%

BRHIP3036936// astrotactin 2 [Mus musculus]// 0// 858aa// 96%

BRHIP3037543// cyclin G associated kinase [Homo sapiens]// 4.00E-40// 84
aa// 78%

BRHIP3037810

BRHIP3038030

BRHIP3038735

BRHIP3039430

BRHIP3039509// Amiloride-sensitive sodium channel delta-subunit (Epithelial Na⁺ channel delta subunit) (Delta ENaC) (Nonvoltage-gated sodium channel 1 delta subunit) (SCNED) (Delta NaCH).// 0// 588aa// 92%

BRHIP3039592

BRHIP3040878

BRHIP3041587// Myosin light chain kinase, skeletal muscle (EC 2.7.1.117) (MLCK).// 2.00E-24// 76aa// 61%

BRHIP3042817

BRHIP3043012

BRSSN2004303

BRSSN2004710// cAMP-dependent 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17) (DPDE4) (PDE32).// 1.00E-59// 108aa// 88%

BRSSN2008464

BRSSN2011843

BRSSN2012157

BRSSN2012198

BRSSN2013696

BRSSN2015497// putative RNA binding protein [Homo sapiens]// 4.00E-16// 65aa// 29%

BRSSN2018218

BRSTN2000312

BRSTN2006466// Glutamate decarboxylase, 65 kDa isoform (EC 4.1.1.15) (GAD-65) (65 kDa glutamic acid decarboxylase).// 2.00E-77// 140aa// 80%

BRSTN2006638// synaptotagmin interacting protein 1 [Rattus norvegicus]//
2.00E-74// 147aa// 45%

BRSTN2008475// growth arrest-specific 11; growth arrest specific 11 [Homo sapiens]// 6.00E-36// 71aa// 98%

BRSTN2009247

BRSTN2010089// tumor differentially expressed 1, like; membrane protein TMS-2 [Mus musculus]// 0// 413aa// 91%

BRSTN2010416

BRSTN2011688

BRSTN2011899

BRSTN2011961// Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1) (Prolyl 4- hydroxylase beta subunit) (Cellular thyroid hormone binding protein) (P55).// 3.00E-90// 160aa// 86%

BRSTN2012069// Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu).// 0// 441aa// 95%

BRSTN2015699

BRSTN2015788

BRSTN2016892// BUP protein [Homo sapiens]// 1.00E-56// 105aa// 100%

BRSTN2016918// Glial fibrillary acidic protein, astrocyte (GFAP).// 0// 367aa// 86%

BRSTN2016992// DRR1 protein (TU3A protein).// 4.00E-62// 118aa// 81%

BRSTN2017104

BRSTN2017151// COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis); COP9 complex S7a [Mus musculus]// 7.00E-24// 54aa// 98%

BRSTN2017184

BRSTN2018712

BRTHA2000969

BRTHA2001304

BRTHA2001953

BRTHA2002091

BRTHA2003759

BRTHA2005448// calpain 12 [Mus musculus]// 0// 300aa// 87%

BRTHA2006720

BRTHA2008502

BRTHA2008598

BRTHA2010672// neutral protease large subunit [Homo sapiens].// 3.00E-39
// 117aa// 71%

BRTHA2012189

BRTHA2014647

BRTHA2018304

BRTHA2019726// Ig gamma-1 chain C region.// 0// 314aa// 95%

BRTHA2019743

BRTHA2020400// Ig lambda chain V-IV region Bau.// 2.00E-45// 82aa// 78%

BRTHA2020566

BRTHA2020642// DRR1 protein (TU3A protein).// 5.00E-19// 120aa// 50%

BRTHA2020695

BRTHA2020721// Ig gamma-1 chain C region.// 0// 315aa// 95%

BRTHA2020781

BRTHA2020910// Tubulin beta-4 chain (Tubulin beta-III).// 1.00E-163// 28
3aa// 93%

BRTHA2021212

BRTHA2021440

BRTHA2021450

BRTHA2022074

BRTHA2022914

BRTHA2022968// NG-CAM related cell adhesion molecule precursor (NR-CAM)
(BRAVO).// 7.00E-45// 95aa// 54%

BRTHA2023402

BRTHA2023437

BRTHA2024177

BRTHA2024354

BRTHA2024712// T-box transcription factor TBX2 (T-box protein 2).// 6.00
E-65// 123aa// 83%

BRTHA2025869// Neurofilament triplet L protein (68 kDa neurofilament pro
tein) (Neurofilament light polypeptide) (NF-L).// 1.00E-157// 306aa// 80
%

BRTHA2026071// TH1 drosophila homolog [Homo sapiens]// 7.00E-21// 45aa//
100%

BRTHA2026290// Ral guanine nucleotide dissociation stimulator-like 2 (Ra
lGDS-like factor) (RAS-associated protein RAB2L).// 3.00E-17// 116aa// 2
4%

BRTHA2026311// Protein disulfide isomerase A6 precursor (EC 5.3.4.1) (Pr
otein disulfide isomerase P5).// 0// 379aa// 87%

BRTHA2027227

BRTHA2027229

BRTHA2027250// Synaptotagmin B (Synaptic vesicle protein 0-P65-B).// 6.0
0E-46// 99aa// 35%

BRTHA2028297

BRTHA2029969

BRTHA2030036

BRTHA2030213

BRTHA2031517

BRTHA2031917// Ciliary neurotrophic factor receptor alpha precursor (CNT
FR alpha).// 1.00E-107// 181aa// 88%

BRTHA2032763

BRTHA2033122

BRTHA2033155// Beta-1,4 N-acetylgalactosaminyltransferase (EC 2.4.1.92)

((N- acetylneuraminy)-galactosylglucosylceramide) (GM2/GD2 synthase) (GalNAc-T).// 2.00E-43// 95aa// 65%

BRTHA2033320

BRTHA2033469

BRTHA2033683// Urea transporter, erythrocyte.// 1.00E-153// 259aa// 93%

BRTHA2034281

BRTHA2034576

BRTHA2035743// activated p21cdc42Hs kinase [Homo sapiens]// 0// 417aa// 73%

BRTHA2036055

BRTHA2036295

BRTHA2037247

BRTHA2038279

BRTHA2038345

BRTHA2038353

BRTHA3000456// Zinc finger protein HZF10.// 1.00E-134// 212aa// 57%

BRTHA3002411

BRTHA3003225

BRTHA3003417

BRTHA3003736// TFIIH basal transcription factor complex helicase XPB subunit (EC 3.6.1.-) (Basic transcription factor 2 89 kDa subunit) (BTF2-p89) (TFIIH 89 kDa subunit) (DNA-repair protein complementing XP-B cells) (Xeroderma pigmentosum group B complementing protein) (DNA excision repair protein ERCC-3).// 0// 520aa// 96%

BRTHA3005988

BRTHA3006593

BRTHA3007469

BRTHA3007662

BRTHA3009858

BRTHA3010135// LAR protein precursor (Leukocyte antigen related) (EC 3.1.3.48).// 0// 422aa// 100%

BRTHA3010212// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).// 0// 397aa// 69%

BRTHA3010469// NMN adenylyltransferase; nicotinamide mononucleotide adenylyl transferase [Homo sapiens]// 2.00E-30// 61aa// 50%

BRTHA3010530// ubiquitin-protein ligase e3 componen n-recognin [Mus musculus]// 1.00E-161// 264aa// 85%

BRTHA3010540

BRTHA3010717// secretory carrier membrane protein 5 [Mus musculus]// 1.00E-107// 186aa// 79%

BRTHA3011187// hect domain and RLD 2 [Homo sapiens]// 7.00E-17// 51aa// 34%

BRTHA3011194// Chloride channel protein 3 (ClC-3).// 0// 622aa// 89%

BRTHA3011229

BRTHA3011265// Spindlin (30000 Mr metaphase complex) (SSEC P).// 5.00E-69// 120aa// 91%

BRTHA3011306

BRTHA3011361

BRTHA3011510

BRTHA3011892

BRTHA3011998// rhomboid (veinlet, Drosophila)-like; Rhomboid, drosophila, homolog of [Homo sapiens]// 9.00E-31// 110aa// 51%

BRTHA3012265// pendrin [Homo sapiens].// 8.00E-44// 300aa// 34%

BRTHA3013860

BRTHA3013882

BRTHA3014000// rapa-1 [Homo sapiens]// 0// 1059aa// 90%

BRTHA3014105

BRTHA3014507

BRTHA3014547// Ankyrin 1 (Erythrocyte ankyrin) (Ankyrin R) (Ankyrins 2.1 and 2.2).// 3.00E-85// 205aa// 34%

BRTHA3014835

BRTHA3014854

BRTHA3014920

BRTHA3016616

BRTHA3017791

BRTHA3018409// synaptotagmin-like 4; granuphilin-a; granuphilin-b; granuphilin// 2.00E-56// 160aa// 41%

BRTHA3018623

BRTHA3019183// Ca²⁺-dependent activator protein for secretion; Ca²⁺-dependent activator protein for secretion [Mus musculus]// 4.00E-67// 122aa// 96%

BRTHA3020369

BRTHA3020771

BRTHA3021569

BRTHA3021708// FERM, RhoGEF, and pleckstrin domain protein 1; chondrocyte-derived ezrin-like protein [Homo sapiens]// 2.00E-66// 122aa// 64%

BRTHA3021786

BRTHA3021971// oxidation resistance 1; oxidation resistance 1; hypothetical protein FLJ10125 [Homo sapiens]// 1.00E-76// 136aa// 50%

BRTHA3022641

BRTHA3023403// phospholipase C, epsilon [Homo sapiens]// 0// 689aa// 90%

BRTHA3023590

BRTHA3023929

BRTHA3024600

BRTHA3025073// Actin cross-linking family protein 7 (Macrophin) (Trabeculin- α) (620 kDa actin-binding protein) (ABP620).// 0// 685aa// 97%

BRTHA3026161

BRTHA3026180

BRTHA3026556

BRTHA3026916// Ral guanine nucleotide dissociation stimulator (RalGEF) (RalGDS).// 0// 728aa// 85%

BRTHA3027171

BRTHA3027318

BRTHA3027638

BRTHA3027820

BRTHA3027879

BRTHA3027957// megacaryocytic acute leukemia protein [Homo sapiens]// 3.00E-36// 95aa// 41%

BRTHA3028339// YY1-associated factor 2 [Homo sapiens]// 4.00E-26// 55aa// 63%

BRTHA3028505

CERVX2000812

CERVX2000968// F-actin binding protein b-Nexilin [Rattus norvegicus].// 1.00E-112// 312aa// 92%

CHONS2000797// T-box transcription factor TBX15 (T-box protein 15) (MmTBx8).// 0// 451aa// 90%

CHONS2001287// Insulin-like growth factor binding protein 3 precursor (IGFBP-3) (IBP-3) (IGF-binding protein 3).// 1.00E-117// 201aa// 77%

CHONS2001797

CHONS2001834// tumor endothelial marker 7 precursor [Homo sapiens]// 1.00E-147// 246aa// 98%

CHONS2002419

CHONS2002829// adipocyte enhancer binding protein 1 precursor [Homo sapiens]// 0// 542aa// 77%

COLON2001829// Dopamine- and cAMP-regulated neuronal phosphoprotein (DARPP-32).// 6.00E-84// 157aa// 77%

COLON2001866

COLON2004351// Probable beta-1,3-galactosyltransferase 8 (EC 2.4.1.-) (UDP-galactose:beta-N- acetylglucosamine beta-1,3-galactosyltransferase 8) // 4.00E-46// 93aa// 47%

COLON2004911// Oxygen-regulated protein 1 (Retinitis pigmentosa RP1 protein) (Retinitis pigmentosa 1 protein).// 2.00E-31// 110aa// 48%

COLON2005623// 2-19 protein precursor.// 3.00E-68// 121aa// 54%

COLON2005735// Blood group RH(CE) polypeptide (Rhesus C/E antigens) (RH30A) (RHIXB) (RH polypeptide 1) (RHPI).// 0// 353aa// 95%

CTONG2001932// bromodomain adjacent to zinc finger domain, 2B [Homo sapiens]// 0// 385aa// 66%

CTONG2003517

CTONG2006235// ubiquitin-protein ligase e3 componen n-recognin [Mus musculus]// 1.00E-24// 82aa// 30%

CTONG2008989// Gap junction beta-5 protein (Connexin 31.1) (Cx31.1).// 7.00E-74// 123aa// 57%

CTONG2009033

CTONG2009570// rab11 binding protein [Bos taurus].// 0// 400aa// 90%

CTONG2010330// Homo sapiens phospholipase A2, group IVB (cytosolic) (PLA2G4B)// 1.00E-122// 222aa// 45%

CTONG2010633

CTONG2011801// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7).// 3.00E-62// 104aa// 50%

CTONG2012123// Mus musculus enabled homolog (Drosophila) (Enah), mRNA// 1.00E-77// 155aa// 74%

CTONG2014206// oxidation resistance 1; oxidation resistance 1; hypothetical protein FLJ10125 [Homo sapiens]// 1.00E-127// 221aa// 82%

CTONG2014959

CTONG2020582// Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA 1

igase) (Acyl- activating enzyme).// 1.00E-157// 269aa// 54%
CTONG2026987
CTONG2027150
CTONG2027591// Mus musculus pecanex homolog (Drosophila) (Pcnx), mRNA.//
0// 347aa// 81%
CTONG2027783
CTONG2027959
CTONG3001605// putative tumor suppressor [Homo sapiens]// 1.00E-35// 77a
a// 45%
CTONG3002518
CTONG3002588
CTONG3003669// high-glucose-regulated protein 8 [Homo sapiens]// 1.00E-1
01// 170aa// 79%
CTONG3008223
D90ST2003106// Homo sapiens SMART/HDAC1 associated repressor protein (SH
ARP), mRNA// 0// 486aa// 82%
D90ST2003989
D90ST2004417// 60S ribosomal protein L13 (Breast basic conserved protein
1).// 1.00E-100// 185aa// 88%
DFNES2001829
DFNES2011221
ERLTF2001452
ERLTF2001835
ERLTF2002178// Kelch-like protein X.// 1.00E-138// 251aa// 50%
ERLTF2002369
FCBBF3001018// Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) (HMG-CoA lya
se) (HL) (3- hydroxy-3-methylglutarate-CoA lyase).// 5.00E-88// 152aa//
73%
FCBBF3002188

FCBBF3005160

FCBBF3012443

FCBBF3020030// Transcription intermediary factor 1-alpha (TIF1-alpha).//
0// 423aa// 80%

FCBBF3021191// Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-
gamma) (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosph
atase 1C).// 0// 441aa// 80%

FCBBF3024911// WHSC1L1 protein isoform short; Wolf-Hirschhorn syndrome c
andidate 1-like 1 protein [Homo sapiens]// 1.00E-124// 217aa// 91%

FCBBF5000384// SWI/SNF related, matrix associated, actin dependent regul
ator of chromatin, subfamily d, member 3; Rsc6p [Homo sapiens]// 0// 394
aa// 84%

FEBRA2000805

FEBRA2002260

FEBRA2012625

FEBRA2013069

FEBRA2013570// 2-oxoisovalerate dehydrogenase alpha subunit, mitochondri
al precursor (EC 1.2.4.4) (Branched-chain alpha-keto acid dehydrogenase
component alpha chain (E1)) (BCKDH E1-alpha).// 0// 391aa// 95%

FEBRA2017736

FEBRA2017811

FEBRA2023498// Leucine-rich repeat protein LRRC3 precursor.// 2.00E-63//
116aa// 86%

FEBRA2026582// Homo sapiens protein (peptidyl-prolyl cis/trans isomerase
) NIMA-interacting, 4 (parvulin) (PIN4)// 7.00E-25// 79aa// 100%

FEBRA2026977

FEBRA2028222

FEBRA2028457// Nucleolin (Protein C23).// 0// 360aa// 82%

FEHRT2001482

FEHRT2002708// solute carrier family 22 (organic cation transporter)-like 2 [Mus musculus].// 6.00E-42// 90aa// 44%

FEKID2001001

FEKID2001201

FEKID2002231

FEKID2002493// WNT-14 protein precursor.// 1.00E-100// 174aa// 61%

FEKID2002637// Serine/threonine protein phosphatase PP1-alpha 1 catalytic subunit (EC 3.1.3.16) (PP-1A).// 0// 297aa// 99%

FELNG2000720// CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM).// 1.00E-123// 219aa// 91%

FELNG2001613

FELNG2001706// transcriptional co-activator with PDZ-binding motif (TAZ); transcriptional co-activator with PDZ-binding motif (TAZ); DKFZP586I1419 protein [Homo sapiens]// 2.00E-21// 45aa// 97%

FELNG2001953// JAK binding protein [Homo sapiens]// 6.00E-96// 174aa// 82%

HCASM2007773

HCASM2008154// RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein).// 1.00E-104// 219aa// 48%

HCHON2009766

HEART2002531

HHGPC2008185// jerky [Mus musculus]// 0// 397aa// 75%

HLUNG2012600

HSYRA2004550// Potential phospholipid-transporting ATPase IIB (EC 3.6.3.13).// 0// 433aa// 92%

HSYRA2007338

JCMCL1000159// Interferon-gamma receptor alpha chain precursor (CDw119).// 4.00E-65// 122aa// 78%

JCMCL2000273// Integrin alpha-M precursor (Cell surface glycoprotein MAC

-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1) (Neutrophil adherence receptor).// 0// 536aa// 96%

JCMC2002095// P-selectin glycoprotein ligand 1 precursor (PSGL-1) (Selectin P ligand) (CD162 antigen).// 1.00E-21// 48aa// 72%

JCMC2002751// Von Willebrand factor precursor (vWF).// 2.00E-42// 83aa// 37%

KIDNE2004531// Lag protein [Mus musculus]// 1.00E-109// 197aa// 78%

KIDNE2010049// Glycerol kinase 2 (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase 2) (Glycerokinase 2) (GK 2).// 8.00E-87// 176aa// 34%

KIDNE2014496

KIDNE2015987// Uromodulin precursor (Tamm-Horsfall urinary glycoprotein) (THP).// 0// 433aa// 86%

KIDNE2016464

KIDNE2017153

KIDNE2018268

LIVER2008465

LYMPB1000158

LYMPB2001387

LYMPB2002236// Gene terminal protein (Membrane protein LMP-2A/LMP-2B).// 3.00E-75// 153aa// 55%

LYMPB2002344

LYMPB2002458// Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Miotendinous antigen) (Glioma-associated-extracellular matrix antigen) (GP 150-225).// 1.00E-115// 193aa// 45%

LYMPB2002478

MESAN2007032

MESAN2009156

MESAN2014624// tumor differentially expressed 1, like; membrane protein TMS-2 [Mus musculus]// 2.00E-71// 124aa// 52%

MESAN2016304

MESAN2017133

MESTC2000170

NIIESE2000698// WD-repeat protein 1 (Actin interacting protein 1) (NORI-1)
).// 0// 558aa// 92%

NETRP2000439

NETRP2000961// Cytosolic purine 5'-nucleotidase (EC 3.1.3.5).// 0// 368a
a// 100%

NETRP2002082

NETRP2003103

NETRP2003268

NETRP2003448// Ras-related protein RAL-B.// 4.00E-97// 189aa// 83%

NETRP2003539

NETRP2004017// nuclear transcription factor Y, gamma; CCAAT-binding tran
scription factor subunit C; transactivator HSM-1; histone H1 transcripti
on factor large subunit 2A [Homo sapiens]// 6.00E-90// 193aa// 59%

NETRP2004090

NETRP2004434

NETRP2005282

NETRP2005849

NETRP2005972

NETRP2006468

NETRP2007945

NETRP2008488

NETRP2008582// Adipophilin (Adipose differentiation-related protein) (AD
RP).// 1.00E-19// 100aa// 44%

NOVAR2000783

NT2NE2011107

NT2NE2016041

NT2RI2004818// 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
beta 1 (EC 3.1.4.11) (PLC-beta-1) (Phospholipase C-beta-1) (PLC-I) (PLC
-154).// 0// 883aa// 91%

NT2RI2009233

NT2RI2010795

NT2RI2012542

NT2RI2015533

NT2RI2023671

NT2RI2028537

NT2RI3001573// F-box protein FBL10 [Mus musculus].// 3.00E-78// 223aa//
62%

NT2RI3001967// Ankyrin homolog precursor.// 6.00E-13// 68aa// 30%

NT2RI3005861

NT2RI3005923// Cadherin-related tumor suppressor precursor (Fat protein)
.// 1.00E-116// 370aa// 28%

NT2RI3007095// Mus musculus neuregulin 1 (Nrg1), mRNA.// 0// 861aa// 96%

NT2RI3008179// thyroid hormone receptor-associated protein, 240 kDa subu
nit [Homo sapiens]// 0// 562aa// 43%

NT2RI3009480// Transcription factor Sp3 (SPR-2) (Fragment).// 1.00E-43//
78aa// 69%

NT2RI3009524// Crumbs protein homolog 1 precursor.// 1.00E-178// 375aa//
31%

NT2RP7003439

NT2RP7007387

NT2RP7014178

NT2RP7014778

NT2RP7016508// YN21_CAEEL Putative ATP-dependent RNA helicase T26G10.1
in chromosome III// 1.00E-157// 388aa// 69%

NT2RP7017139

NT2RP7019682

NT2RP7020343

NT2RP8000633

NT2RP8001363// signal peptide, CUB domain, EGF-like 1 [Mus musculus]// 0
// 357aa// 87%

NT2RP8001407

NT2RP8001584// alpha integrin binding protein 63 [Homo sapiens]// 1.00E-
17// 74aa// 30%

NT2RP8001604// CUB and Sushi multiple domains 1 [Homo sapiens]// 0// 754
aa// 65%

NT2RP8001605

NT2RP8003490// LIM/homeobox protein LMX1A (LMX-1) (LIM-homeobox protein
1).// 0// 344aa// 90%

NT2RP8003657

NT2RP8003787// vanilloid receptor-related osmotically activated channel;
OSM9-like transient receptor potential channel 4; transient receptor po
tential channel 12; transient receptor potential, drosophila, homolog of
, 12 [Homo sapiens]// 1.00E-118// 221aa// 44%

NT2RP8005546// schlafen 3 [Mus musculus]// 1.00E-34// 92aa// 29%

NT2RP8006452// Flightless-I protein.// 1.00E-14// 79aa// 30%

NT2RP8006521

NT2RP8007416

NT2RP8007503

NT2RP8007920

NT2RP8008057// cartilage intermediate layer protein [Homo sapiens]// 0//
564aa// 49%

NT2RP8009119

NT2RP8009248

NTONG2002278

NTONG2003805// Zinc finger protein 45 (BRC1744).// 0// 438aa// 98%

NTONG2004829

NTONG2008483// zinc finger protein 106 [Homo sapiens]// 0// 607aa// 72%

NTONG2009468

OCBBF2000831// AMBP protein precursor [Contains: Alpha-1-microglobulin; Inter-alpha- trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30)].// 9.00E-23// 54aa// 36%

OCBBF2003518// Myosin heavy chain, non-muscle (Zipper protein) (Myosin I I).// 3.00E-14// 118aa// 21%

OCBBF2004478// Homo sapiens cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) (CELSR2), mRNA// 4.00E-96// 177aa// 80%

OCBBF2007039// ADAM-TS 7 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAMTS-7) (ADAM-TS7).// 1.00E-143// 293aa// 36%

OCBBF2009536// Mus musculus amiloride-sensitive cation channel 1, neuronal (degenerin) (Accn1)// 0// 471aa// 95%

OCBBF2014745

OCBBF2016928// zinc finger protein [Homo sapiens]// 0// 449aa// 88%

OCBBF2018229

OCBBF2018618// Adenosine A1 receptor.// 1.00E-155// 273aa// 83%

OCBBF2019761

OCBBF2024589// Dihydropyrimidinase related protein-1 (DRP-1) (Collapsin response mediator protein 1) (CRMP-1).// 0// 528aa// 92%

OCBBF2024779

OCBBF2025631

OCBBF2030927// matrilin 4 isoform 2 precursor [Homo sapiens]// 2.00E-39// 138aa// 28%

OCBBF2036019// NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondr

ial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-20KD) (CI-20KD) (PSS
T subunit).// 7.00E-36// 76aa// 97%

OCBBF3000743

OCBBF3000830

OCBBF3001076

OCBBF3001202// suppression of tumorigenicity 5 [Homo sapiens]// 0// 532a
a// 87%

OCBBF3001333// ubiquitin UBF-fl [Homo sapiens]// 1.00E-166// 279aa// 58%
OCBBF3001616

OCBBF3003745

OCBBF3004487// Probable ATP-dependent RNA helicase p47.// 1.00E-140// 24
5aa// 100%

OCBBF3004908

OCBBF3005330// FYVE finger-containing phosphoinositide kinase (EC 2.7.1.
68) (1- phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-k
inase) (p235).// 0// 878aa// 86%

OCBBF3005843

OCBBF3006986// CDC4-like protein (Beige-like protein) (Fragment).// 1.00
E-112// 299aa// 33%

OCBBF3007078

OCBBF3007704

OCBBF3008392// bromodomain adjacent to zinc finger domain, 2A; TTF-I int
eracting peptide 5 [Homo sapiens]// 0// 504aa// 92%

OCBBF3008835

OCBBF3009244// pantothenate kinase 1 beta [Mus musculus]// 1.00E-154// 2
67aa// 89%

OCBBF3019269// Homo sapiens Dvl-binding protein IDAX (inhibition of the
Dvl and Axin complex) (IDAX)// 1.00E-100// 168aa// 84%

OCBBF3020263// Zinc finger protein 135.// 4.00E-90// 144aa// 59%

OCBBF3020414

OCBBF3021086

OCBBF3021166

OCBBF3021361// rapa-1 [Homo sapiens]// 3.00E-50// 330aa// 50%

OCBBF3021502

OCBBF3021515

OCBBF3022123

OCBBF3022166// Nuclear receptor co-repressor 2 (N-CoR2) (Silencing mediator of retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Thyroid-, retinoic-acid-receptor-associated co-repressor) (T3 receptor- associating factor) (TRAC) (CTG26).// 2.00E-38// 75aa// 92%

OCBBF3022576

OCBBF3022827// putative Rab5 GDP/GTP exchange factor homologue [Homo sapiens]// 0// 384aa// 90%

OCBBF3023175// LPS-responsive beige-like anchor [Mus musculus]// 0// 999aa// 63%

OCBBF3023543

OCBBF3023913// Mus musculus protein phosphatase 1, regulatory (inhibitor) subunit 1C (Ppp1r1c)// 1.00E-154// 302aa// 44%

OCBBF3023993

OCBBF3025127

OCBBF3025131

OCBBF3025475// Renal sodium/dicarboxylate cotransporter (Na(+)/dicarboxylate cotransporter).// 1.00E-155// 279aa// 50%

OCBBF3025503// Eyes absent homolog 1.// 0// 423aa// 89%

OCBBF3025630// Brefeldin A-inhibited guanine nucleotide-exchange protein 1 (Brefeldin A-inhibited GEP 1) (p200 ARF-GEP1) (p200 ARF guanine nucleotide exchange factor).// 1.00E-132// 235aa// 96%

OCBBF3025887

OCBBF3025901

OCBBF3026088

OCBBF3026361

OCBBF3026979// Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1) (Nel-related protein 1).// 0// 795aa// 94%

OCBBF3027969// myosin IIIA [Homo sapiens]// 3.00E-84// 187aa// 36%

OCBBF3028001// Rattus norvegicus potassium channel subunit (Slack) (Slack), mRNA// 0// 407aa// 76%

PEBLM2001803

PEBLM2003935

PEBLM2005615// C-C chemokine receptor type 7 precursor (C-C CKR-7) (CC-C KR-7) (CCR-7) (MIP-3 beta receptor) (EBV-induced G protein-coupled receptor 1) (EBI1) (BLR2).// 0// 351aa// 92%

PEBLM2006298

PERIC2003349

PLACE5000492// 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta 1 (EC 3.1.4.11) (PLC-delta-1) (Phospholipase C-delta-1) (PLC-III) .// 0// 505aa// 91%

PLACE5000522

PLACE5000527

PLACE6000012// cation-chloride cotransporter-interacting protein [Homo sapiens]// 3.00E-19// 54aa// 54%

PLACE6000055// neuronal differentiation related protein [Mus musculus]// 0// 416aa// 90%

PLACE6001933// Epidermal growth factor receptor precursor (EC 2.7.1.112) .// 1.00E-40// 79aa// 98%

PLACE6003004// rTS beta protein [Homo sapiens]// 0// 388aa// 93%

PLACE6008315// similar to ALPHA-ACTININ, SARCOMERIC (F-ACTIN CROSS LINKING PROTEIN) (D. melanogaster) [Homo sapiens].// 1.00E-76// 121aa// 100%

PLACE6010925// NY-REN-50 antigen [Homo sapiens]// 0// 345aa// 98%

PLACE6010936// orphan G protein-coupled receptor GPR26 [Rattus norvegicus]// 1.00E-62// 112aa// 63%

PLACE6016030// Wilms tumor 1-associating protein (WT1-associated protein).// 1.00E-73// 138aa// 91%

PLACE6019542

PLACE6019600// Ras-related protein Rab-12 (Fragment).// 1.00E-45// 92aa// 85%

PLACE6019674

PLACE7000266// titin [Homo sapiens]// 2.00E-36// 218aa// 24%

PLACE7000707

PLACE7001759// Arylacetamide deacetylase (EC 3.1.1.-) (AADAC).// 8.00E-41// 97aa// 36%

PLACE7002303// Pituitary homeobox 2 (RIEG bicoid-related homeobox transcription factor) (Solurshin) (ALL1 responsive protein ARP1).// 1.00E-145// 256aa// 80%

PLACE7003639

PLACE7003684

PLACE7003985// Estradiol 17 beta-dehydrogenase 1 (EC 1.1.1.62) (17-beta-HSD 1) (Placental 17-beta-hydroxysteroid dehydrogenase) (20 alpha-hydroxysteroid dehydrogenase) (20-alpha-HSD) (E2DH).// 1.00E-164// 293aa// 89%

PLACE7004103// Vigilin (High density lipoprotein-binding protein) (HDL-binding protein).// 0// 701aa// 91%

PLACE7004961// Dynamin-1 (EC 3.6.1.50) (D100) (Dynamin, brain) (B-dynamin).// 2.00E-18// 49aa// 68%

PLACE7005169// zinc finger protein 292 [Mus musculus]// 0// 953aa// 76%

PLACE7005671

PLACE7005840

PLACE7006090// Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20) (Alpha-glucosidase); Glucoamylase (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)].// 9.00E-59// 107aa// 86%

PLACE7006240

PLACE7006268// Histone acetyltransferase type B catalytic subunit (EC 2.3.1.48).// 1.00E-67// 124aa// 100%

PLACE7006498// Guanine nucleotide-binding protein, alpha-12 subunit (G alpha 12).// 1.00E-160// 277aa// 99%

PLACE7006540

PLACE7007379// carboxypeptidase Z.precursor [Homo sapiens]// 1.00E-149// 245aa// 99%

PLACE7007973

PLACE7008136

PLACE7008766

PLACE7009563// Melanoma-associated antigen 11 (MAGE-11 antigen).// 1.00E-162// 284aa// 89%

PLACE7009757// Transcription factor Sp3 (SPR-2) (Fragment).// 3.00E-44// 79aa// 70%

PLACE7009936// Active breakpoint cluster region-related protein.// 1.00E-114// 204aa// 99%

PLACE7010567

PLACE7011269

PLACE7011559// Death-associated protein kinase 1 (EC 2.7.1.-) (DAP kinase 1).// 1.00E-153// 263aa// 88%

PLACE7012111// ADAM 12 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 12) (Meltrin alpha).// 0// 662aa// 96%

PLACE7012127// AAA-ATPase TOB3 [Homo sapiens]// 9.00E-64// 118aa// 91%

PLACE7013060

PLACE7014247// Phosphatidylinositol 3-kinase catalytic subunit, gamma is

oform (EC 2.7.1.137) (PI3-kinase P110 subunit gamma) (PtdIns-3-kinase P110) (PI3K) (PI3Kgamma).// 4.00E-50// 93aa// 100%

PLACE7014396

PLACE7015238

PLACE7015647

PLACE7016214

PLACE7016321

PLACE7016454

PLACE7016526// Lon protease homolog, mitochondrial precursor (EC 3.4.21.-) (Lon protease-like protein) (LONP) (LONHs).// 0// 865aa// 90%

PLACE7018304

PLACE7018349

PLACE7018452

PLACE7018479

PLACE7018512

PROST2002078// RNA-binding protein with multiple splicing homolog (RBP-M S) (HEart, RRM Expressed Sequence) (Hermes).// 7.00E-90// 161aa// 77%

PROST2007444

PROST2016566// erythroblast macrophage protein [Mus musculus]// 6.00E-82// 144aa// 91%

PROST2017578

PROST2017729

PROST2017749

PROST2017910

PUAEN2000594// Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1) (PABP1).// 5.00E-60// 117aa// 92%

PUAEN2000684// Mus musculus soc-2 (suppressor of clear) homolog// 5.00E-28// 107aa// 26%

PUAEN2006639// Vegetatible incompatibility protein HET-E-1.// 1.00E-46//

89aa// 36%

RECTM2001519

SKMUS2008585// protein phosphatase [Homo sapiens]// 1.00E-112// 198aa//
100%

SKMUS2009479

SKMUS2009557

SKNMC2003639

SKNSH2007306// Sperm-specific antigen 2 (Cleavage signal-1 protein) (CS-
1).// 1.00E-102// 194aa// 85%

SMINT2003641

SMINT2009292

SMINT2009895

SMINT2010753// Probable kinesin light chain 3 (KLC 3).// 0// 528aa// 85%

SMINT2011406// Interferon-regulated resistance GTP-binding protein MxB (P78-related protein).// 1.00E-90// 165aa// 100%

SMINT2011509// Homo sapiens polymerase (DNA directed), lambda (POLL), mRNA// 1.00E-145// 254aa// 95%

SMINT2012040

SMINT2012179// LCAT-like lysophospholipase [Homo sapiens]// 1.00E-123//
205aa// 99%

SMINT2014166

SMINT2014721// Peroxisomal carnitine octanoyltransferase (EC 2.3.1.-) (COT).// 0// 611aa// 95%

SMINT2017964

SMINT2019105

SPLEN2001227

SPLEN2007689// Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH oxidase factor 1) (47 kDa neutrophil oxidase factor) (p47-phox) (NCF-47K) (47 kDa autosomal chronic granulomatous disease protein).// 2.00E-75// 13

5aa// 99%

SPLEN2011252

SPLEN2012571// Zinc finger protein 202.// 1.00E-77// 203aa// 32%

SPLEN2017999

SPLEN2019092

SPLEN2019480

SPLEN2021231

SPLEN2021991

SPLEN2022785

SPLEN2022920

SPLEN2024571

SPLEN2025012// Ig alpha-1 chain C region.// 0// 318aa// 92%

SPLEN2027852

SPLEN2028417// Homeobox protein HLX1 (Homeobox protein HB24).// 0// 364a
a// 74%

SPLEN2028593

SPLEN2031004

SPLEN2032677

SPLEN2033996// pan-hematopoietic expression; tumor-suppressing STF cDNA
6; TSSC6 tumor-suppressing STF cDNA 6; tumor suppressing subtransferable
candidate 6 [Homo sapiens]// 2.00E-63// 111aa// 100%

SPLEN2034551// LIS1-interacting protein NUDE1, rat homolog [Homo sapiens
]// 2.00E-71// 136aa// 100%

SPLEN2034601

SPLEN2034934// shroom [Mus musculus]// 2.00E-49// 90aa// 68%

SPLEN2035615

SPLEN2036608

SPLEN2037077

SPLEN2042051

STOMA2003894

STOMA2004663// T-cell receptor alpha chain V region RL-5 precursor.// 9.00E-36// 75aa// 65%

SYNOV2003326// Glucocorticoid-induced leucine zipper protein (Delta sleep-inducing peptide immunoreactor) (DSIP-immunoreactive peptide) (DIP protein) (hDIP) (TSC-22-like protein) (TSC-22R).// 3.00E-65// 125aa// 93%

SYNOV2017179// EBP50-PDZ interactor of 64 kD [Homo sapiens]// 0// 485aa// 94%

SYNOV3000345// upregulated by 1,25-dihydroxyvitamin D-3 [Homo sapiens]// 5.00E-65// 142aa// 36%

SYNOV4000598

SYNOV4003174// unconventional myosin from rat 4 for myosin I heavy chain [Rattus norvegicus]// 0// 650aa// 97%

SYNOV4004210

SYNOV4009139// hyaluronoglucosaminidase 2; lysosomal hyaluronidase; PH-20 homolog; hyaluronidase 2 [Homo sapiens]// 0// 429aa// 90%

SYNOV4009575

TIESE2000609// SON protein (SON3).// 1.00E-177// 315aa// 86%

TIESE2000904// zinc finger protein 304 [Homo sapiens]// 0// 325aa// 49%

TIESE2002665// Bumetanide-sensitive sodium-(potassium)-chloride cotransporter 1 (Basolateral Na-K-Cl symporter).// 6.00E-60// 129aa// 31%

TBAES2003917// NG28 protein [Mus musculus]// 0// 479aa// 58%

TBAES2005361

TBAES2007428// N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase [Homo sapiens]// 0// 427aa// 82%

TBAES2007548

TBAES2007862

TESOP2002005

TESOP2003308

TESOP2004110

TESOP2008556

TESTI1000459

TESTI2001364// lactate dehydrogenase A -like [Homo sapiens]// 1.00E-113/
/ 204aa// 81%

TESTI2001915// actin filament associated protein [Homo sapiens]// 1.00E-
96// 183aa// 81%

TESTI2003768// Chloride channel protein 3 (ClC-3).// 2.00E-23// 47aa// 9
0%

TESTI2004452

TESTI2004601// NYD-TSPG protein [Homo sapiens]// 1.00E-45// 116aa// 35%

TESTI2004971

TESTI2005112// NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondr
ial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-30KD) (CI-30KD).// 1
.00E-110// 189aa// 100%

TESTI2005153

TESTI2005564

TESTI2006543

TESTI2007490// 2-hydroxyacylsphingosine 1-beta-galactosyltransferase pre
cursor (EC 2.4.1.45) (UDP-galactose-ceramide galactosyltransferase) (Cer
amide UDP-galactosyltransferase) (Cerebroside synthase).// 0// 510aa// 9
4%

TESTI2008636

TESTI2009497// GPI-anchored protein p137 (p137GPI).// 0// 455aa// 76%

TESTI2009739// Myosin heavy chain, smooth muscle isoform (SMMHC).// 3.00
E-14// 104aa// 20%

TESTI2011020

TESTI2011033

TESTI2018335

TESTI2018687

TESTI2018867

TESTI2021112

TESTI2021654// thymidylate kinase family LPS-inducible member; thymidylate kinase homologue [Mus musculus]// 9.00E-19// 196aa// 74%

TESTI2022323// Olfactory receptor 2H1 (Hs6M1-16) (Olfactory receptor 6-2) (OR6-2) (OLFR42A-9004.14/9026.2).// 1.00E-174// 303aa// 95%

TESTI2023053

TESTI2023903// ubiquilin 1 [Homo sapiens]// 2.00E-53// 156aa// 34%

TESTI2024267

TESTI2026024// early development regulator 2 (homolog of polyhomeotic 2) ; polyhomeotic 2 protein [Mus musculus]// 1.00E-116// 198aa// 89%

TESTI2026284

TESTI2028613

TESTI2030519

TESTI2030901// glutathione S-transferase theta 1 [Homo sapiens]// 4.00E-18// 68aa// 57%

TESTI2033905

TESTI2034913// Keratin, type II cytoskeletal 8 (Cytokeratin 8) (K8) (CK 8).// 1.00E-64// 137aa// 69%

TESTI2035962

TESTI2036285// ubiquitin C [Rattus norvegicus]// 1.00E-78// 166aa// 91%

TESTI2036822

TESTI2037085

TESTI2037209

TESTI2037572

TESTI2037657// Integral membrane glycoprotein gp210 precursor.// 1.00E-147// 260aa// 48%

TESTI2037877

TESTI2038733

TESTI2039342

TESTI2039732

TESTI2039738

TESTI2040372

TESTI2040377// Mitogen-activated protein kinase kinase kinase 1 (EC 2.7.1.-) (MAPK/ERK kinase kinase 1) (MEK kinase 1) (MEKK 1).// 1.00E-13// 56aa// 28%

TESTI2041362

TESTI2041976

TESTI2046188

TESTI2049041

TESTI2049062// peroxisomal 2,4-dienoyl-CoA reductase [Homo sapiens]// 6.00E-51// 106aa// 63%

TESTI2051742

TESTI2052110

TESTI2052202

TESTI2052670// Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).// 2.00E-44// 139aa// 32%

TESTI2052799

TESTI4000370

TESTI4000534

TESTI4000600

TESTI4000621// Snf2-related CBP activator protein [Homo sapiens]// 0// 1397aa// 62%

TESTI4000703

TESTI4000957

TESTI4001037

TESTI4001348

TESTI4001517// Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (C K 18).// 7.00E-52// 103aa// 78%

TESTI4001569

TESTI4001679// RING finger protein 4.// 2.00E-92// 165aa// 86%

TESTI4002003

TESTI4002072

TESTI4002141

TESTI4002195

TESTI4002520

TESTI4002774// oxysterol binding protein 2 [Mus musculus]// 3.00E-48// 1 25aa// 35%

TESTI4002799// DNA-directed RNA polymerase I 135 kDa polypeptide (EC 2.7 .7.6) (RNA polymerase I subunit 2) (RPA135).// 0// 1001aa// 88%

TESTI4002868// DNA-binding protein RFX5 (Regulatory factor X subunit 5). // 5.00E-40// 76aa// 47%

TESTI4002889

TESTI4003179

TESTI4003279

TESTI4003319

TESTI4003404

TESTI4003565

TESTI4003574

TESTI4003579// FH1/FH2 domains-containing protein (Formin homolog overex pressed in spleen) (FHOS).// 1.00E-111// 207aa// 53%

TESTI4003602

TESTI4003703// retinoblastoma-associated protein RAP140 [Homo sapiens]// 5.00E-46// 101aa// 40%

TESTI4003733

TESTI4003796// Zinc finger protein 189.// 1.00E-79// 148aa// 45%

TESTI4003944// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7)
./ 8.00E-32// 162aa// 23%

TESTI4004031

TESTI4004210

TESTI4004539

TESTI4004653// CTL2 gene [Homo sapiens]// 0// 292aa// 51%

TESTI4004695

TESTI4004917// Dynein beta chain, ciliary.// 0// 560aa// 73%

TESTI4005013

TESTI4005322// Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).
// 0// 339aa// 69%

TESTI4005399

TESTI4005470// Transcriptional repressor CTCF.// 1.00E-155// 249aa// 68%

TESTI4005653// SON DNA binding protein; SON DNA-binding protein; SON DNA
-binding protein, KIAA1019; NRE-binding protein [Homo sapiens]// 0// 112
2aa// 77%

TESTI4006441

TESTI4006539

TESTI4007565

TESTI4007671// Mus musculus quiescin Q6 (Qscn6), mRNA.// 1.00E-111// 207
aa// 44%

TESTI4007965// Adapter-related protein complex 1 gamma 1 subunit (Gamma-
adaptin) (Golgi adaptor HA1/AP1 adaptin gamma subunit) (Clathrin assembl
y protein complex 1 gamma large chain).// 0// 766aa// 93%

TESTI4008086

TESTI4008305

TESTI4009501

TESTI4010544

TESTI4010721

TESTI4010902// Echinoderm microtubule-associated protein-like 4 (EMAP-4)
(Restrictedly overexpressed proliferation-associated protein) (Ropp 120
).// 1.00E-56// 135aa// 35%

TESTI4010979

TESTI4011616

TESTI4011744

TESTI4011926

TESTI4012258

TESTI4012382

TESTI4012623

TESTI4012956

TESTI4012960

TESTI4013474// PTPL1-associated RhoGAP 1 [Homo sapiens]// 1.00E-133// 28
3aa// 33%

TESTI4013742// antigen identified by monoclonal antibody 2A8 [Mus muscul
us]// 0// 640aa// 70%

TESTI4013774

TESTI4013960

TESTI4013962

TESTI4014262

TESTI4014415

TESTI4014891

TESTI4014908// dedicator of cyto-kinesis 2 [Mus musculus]// 0// 825aa//
92%

TESTI4014932// Integral membrane glycoprotein gp210 precursor.// 0// 580
aa// 40%

TESTI4014977

TESTI4015129

TESTI4015339

TESTI4016848

TESTI4017229

TESTI4017382// Copine VII.// 1.00E-152// 250aa// 72%

TESTI4017647// homolog-like; Jerky, mouse, homolog-like [Homo sapiens]//
2.00E-07// 67aa// 37%

TESTI4017854

TESTI4018436// Ubiquitin fusion degradation protein 1 homolog (UB fusion
protein 1).// 5.00E-70// 125aa// 100%

TESTI4018506// tomosyn [Rattus norvegicus]// 0// 689aa// 85%

TESTI4019149

TESTI4020342// H326 [Homo sapiens]// 0// 370aa// 61%

TESTI4020596// calpain 5 [Homo sapiens]// 0// 629aa// 98%

TESTI4020819// complement-clq tumor necrosis factor-related protein 6 [H
omo sapiens]// 2.00E-74// 135aa// 87%

TESTI4021129

TESTI4021197// Regulator of G-protein signaling 3 (RGS3) (RGP3).// 0// 4
79aa// 92%

TESTI4021377

TESTI4021569// ATP-binding cassette, sub-family B, member 8, mitochondri
al precursor (Mitochondrial ATP-binding cassette 1) (M-ABC1).// 0// 343a
a// 77%

TESTI4021713// synaptonemal complex protein 2 [Homo sapiens]// 1.00E-46/
/ 108aa// 40%

TESTI4021821

TESTI4022158// transmembrane receptor Unc5H2 [Rattus norvegicus]// 0// 8
12aa// 87%

TESTI4023096// solute carrier family 12 (potassium/chloride transporters
, member 6; potassium/chloride transporter 3 [Homo sapiens]// 0// 901aa
// 89%

TESTI4023172

TESTI4023654

TESTI4024240

TESTI4024245

TESTI4024294// WW domain binding protein 2 [Mus musculus]// 3.00E-30// 6
8aa// 48%

TESTI4024494// zinc-binding protein Rbcc728 [Homo sapiens]// 1.00E-111//
190aa// 46%

TESTI4025062

TESTI4025401

TESTI4025908

TESTI4026080// family member, chromosome-associated protein C [Homo sapi
ens]// 0// 1137aa// 88%

TESTI4026680

TESTI4027139

TESTI4027170

TESTI4027262

TESTI4027660

TESTI4028042// NYD-SP11 protein [Homo sapiens]// 0// 610aa// 90%

TESTI4028182// 116 kDa U5 small nuclear ribonucleoprotein component (U5
snRNP- specific protein, 116 kDa) (U5-116 kDa).// 0// 642aa// 95%

TESTI4029023

TESTI4029297

TESTI4029651

TESTI4029676

TESTI4029731

TESTI4029743

TESTI4030319

TESTI4030673

TESTI4030864

TESTI4031066

TESTI4031173// Contactin 2 precursor (Axonin-1) (Axonal glycoprotein TAG-1) (Transient axonal glycoprotein 1) (TAX-1).// 1.00E-29// 93aa// 30%

TESTI4031818

TESTI4032128// Amyloid-like protein 2 precursor (Amyloid protein homolog) (APPH) (CDEI-box binding protein) (CDEBP).// 0// 564aa// 84%

TESTI4032270

TESTI4032375

TESTI4032834// trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit); thyroid hormone receptor-associated protein, 230 kDa subunit [Homo sapiens]// 0// 359aa// 66%

TESTI4032856

TESTI4032913// Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).// 1.00E-30// 106aa// 30%

TESTI4033177// Dual specificity protein phosphatase 8 (EC 3.1.3.48) (EC 3.1.3.16) (Dual specificity protein phosphatase hVH-5).// 2.00E-57// 110aa// 92%

TESTI4034633

TESTI4034973

TESTI4035770

TESTI4035872

TESTI4035898

TESTI4035989

TESTI4036012

TESTI4036048// Sorting nexin 1.// 0// 457aa// 90%

TESTI4037228

TESTI4037949// Kelch-like protein X.// 1.00E-129// 241aa// 44%

TESTI4038047

TESTI4038758

TESTI4039451// B29 protein [Homo sapiens]// 3.00E-34// 73aa// 38%

TESTI4039575// Telomeric repeat binding factor 1.// 2.00E-12// 62aa// 10
0%

TESTI4039744

TESTI4039904// Zinc finger protein 85 (Zinc finger protein HPF4) (HTF1).
// 0// 298aa// 72%

TESTI4040197

TESTI4040559// Cyclic-nucleotide-gated olfactory channel (Cyclic-nucleot
ide-gated cation channel 2) (CNG channel 2) (CNG-2) (CNG2) (Aorta CNG ch
annel) (RACNG).// 0// 600aa// 90%

TESTI4040598

TESTI4040804

TESTI4041049// leucine-rich neuronal protein [Homo sapiens]// 2.00E-72//
136aa// 90%

TESTI4041482// Rattus norvegicus SEC15 homolog (S. cerevisiae) (Sec15),
mRNA// 0// 700aa// 88%

TESTI4041832

TESTI4041984// latent transforming growth factor beta binding protein 4
[Homo sapiens]// 0// 732aa// 86%

TESTI4042420

TESTI4042846

TESTI4043067

TESTI4043166// lymphocyte specific formin related protein; formin-relate
d gene in leukocytes [Mus musculus]// 1.00E-137// 257aa// 60%

TESTI4043223

TESTI4043371

TESTI4043378

TESTI4044076

TESTI4044291

TESTI4044770

TESTI4045168

TESTI4045330

TESTI4045470

TESTI4046073// Rho-GTPase-activating protein 6 (Rho-type GTPase-activating protein RhoGAPX-1).// 1.00E-75// 177aa// 36%

TESTI4046090

TESTI4046245

TESTI4046328

TESTI4046450

TESTI4046873

TESTI4046962

TESTI4047119// AIM-1 protein [Homo sapiens]// 1.00E-38// 82aa// 35%

TESTI4047305

TESTI4047328// otogelin [Mus musculus]// 0// 1009aa// 65%

TESTI4047437

TESTI4047569

TESTI4047746

TESTI4047808

TESTI4048232

TESTI4048296

TESTI4048545

TESTI4048619

TESTI4049110

TESTI4049552

TESTI4049562

TESTI4049677

TESTI4049786// Hexokinase, type I (EC 2.7.1.1) (HK I) (Brain form hexoki

nase).// 0// 892aa// 99%

TESTI4049863

TESTI4049899// deleted in malignant brain tumors 1 isoform c precursor [
Homo sapiens]// 6.00E-44// 79aa// 45%

TESTI4050293

TESTI4050954

TESTI4051015// Aquaporin 7 (Aquaporin-7 like) (Aquaporin adipose) (AQPap
).// 7.00E-17// 45aa// 86%

TESTI4051054

TESTI4051388

TESTI4051424// M-protein, striated muscle.// 0// 511aa// 43%

TESTI4051504

TESTI4051747

TESTI4051858

TESTI4051865// Tight junction protein ZO-3 (Zonula occludens 3 protein)
(Zona occludens 3 protein) (Tight junction protein 3).// 0// 825aa// 88%

TESTI4051952

TESTI4052132

TESTI4052217

TESTI4052219// Potential phospholipid-transporting ATPase IH (EC 3.6.3.1
3).// 0// 670aa// 92%

TESTI4052430

TESTI4052598// C-type lectin-like receptor-1 [Homo sapiens]// 7.00E-29//
67aa// 33%

TESTI4052775// Krueppel-related zinc finger protein 1 (HKR1 protein) (Fr
agment).// 1.00E-29// 78aa// 32%

THYMU2008207

THYMU2038199

THYMU3000390

THYMU3000776

THYMU3001082

THYMU3001593

THYMU3001776

THYMU3002825// alpha 1,2-mannosidase [Homo sapiens]// 1.00E-169// 282aa/
/ 100%

THYMU3002887

THYMU3003007

THYMU3003350

THYMU3003958

THYMU3004628

THYMU3004632

THYMU3007308

THYMU3007559

THYMU3008105// Zinc finger protein 74.// 0// 490aa// 90%

THYMU3008935

THYMU3009643

THYMU3009755

THYMU3011012

THYMU3011244

THYMU3011360

THYMU3011534

THYMU3011556

THYMU3011717// exocyst component protein 70 kDa homolog (S. cerevisiae)/
/ 1.00E-25// 62aa// 100%

THYMU3012402// Importin alpha-1 subunit (Karyopherin alpha-1 subunit) (S
RP1-beta) (RAG cohort protein 2) (Nucleoprotein interactor 1) (NPI-1).//
0// 322aa// 95%

THYMU3012907

THYMU3012983// zinc finger protein 14 (KOX 6); G1OT-4 for gonadotropin i
nducible transcription repressor-4 [Homo sapiens]// 1.00E-156// 265aa//
54%

THYMU3013114

THYMU3013197

THYMU3013241

THYMU3013470

THYMU3013785// novel SH2-containing protein 3 [Homo sapiens]// 0// 457aa
// 90%

THYMU3013897

THYMU3014038

THYMU3014173// HLA class I histocompatibility antigen, alpha chain E*010
1/E*0102 precursor.// 8.00E-26// 60aa// 57%

THYMU3014372// DNA replication licensing factor MCM2 (Nuclear protein BM
28).// 0// 743aa// 96%

THYMU3014620// F-box protein Lilina [Homo sapiens].// 1.00E-123// 239aa/
/ 100%

THYMU3014701

THYMU3015042

THYMU3015457

THYMU3015571// 10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa
chaperonin) (CPN10).// 5.00E-18// 44aa// 100%

THYMU3015647// serpentine receptor (secretin receptor superfamily member
with s; serpentine receptor; secretin receptor [Mus musculus]// 4.00E-5
7// 151aa// 30%

THYMU3016518// Ig gamma-1 chain C region.// 0// 304aa// 94%

THYMU3016822// erythroblast macrophage protein [Mus musculus]// 1.00E-42
// 80aa// 97%

THYMU3017761

THYMU3018151

THYMU3018896

THYMU3019095

THYMU3019476

THYMU3019605

THYMU3019916

THYMU3020221// Ig gamma-1 chain C region.// 0// 315aa// 95%

THYMU3020869// BMAL1 protein (Brain and muscle ARNT-like 1) (Member of PAS protein 3) (MOP3) (BHLH-PAS protein JAP3).// 1.00E-45// 89aa// 83%

THYMU3020970

THYMU3021404// differentiation-associated Na-dependent inorganic phosphate cotr; differentiation-associated Na-dependent inorganic phosphate cotransporter [Homo sapiens]// 0// 417aa// 75%

THYMU3021586// Sterol regulatory element binding protein-1 (SREBP-1) (Sterol regulatory element-binding transcription factor 1).// 0// 774aa// 86%

THYMU3021755// solute carrier family 4, sodium bicarbonate cotransporter, member 8 [Homo sapiens]// 1.00E-169// 294aa// 93%

THYMU3021900

THYMU3022211

THYMU3022434// Monocytic leukemia zinc finger protein (Zinc finger protein 220).// 0// 537aa// 81%

THYMU3022528

THYMU3022668

THYMU3022982

THYMU3023107

THYMU3023394

THYMU3023400// amino acid transporter 2 [Homo sapiens]// 4.00E-19// 71aa// 25%

THYMU3023797

THYMU3024164

THYMU3024339

THYMU3025118// Cell surface glycoprotein MUC18 precursor (Melanoma-associated antigen MUC18) (Melanoma-associated antigen A32) (S-endo 1 endothelial-associated antigen) (CD146 antigen) (Melanoma adhesion molecule).// 0// 493aa// 95%

THYMU3025313

THYMU3025642

THYMU3025683// Ras interaction/interference protein 1.// 8.00E-36// 111aa// 30%

THYMU3025772

THYMU3026000// zinc finger protein interacting with K protein 1 [Mus musculus]// 0// 335aa// 70%

THYMU3026306// alpha 1,2-mannosidase [Homo sapiens]// 1.00E-169// 282aa// 100%

THYMU3026350

THYMU3026479// secretory pathway component Sec31B-1 [Homo sapiens]// 0// 385aa// 95%

THYMU3026532// Integrin beta-2 precursor (Cell surface adhesion glycoproteins LFA-1/CR3/p150,95 beta-subunit) (CD18) (Complement receptor C3 beta-subunit).// 0// 701aa// 93%

THYMU3026783

THYMU3026869

THYMU3027251

THYMU3027540

THYMU3027655

THYMU3027671// extra spindle poles, S. cerevisiae, homolog of [Homo sapiens]// 1.00E-176// 306aa// 91%

THYMU3028075

THYMU3028461

THYMU3028702// chromosome condensation-related SMC-associated protein 1;
chromosome condensation-related SMC-associated protein 1; KIAA0159 gene
product [Homo sapiens]// 0// 1278aa// 91%

THYMU3029188

THYMU3029318

THYMU3029421

THYMU3029719// AAA-ATPase TOB3 [Homo sapiens]// 6.00E-52// 105aa// 85%

THYMU3029774

THYMU3029795

THYMU3030072// Zinc finger protein 84 (Zinc finger protein HPF2).// 0//
365aa// 51%

THYMU3030706

THYMU3030752

THYMU3031146

THYMU3031402

THYMU3031612

THYMU3031868

THYMU3031878

THYMU3032032// Natural killer cell receptor BY55 precursor (CD160 antigen).// 2.00E-20// 46aa// 95%

THYMU3032798// Focal adhesion kinase 2 (EC 2.7.1.112) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase beta) (CAK beta).// 0// 51
2aa// 85%

THYMU3032867

THYMU3033626

THYMU3033630

THYMU3033649// T-cell surface glycoprotein CD3 zeta chain precursor (T-c

ell receptor T3 zeta chain).// 2.00E-57// 110aa// 94%

THYMU3033754// basement membrane-induced gene [Homo sapiens]// 6.00E-25/
/ 89aa// 32%

THYMU3033759// Eukaryotic translation initiation factor 4 gamma (eIF-4-g
amma) (eIF- 4G) (eIF4G) (P220).// 0// 522aa// 68%

THYMU3034099

THYMU3034453

THYMU3034616

THYMU3034671// histone deacetylase 7A, isoform b; histone deacetylase 7A
; histone deacetylase 7 [Homo sapiens]// 0// 412aa// 96%

THYMU3034853

THYMU3034867

THYMU3034983

THYMU3036200

THYMU3036310

THYMU3036934

THYMU3036953// mosaic serine protease [Homo sapiens]// 3.00E-13// 100aa/
/ 39%

THYMU3037052// HIV TAT specific factor 1; cofactor required for Tat acti
vation of HIV-1 transcription [Homo sapiens]// 1.00E-31// 80aa// 45%

THYMU3037192// potassium large conductance calcium-activated channel, su
bfamily M, alpha member 1 [Mus musculus]// 8.00E-94// 166aa// 100%

THYMU3037617

THYMU3037772// Ig gamma-1 chain C region.// 0// 313aa// 94%

THYMU3037827

THYMU3037856

THYMU3037867

THYMU3037909

THYMU3037980

THYMU3038158// Acetylcholinesterase collagenic tail peptide precursor (AChE Q subunit) (Acetylcholinesterase-associated collagen).// 1.00E-138// 237aa// 79%

THYMU3038167

THYMU3038214

THYMU3038266

THYMU3038347// tumor stroma and activated macrophage protein DLM-1 [Homo sapiens]// 3.00E-93// 159aa// 100%

THYMU3038375// interrupting locus; SCL interrupting locus [Homo sapiens]// 0// 573aa// 96%

THYMU3038603// WW domain binding protein 2 [Mus musculus]// 3.00E-48// 113aa// 98%

THYMU3038687

THYMU3038759

THYMU3038879

THYMU3038970

THYMU3039807

THYMU3039846

THYMU3040068

THYMU3040126

THYMU3040146

THYMU3040168

THYMU3040172// T-cell differentiation antigen CD6 precursor (T12) (TP120).// 0// 563aa// 84%

THYMU3040725

THYMU3040746// Ig gamma-2 chain C region.// 1.00E-166// 282aa// 88%

THYMU3040816// VAMP (vesicle-associated membrane protein)-associated protein B and C; VAMP-associated protein C; VAMP-associated protein B; VAMP-associated 33 kDa protein [Homo sapiens]// 1.00E-45// 91aa// 100%

THYMU3040829// Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) (A18 hnRNP).// 7.00E-34// 70aa// 100%

THYMU3040830// AD-012 protein [Homo sapiens]// 1.00E-28// 84aa// 97%

THYMU3041354

THYMU3041386

THYMU3041428// Homo sapiens prp28, U5 snRNP 100 kd protein [Homo sapiens]
]// 0// 599aa// 87%

THYMU3041573

THYMU3041603// gamma-tubulin complex protein 2 [Homo sapiens]// 1.00E-27
// 59aa// 100%

THYMU3041736

THYMU3041918

THYMU3042075

THYMU3042321

THYMU3042758

THYMU3043200// Splicing factor 3A subunit 3 (Spliceosome associated protein 61) (SAP 61) (SF3a60).// 0// 479aa// 95%

THYMU3043327

THYMU3043482

THYMU3043688

THYMU3043779// Phospholipid scramblase 4 (PL scramblase 4) (Ca²⁺ dependent phospholipid scramblase 4).// 6.00E-69// 123aa// 93%

THYMU3043883

THYMU3043993

THYMU3044075

THYMU3044188

THYMU3044441

THYMU3044445

THYMU3045510// dedicator of cyto-kinesis 2 [Mus musculus]// 0// 321aa//

85%

THYMU3045673

THYMU3045692

THYMU3045704

THYMU3046140

THYMU3046360// F-box only protein 3.// 0// 393aa// 95%

THYMU3047115// Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 (EC 3.6.3.8) (Calcium pump 1) (SERCA1) (SR Ca(2+)-ATPase 1) (Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform) (Endoplasmic reticulum class 1/2 Ca(2+) ATPase).// 0// 826aa// 95%

THYMU3047144

THYMU3047156

THYMU3047513

THYMU3047542

THYMU3047760// cleft lip and palate associated transmembrane protein 1 [Homo sapiens]// 3.00E-46// 80aa// 59%

THYMU3047891// oxidoreductase UCPA [Homo sapiens]// 8.00E-59// 111aa// 84%

TKIDN2000319

TKIDN2003396// Homo sapiens paternally expressed 10 (PEG10), mRNA// 3.00E-17// 310aa// 22%

TKIDN2010602

TKIDN2011051

TKIDN2011160// ADAM-TS 3 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 3) (ADAMTS-3) (ADAM-TS3) (Fragment).// 1.00E-114// 176aa// 64%

TLIVE2000142

TLIVE2001616// Zinc finger protein 84 (Zinc finger protein HPF2).// 1.00E-177// 285aa// 50%

TLIVE2007736// solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulatory factor 1 [Homo sapiens]// 2.00E-95// 172aa// 85%

TLIVE2008797

TLUNG2000654// Keratin, type II cytoskeletal 7 (Cytokeratin 7) (K7) (CK7).// 0// 361aa// 79%

TLUNG2001445// Ig alpha-1 chain C region.// 0// 326aa// 92%

TLUNG2001600// Ig gamma-4 chain C region.// 0// 311aa// 95%

TLUNG2001810

TLUNG2002055

TRACH2011057// D-type cyclin-interacting protein 1; MAID protein [Homo sapiens]// 3.00E-89// 161aa// 89%

TRACH2013585

TRACH2019080

TRACH2022113

TRACH2024730// SH3-domain binding protein 4 [Homo sapiens]// 1.00E-178// 320aa// 47%

TRACH3002188

TRACH3002293

TRACH3002752// ubiquitin-protein ligase e3 component n-recognin [Mus musculus]// 1.00E-24// 82aa// 30%

TRACH3002890

TRACH3003037// Putative Rho/Rac guanine nucleotide exchange factor (Rho/Rac GEF) (Faciogenital dysplasia protein homolog).// 3.00E-75// 175aa// 30%

TRACH3003357// SH3 domain protein D19; SH3 domain containing protein D19; SH3 domain-containing protein [Mus musculus]// 0// 321aa// 76%

TRACH3003458// Zinc finger protein 208.// 0// 436aa// 62%

TRACH3003872

TRACH3004113

TRACH3004288

TRACH3004412// clusterin-like 1 (retinal); unknown prepropeptide specific to rod photoreceptor [Homo sapiens]// 0// 445aa// 95%

TRACH3004424// Zinc finger protein 91 (Zinc finger protein HTF10) (HPF7)
.// 0// 559aa// 59%

TRACH3004596

TRACH3004747// organic anion transporter OATP-E [Homo sapiens]// 1.00E-1
29// 251aa// 40%

TRACH3005173// Breakpoint cluster region protein (EC 2.7.1.-).// 9.00E-8
5// 157aa// 83%

TRACH3005191// androgen-induced prostate proliferative shutoff associated protein [Homo sapiens]// 0// 516aa// 87%

TRACH3005274// Glycosyltransferase ALG11 (EC 2.4.1.-).// 1.00E-47// 104aa// 37%

TRACH3005699// mucin 16; CA125 ovarian cancer antigen [Homo sapiens]// 0
// 1037aa// 90%

TRACH3006379// Keratin, type II cytoskeletal 7 (Cytokeratin 7) (K7) (CK7).// 1.00E-106// 212aa// 74%

TRACH3006397

TRACH3006717

TRACH3006800// mucin 16; CA125 ovarian cancer antigen [Homo sapiens]// 0
// 901aa// 90%

TRACH3007274

TRACH3007625// Hemolysin III (HLY-III).// 8.00E-06// 60aa// 25%

TRACH3007689

TRACH3007995

TRACH3008042// Membrane component, chromosome 17, surface marker 2 (Ovarian carcinoma antigen CA125) (1A1-3B) (Next to BRCA1 gene 1 protein).//
0// 327aa// 100%

TRACH3008508// GC-rich sequence DNA-binding factor homolog.// 1.00E-109/
/ 198aa// 85%

TRACH3008632

TRACH3009008// Thioredoxin reductase (EC 1.6.4.5).// 0// 456aa// 95%

TRACH3009061// ATP-binding cassette, sub-family A, member 1 (ATP-binding
cassette transporter 1) (ATP-binding cassette 1) (ABC-1).// 1.00E-138//
265aa// 41%

TRACH3009701// dynein, axonemal, heavy polypeptide 9, isoform 2// 1.00E-
165// 329aa// 36%

TRACH3010079// Homo sapiens COP9 constitutive photomorphogenic homolog s
ubunit 5 (Arabidopsis) (COPS5)// 1.00E-143// 246aa// 91%

TRACH3010167// Transcription factor Sp3 (SPR-2) (Fragment).// 1.00E-40//
72aa// 67%

TRACH3010342// Nuclear receptor ROR-gamma (Nuclear receptor RZR-gamma)./
/ 4.00E-46// 86aa// 100%

TRACH3010382

TRACH3011082// Ig kappa chain V-III region HAH precursor.// 3.00E-51// 1
00aa// 77%

TRACH3011184// Ig kappa chain V-III region CLL precursor (Rheumatoid fac
tor).// 5.00E-53// 101aa// 78%

TRACH3011282// Allograft inflammatory factor-1 (AIF-1) (Ionized calcium-
binding adapter molecule 1).// 5.00E-46// 94aa// 56%

TRACH3011313// Branched-chain amino acid aminotransferase, cytosolic (EC
2.6.1.42) (BCAT(C)) (ECA39 protein).// 0// 320aa// 88%

TRACH3011454

TRACH3011503// UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX
) (Sperm- associated antigen 2) [Includes: UDP-N-acetylgalactosamine pyr
ophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophospho
rylase (EC 2.7.7.23) (AGX-2)].// 1.00E-109// 197aa// 55%

TRACH3011538

TRACH3012106// erythrocyte protein band 4.1-like 3 [Mus musculus]// 0//
610aa// 74%

TRACH3012460

TRACH3012659// Ig heavy chain V-III region VH26 precursor.// 4.00E-51//
95aa// 86%

TRACH3012718

TRACH3012864

TRACH3012891// ATPase, Class I, type 8B, member 1; benign recurrent intrahepatic cholestasis; progressive familial intrahepatic cholestasis 1, Byler disease; familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent); ATPase, Class I, type 8B, member 1 [Homo sapiens]// 6.00E-42// 85aa// 84%

TRACH3013043

TRACH3013072

TRACH3013684

TRACH3013900

TRACH3014063

TRACH3014183

TRACH3014580

TRACH3015136// Polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) (Protein- UDP acetylgalactosaminyltransferase) (UDP-GalNAc:polypeptide, N- acetylgalactosaminyltransferase) (GalNAc-T1).// 3.00E-67// 117aa//
56%

TRACH3015346

TRACH3015354

TRACH3015467

TRACH3015951// Zinc finger protein 151 (Myc-interacting zinc finger protein) (Miz-1 protein).// 4.00E-53// 156aa// 26%

TRACH3016264

TRACH3016368

TRACH3016455// calpain 10, isoform e; calcium-activated neutral protease
[Homo sapiens]// 1.00E-162// 267aa// 91%

TRACH3016805// Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythr
oid).// 1.00E-30// 106aa// 30%

TRACH3016885

TRACH3016992

TRACH3017409

TRACH3018108// 51 kDa FK506-binding protein (FKBP51) (Peptidyl-prolyl ci
s-trans isomerase) (EC 5.2.1.8) (PPiase) (Rotamase).// 0// 407aa// 89%

TRACH3018191

TRACH3018240

TRACH3018261// 1,2-alpha-mannosidase IC [Homo sapiens]// 4.00E-76// 139a
a// 100%

TRACH3018519// Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (
p102).// 1.00E-22// 47aa// 100%

TRACH3018524// Protein-tyrosine phosphatase beta precursor (EC 3.1.3.48)
(R-PTP- beta).// 0// 1251aa// 96%

TRACH3018606// SH3/ankyrin domain gene 3 [Rattus norvegicus]// 8.00E-26/
/ 80aa// 68%

TRACH3018783

TRACH3018907// Ig alpha-1 chain C region.// 0// 325aa// 92%

TRACH3018943

TRACH3019058// Ig delta chain C region.// 1.00E-78// 137aa// 99%

TRACH3019370// ATP-binding cassette, sub-family A, member 1 (ATP-binding
cassette transporter 1) (ATP-binding cassette 1) (ABC-1).// 1.00E-122//
264aa// 34%

TRACH3019621// UDP-N-acetylglucosamine--dolichyl-phosphate N- acetylgluc

osaminephosphotransferase (EC 2.7.8.15) (GPT) (G1PT) (N-acetylglucosamin
e-1-phosphate transferase) (GlcNAc-1-P transferase).// 0// 367aa// 89%
TRACH3019807// Antigen LY-9 precursor.// 4.00E-47// 103aa// 48%
TRACH3020137
TRACH3020563
TRACH3020605
TRACH3020769// Myosin heavy chain, nonmuscle type B (Cellular myosin hea
vy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).// 2.00E-31
// 159aa// 21%
TRACH3020930// Ig gamma-1 chain C region.// 1.00E-166// 284aa// 80%
TRACH3021023// Ig delta chain C region.// 0// 354aa// 92%
TRACH3021335
TRACH3021373// autoantigen [Homo sapiens]// 0// 836aa// 86%
TRACH3021544// ubiquitin-specific processing protease [Homo sapiens]// 1
.00E-127// 276aa// 44%
TRACH3021778// Nucleolin (Protein C23).// 6.00E-50// 100aa// 85%
TRACH3021834
TRACH3021883// Neuronal PAS domain protein 2 (Neuronal PAS2) (Member of
PAS protein 4) (MOP4).// 2.00E-73// 140aa// 75%
TRACH3022109// rec [Homo sapiens]// 1.00E-107// 173aa// 59%
TRACH3022198
TRACH3022296// DnaJ homolog subfamily B member 1 (Heat shock 40 kDa prot
ein 1) (Heat shock protein 40) (HSP40).// 9.00E-32// 63aa// 56%
TRACH3022732
TRACH3022758// dual oxidase 1 [Homo sapiens]// 0// 546aa// 97%
TRACH3022960// Dynein beta chain, ciliary.// 0// 386aa// 35%
TRACH3023063
TRACH3023203
TRACH3023242

TRACH3023373// Colorectal mutant cancer protein (MCC protein).// 0// 638
aa// 84%

TRACH3023516// 65 kDa FK506-binding protein precursor (EC 5.2.1.8) (FKBP
65) (FKBPRP) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (
Immunophilin FKBP65).// 0// 333aa// 60%

TRACH3023752

TRACH3023945

TRACH3023960// dynein, axonemal, heavy polypeptide 8 [Homo sapiens]// 0/
/ 551aa// 69%

TRACH3024020// calcium/calmodulin-dependent protein kinase kinase 1, alp
ha [Rattus norvegicus]// 1.00E-119// 208aa// 91%

TRACH3024081// Potential phospholipid-transporting ATPase ID (EC 3.6.3.1
3) (Fragment).// 5.00E-79// 136aa// 72%

TRACH3024342

TRACH3024423

TRACH3024428

TRACH3024512

TRACH3024671// squamous cell carcinoma antigen recognized by T cell [Hom
o sapiens]// 0// 602aa// 96%

TRACH3024823

TRACH3025316// Importin alpha-6 subunit (Karyopherin alpha-5 subunit) (I
mportin alpha S2).// 1.00E-165// 288aa// 92%

TRACH3025346// Organic cation/carnitine transporter 2 (Solute carrier fa
mily 22, member 5) (High-affinity sodium-dependent carnitine cotransport
er).// 1.00E-108// 195aa// 88%

TRACH3025520

TRACH3026283// ataxin 2; olivopontocerebellar ataxia 2, autosomal domina
nt [Homo sapiens]// 1.00E-100// 179aa// 69%

TRACH3026299// Ig delta chain C region.// 0// 353aa// 92%

TRACH3026303

TRACH3026542

TRACH3026650// Actin cross-linking family protein 7 (Macrophin) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).// 0// 351aa// 82%

TRACH3026676

TRACH3026949

TRACH3027229// Homo sapiens diacylglycerol 0-acyltransferase homolog 2 (mouse) (DGAT2), mRNA// 1.00E-64// 252aa// 48%

TRACH3027681

TRACH3027701// phosphatidylinositol 4-kinase type II [Homo sapiens]// 1.00E-158// 265aa// 68%

TRACH3028164

TRACH3028180// Zinc finger protein 29 (Zfp-29).// 0// 530aa// 86%

TRACH3028441// Ig delta chain C region.// 0// 355aa// 92%

TRACH3028597// pallidin [Homo sapiens]// 4.00E-21// 48aa// 100%

TRACH3028837// Smoothelin.// 0// 564aa// 60%

TRACH3028855

TRACH3029139

TRACH3029329

TRACH3029462// Actin cross-linking family protein 7 (Macrophin) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620).// 0// 735aa// 59%

TRACH3029520

TRACH3029592

TRACH3029670// Ig delta chain C region.// 0// 355aa// 92%

TRACH3030176// CDC4-like protein (Beige-like protein) (Fragment).// 1.00E-123// 278aa// 37%

TRACH3030855// Placental thrombin inhibitor (Cytoplasmic antiprotease) (CAP) (Protease inhibitor 6).// 1.00E-157// 272aa// 94%

TRACH3031316// Ig kappa chain V-IV region B17 precursor.// 2.00E-57// 10

9aa// 81%

TRACH3031660// cAMP-dependent protein kinase type II-beta regulatory chain.// 0// 384aa// 92%

TRACH3031678// Natural resistance-associated macrophage protein 2 (NRAMP 2) (Divalent metal transporter 1) (DMT1).// 0// 358aa// 91%

TRACH3032044

TRACH3032150// Cysteine sulfinic acid decarboxylase (EC 4.1.1.29) (Sulfinolalanine decarboxylase) (Cysteine-sulfinic acid decarboxylase).// 1.00E-126// 205aa// 60%

TRACH3032480

TRACH3032570// Homo sapiens syndecan binding protein (syntenin) (SDCBP), mRNA// 1.00E-167// 296aa// 99%

TRACH3033535

TRACH3034680// Ig delta chain C region.// 1.00E-150// 293aa// 63%

TRACH3035451

TRACH3036004

TRACH3036103// Ig heavy chain V-III region VH26 precursor.// 3.00E-48// 88aa// 75%

TRACH3036278

TRACH3036750// Zinc finger protein 135.// 3.00E-94// 148aa// 48%

TRACH3036792

TRACH3036897

TRACH3036932

TRACH3037505// Ig delta chain C region.// 0// 354aa// 92%

TRACH3038399// Eukaryotic translation initiation factor 2-alpha kinase 3 precursor (EC 2.7.1.-) (PRKR-like endoplasmic reticulum kinase) (Pancreatic eIF2-alpha kinase) (HsPEK).// 0// 912aa// 94%

TSTOM2000235

TSTOM2001571// Casein kinase I, delta isoform (EC 2.7.1.-) (CKI-delta)./

/ 1.00E-144// 248aa// 93%

TSTOM2002611// thiamin pyrophosphokinase [Mus musculus]// 6.00E-64// 119
aa// 65%

TSTOM2002682

TUTER1000014

TUTER2001433// Ig alpha-1 chain C region.// 0// 320aa// 92%

UTERU2000300

UTERU2014998

UTERU2016464

UTERU2016669

UTERU2020226

UTERU2022955

UTERU2023941

UTERU2024042// Casein kinase I, gamma 2 isoform (EC 2.7.1.-) (CKI-gamma
2).// 9.00E-46// 88aa// 73%

UTERU2027369

UTERU2028377

UTERU2029660

UTERU2035926

UTERU2037423// Zinc finger protein 135.// 4.00E-90// 144aa// 59%

UTERU3000670// shroom [Mus musculus]// 0// 1134aa// 62%

UTERU3001029// Echinoderm microtubule-associated protein-like 4 (EMAP-4)
(Restrictedly overexpressed proliferation-associated protein) (Ropp 120
).// 0// 388aa// 58%

UTERU3001394

UTERU3001946// mucin 16; CA125 ovarian cancer antigen [Homo sapiens]// 0
// 613aa// 89%

UTERU3004635// Neuroblast differentiation associated protein AHNAK (Desm
oyokin) (Fragments).// 0// 1453aa// 78%

UTERU3005264

UTERU3005422

UTERU3006538

UTERU3006720

UTERU3007108

UTERU3009775// PAPIN [Rattus norvegicus]// 2.00E-28// 95aa// 90%

UTERU3010029

UTERU3010409// Aortic preferentially expressed protein 1 (APEG-1).// 3.00E-61// 113aa// 100%

UTERU3010604// Indoleamine 2,3-dioxygenase (EC 1.13.11.42) (IDO) (Indole amine- pyrrole 2,3-dioxygenase).// 2.00E-38// 72aa// 55%

UTERU3010892// adaptor-related protein complex 3, delta 1 subunit; adapt in, delta [Homo sapiens]// 3.00E-48// 91aa// 100%

UTERU3010919// Serine/threonine-protein kinase NEK1 (EC 2.7.1.-) (NimA-related protein kinase 1).// 2.00E-58// 106aa// 43%

UTERU3011092

UTERU3011398// Collagen alpha 2(VI) chain precursor.// 1.00E-103// 184aa// 92%

UTERU3011558

UTERU3011579

UTERU3011837// NG-CAM related cell adhesion molecule precursor (NR-CAM) (BRAVO).// 1.00E-47// 126aa// 61%

UTERU3012293// zinc finger protein 14 (KOX 6); GIOT-4 for gonadotropin inducible transcription repressor-4 [Homo sapiens]// 1.00E-160// 278aa// 48%

UTERU3012414// Guanine nucleotide-binding protein, alpha-12 subunit (G alpha 12).// 1.00E-116// 211aa// 89%

UTERU3012476

UTERU3012599

UTERU3012999// Homo sapiens CD27-binding (Siva) protein (SIVA), transcript variant 1, mRNA// 1.00E-56// 104aa// 100%

UTERU3013167

UTERU3013302// nuclear protein [Homo sapiens]// 0// 515aa// 92%

UTERU3014274

UTERU3014647// Sorting nexin 7.// 4.00E-26// 48aa// 44%

UTERU3014906

UTERU3015011// Paxillin.// 1.00E-168// 262aa// 93%

UTERU3015299// NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-20KD) (CI-20KD) (PSS T subunit).// 1.00E-51// 97aa// 98%

UTERU3015647// Embigin precursor (Teratocarcinoma glycoprotein GP-70).// 8.00E-48// 93aa// 78%

UTERU3015844

UTERU3016070// Zinc finger protein 29 (Zfp-29).// 1.00E-94// 196aa// 39%

UTERU3016273

UTERU3016274

UTERU3016308// Smoothelin.// 0// 405aa// 65%

UTERU3017441// plakophilin 4 [Homo sapiens]// 0// 922aa// 88%

UTERU3017626// potassium voltage-gated channel, subfamily G, member 1; potassium channel KH2 [Homo sapiens]// 1.00E-119// 219aa// 87%

UTERU3017995// p47 [Homo sapiens]// 3.00E-55// 113aa// 87%

UTERU3018172

UTERU3018255

UTERU3019708// Regulator of nonsense transcripts 1 (Nonsense mRNA reducing factor 1) (NORF1) (Up-frameshift suppressor 1 homolog).// 0// 336aa// 90%

UTERU3020090

UTERU3021231// five SH3 domains [Mus musculus]// 3.00E-59// 101aa// 78%

UTERU3021850// ADAM-TS 7 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 7) (ADAMTS-7) (ADAM-TS7).// 2.0
OE-80// 163aa// 39%

UTERU3022168// membrane bound C2 domain containing protein [Rattus norvegicus]// 0// 810aa// 77%

UTERU3022588// Cyclic-AMP-dependent transcription factor ATF-2 (Activating transcription factor 2) (cAMP response element binding protein CRE- B P1) (HB16).// 0// 415aa// 85%

UTERU3022922

UTERU3023141

UTERU3023413

【 0 3 2 7 】

【配列表】

<210> 1957

<211> 406

<212> PRT

<213> Homo sapiens

<400> 1957

Met Asp Gly Asn Asp Asn Val Thr Leu Leu Phe Ala Pro Leu Leu Arg

1 5 10 15

Asp Asn Tyr Thr Leu Ala Pro Asn Ala Ser Ser Leu Gly Pro Gly Thr

20 25 30

Asp Leu Ala Leu Ala Pro Ala Ser Ser Ala Gly Pro Gly Pro Gly Leu

35 40 45

Ser Leu Gly Pro Gly Pro Ser Phe Gly Phe Ser Pro Gly Pro Thr Pro

50 55 60

Thr Pro Glu Pro Thr Thr Ser Gly Leu Ala Gly Gly Ala Ala Ser His

65 70 75 80

Gly Pro Ser Pro Phe Pro Arg Pro Trp Ala Pro His Ala Leu Pro Phe
 85 90 95
 Trp Asp Thr Pro Leu Asn His Gly Leu Asn Val Phe Val Gly Ala Ala
 100 105 110
 Leu Cys Ile Thr Met Leu Gly Leu Gly Cys Thr Val Asp Val Asn His
 115 120 125
 Phe Gly Ala His Val Arg Arg Pro Val Gly Ala Leu Leu Ala Ala Leu
 130 135 140
 Cys Gln Phe Gly Leu Leu Pro Leu Leu Ala Phe Leu Leu Ala Leu Ala
 145 150 155 160
 Phe Lys Leu Asp Glu Val Ala Ala Val Ala Val Leu Leu Cys Gly Cys
 165 170 175
 Cys Pro Gly Gly Asn Leu Ser Asn Leu Met Ser Leu Leu Val Asp Gly
 180 185 190
 Asp Met Asn Leu Ser Ile Ile Met Thr Ile Ser Ser Thr Leu Leu Ala
 195 200 205
 Leu Val Leu Met Pro Leu Cys Leu Trp Ile Tyr Ser Trp Ala Trp Ile
 210 215 220
 Asn Thr Pro Ile Val Gln Leu Leu Pro Leu Gly Thr Val Thr Leu Thr
 225 230 235 240
 Leu Cys Ser Thr Leu Ile Pro Ile Gly Leu Gly Val Phe Ile Arg Tyr
 245 250 255
 Lys Tyr Ser Arg Val Ala Asp Tyr Ile Val Lys Val Ser Leu Trp Ser
 260 265 270
 Leu Leu Val Thr Leu Val Val Leu Phe Ile Met Thr Gly Thr Met Leu
 275 280 285
 Gly Pro Glu Leu Leu Ala Ser Ile Pro Ala Ala Val Tyr Val Ile Ala
 290 295 300
 Ile Phe Met Pro Leu Ala Gly Tyr Ala Ser Gly Tyr Gly Leu Ala Thr

305 310 315 320
 Leu Phe His Leu Pro Pro Asn Cys Lys Arg Thr Val Cys Leu Glu Thr
 325 330 335
 Gly Ser Gln Asn Val Gln Leu Cys Thr Ala Ile Leu Lys Leu Ala Phe
 340 345 350
 Pro Pro Gln Phe Ile Gly Ser Met Tyr Met Phe Pro Leu Leu Tyr Ala
 355 360 365
 Leu Phe Gln Ser Ala Glu Ala Gly Ile Phe Val Leu Ile Tyr Lys Met
 370 375 380
 Tyr Gly Ser Glu Met Leu His Lys Arg Asp Pro Leu Asp Glu Asp Glu
 385 390 395 400
 Asp Thr Asp Ile Ser Tyr
 405

<210> 1958

<211> 496

<212> PRT

<213> Homo sapiens

<400> 1958

Met Asp Trp Ala Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
 1 5 10 15
 Val His Ser Gln Ala Gln Leu Val Gln Ser Gly Ala Glu Ala Lys Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Pro Phe
 35 40 45
 Ser Gly Tyr Val Leu His Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

Glu Trp Leu Gly Ser Ile Thr Ala Gly Tyr Asp Ala Thr Lys Tyr Ser
 65 70 75 80
 Gln Arg Phe Gln Asp Arg Ile Thr Ile Thr Arg Asp Thr Ser Ala Ser
 85 90 95
 Thr Val Tyr Leu Glu Trp Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
 100 105 110
 Leu Tyr Cys Ala Arg Glu Gly Asp Glu Asp Tyr Gly Asp Ser Leu Gly
 115 120 125
 Ala Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Pro Ala
 130 135 140
 Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Cys Ser Thr Gln
 145 150 155 160
 Pro Asp Gly Asn Val Val Ile Ala Cys Leu Val Gln Gly Phe Phe Pro
 165 170 175
 Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln Gly Val Thr
 180 185 190
 Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp Leu Tyr Thr
 195 200 205
 Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Leu Ala Gly Lys
 210 215 220
 Ser Val Thr Cys His Val Lys His Tyr Thr Asn Pro Ser Gln Asp Val
 225 230 235 240
 Thr Val Pro Cys Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser
 245 250 255
 Thr Pro Pro Thr Pro Ser Pro Ser Cys Cys His Pro Arg Leu Ser Leu
 260 265 270
 His Arg Pro Ala Leu Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu
 275 280 285
 Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala Ser Gly Val Thr Phe Thr

290	295	300
Trp Thr Pro Ser Ser Gly Lys Ser Ala Val Gln Gly Pro Pro Asp Arg		
305	310	315
Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala		
325	330	335
Glu Pro Trp Asn His Gly Lys Thr Phe Thr Cys Thr Ala Ala Tyr Pro		
340	345	350
Glu Ser Lys Thr Pro Leu Thr Ala Thr Leu Ser Lys Ser Gly Asn Thr		
355	360	365
Phe Arg Pro Glu Val His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala		
370	375	380
Leu Asn Glu Leu Val Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro		
385	390	395
Lys Asp Val Leu Val Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg		
405	410	415
Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr		
420	425	430
Thr Thr Phe Ala Val Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp		
435	440	445
Lys Lys Gly Asp Thr Phe Ser Cys Met Val Gly His Glu Ala Leu Pro		
450	455	460
Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr		
465	470	475
His Val Asn Val Ser Val Val Met Ala Glu Val Asp Gly Thr Cys Tyr		
485	490	495

<210> 1959

<211> 140

<212> PRT

<213> Homo sapiens

<400> 1959

Met Gly Leu Pro His Trp Tyr Pro Thr Pro Leu Pro Pro Gly Met Ala
1 5 10 15
Ala Phe Ala Thr Ala His Leu Leu Tyr Val Trp Ala Phe Gly Phe Ser
20 25 30
Pro Leu Gln Pro Gly Leu Leu Leu Leu Ile Ile Leu Ala Pro Gly Pro
35 40 45
Tyr Leu Ser Leu Val Leu Gln His Leu Glu Pro Asp Met Val Leu Pro
50 55 60
Val Ala Ala Tyr Gly Leu Ile Leu Met Ala Met Leu Trp Arg Gly Leu
65 70 75 80
Ala Gln Gly Gly Ser Ala Gly Trp Gly Ala Leu Leu Phe Thr Leu Ser
85 90 95
Asp Gly Val Leu Ala Trp Asp Thr Phe Ala Gln Pro Leu Pro His Ala
100 105 110
His Leu Val Ile Met Thr Thr Tyr Tyr Ala Ala Gln Leu Leu Ile Thr
115 120 125
Leu Ser Ala Leu Arg Ser Pro Val Pro Lys Thr Asp
130 135 140

<210> 1960

<211> 153

<212> PRT

<213> Homo sapiens

<400> 1960

Met Gly Gln Thr His Ser Cys Ser Gln Ala Pro Ser Val Trp Pro Thr
 1 5 10 15
 Asn Pro Ala Tyr Val Ser Asp Leu Thr Lys Arg Leu Asp Gln Val Tyr
 20 25 30
 Arg Arg Leu Glu Ser Pro Tyr Pro Trp Lys Trp Gly Glu Lys Arg Ile
 35 40 45
 Ser Ser Pro Arg Pro Lys Leu Val Ser Pro Val Val Gly Pro Glu His
 50 55 60
 Pro Glu Leu Trp Lys Leu Thr Val Ala Ser Tyr His Ile Arg Ile Trp
 65 70 75 80
 Ser Gly Asn Gln Val Met Gly Thr Arg Asn His Lys Pro Tyr Tyr Thr
 85 90 95
 Ile Asn Leu Asn Tyr Asn Leu Lys Ile Pro Leu Gln Ser Cys Val Lys
 100 105 110
 Pro Pro Tyr Met Leu Val Val Gly Asn Ile Ala Ile Lys Pro Asp Ser
 115 120 125
 Gln Thr Thr Thr Ser Glu Asn Cys Arg Leu Phe Thr Cys Ile Asp Ser
 130 135 140
 Thr Phe Asp Trp Gln Asn Gly Thr Leu
 145 150

<210> 1961

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1961

Met Lys Ser Trp Glu Asn Phe Ala Phe Arg Val Ser Ser Leu Cys Cys
 1 5 10 15
 Gln Ser Gly Val Gln Trp His Asp Leu Gly Pro Leu Gln Pro Pro Pro
 20 25 30
 Thr Arg Phe Lys Arg Leu Ser Cys Leu Ser Phe Pro Ser Ser Trp Asp
 35 40 45
 Tyr Lys Cys Thr Leu Pro His Pro Asp Val Pro Ala Pro Phe Val Glu
 50 55 60
 Asp Cys Ser Leu Pro Val Glu Leu Ser Trp His Ser Cys Gln Lys Gln
 65 70 75 80
 Phe Thr Arg Ile Val Arg Val Tyr Phe Trp Thr Leu Pro Leu Tyr Leu
 85 90 95
 Val Ser Asn Val Thr Asp Lys Val Lys Asp
 100 105

<210> 1962

<211> 116

<212> PRT

<213> Homo sapiens

<400> 1962

Met Phe Phe Lys Glu Phe Asn Gln Tyr Leu Thr Ser Ala Leu Asn Ile
 1 5 10 15
 Thr Leu Glu Ser Ser Ile Leu Leu Gln Ile Lys His Ile Ile Arg Asn
 20 25 30
 Cys Leu Leu Ser Val Glu Pro Ala Ile Ser Thr Lys His Leu Pro Tyr
 35 40 45
 Gln Ser Phe Gln Leu Phe Gly Phe Asp Phe Met Val Asp Glu Glu Leu

50 55 60
 Lys Val Trp Leu Ile Glu Val Asn Gly Ala Pro Ala Cys Ala Gln Lys
 65 70 75 80
 Leu Tyr Ala Glu Leu Cys Gln Gly Ile Val Asp Ile Ala Ile Ser Ser
 85 90 95
 Val Phe Pro Pro Pro Asp Val Glu Gln Pro Gln Thr Gln Pro Ala Ala
 100 105 110
 Phe Ile Lys Leu
 115

<210> 1963

<211> 235

<212> PRT

<213> Homo sapiens

<400> 1963

Met Phe Phe Trp Leu Ala Asn Phe Val Leu Ala Leu Gly Gln Val Thr
 1 5 10 15
 Leu Ala Gly Ala Phe Ala Ser Tyr Tyr Trp Ala Leu Arg Lys Pro Asp
 20 25 30
 Asp Leu Pro Ala Phe Pro Leu Ile Leu Ala Ile Val Gln Ile Ile Arg
 35 40 45
 Val Ile Leu Glu Tyr Leu Asp Gln Arg Leu Lys Ala Ala Glu Asn Lys
 50 55 60
 Phe Ala Lys Cys Leu Met Thr Cys Leu Lys Cys Cys Phe Trp Cys Leu
 65 70 75 80
 Glu Lys Phe Ile Lys Phe Leu Asn Arg Asn Ala Tyr Ile Met Ile Ala
 85 90 95

Ile Tyr Gly Thr Asn Phe Cys Thr Ser Ala Arg Asn Ala Phe Phe Leu
 100 105 110
 Leu Met Arg Asn Ile Ile Arg Val Ala Val Leu Asp Lys Val Thr Asp
 115 120 125
 Phe Leu Phe Leu Leu Gly Lys Leu Leu Ile Val Gly Ser Val Gly Ile
 130 135 140
 Leu Ala Phe Phe Phe Phe Thr His Arg Ile Arg Ile Val Gln Asp Thr
 145 150 155 160
 Ala Pro Pro Leu Asn Tyr Tyr Trp Val Pro Ile Leu Thr Val Ile Val
 165 170 175
 Gly Ser Tyr Leu Ile Ala His Gly Phe Phe Ser Val Tyr Gly Met Cys
 180 185 190
 Val Asp Thr Leu Phe Leu Cys Phe Leu Glu Asp Leu Glu Arg Asn Asp
 195 200 205
 Gly Ser Ala Glu Arg Pro Tyr Phe Met Ser Ser Thr Leu Lys Lys Leu
 210 215 220
 Leu Asn Lys Thr Asn Lys Lys Ala Ala Glu Ser
 225 230 235

<210> 1964

<211> 327

<212> PRT

<213> Homo sapiens

<400> 1964

Met Leu Leu His Leu Thr Gln His Lys Arg Phe His Ile Thr Glu Asn
 1 5 10 15
 Ser Tyr Gln Cys Lys Asp Cys Gly Lys Ala Phe Asn Trp Phe Ser Thr

20	25	30
Leu Thr Thr His Arg Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys		
35	40	45
Glu Glu Cys Gly Lys Ala Phe Asn Arg Ser Ser His Leu Thr Thr His		
50	55	60
Lys Ile Ile His Thr Gly Glu Lys Pro Tyr Arg Cys Glu Glu Cys Gly		
65	70	75
Lys Ala Phe Asn Arg Ser Ser His Leu Thr Thr His Lys Arg Ile His		
85	90	95
Thr Gly Val Lys Pro Tyr Lys Cys Thr Glu Cys Gly Lys Ala Phe Asn		
100	105	110
Arg Ser Ser His Leu Thr Thr His Arg Ile Ile His Thr Gly Glu Lys		
115	120	125
Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Gln Ser Ser Thr		
130	135	140
Leu Thr Thr His Lys Ile Thr His Ala Gly Glu Lys Pro Tyr Lys Cys		
145	150	155
Glu Glu Cys Gly Lys Ala Phe Tyr Arg Phe Ser Tyr Leu Thr Lys His		
165	170	175
Lys Thr Ser His Thr Gly Glu Lys Phe Tyr Lys Cys Glu Glu Cys Gly		
180	185	190
Lys Gly Phe Asn Trp Ser Ser Ala Leu Thr Lys His Lys Arg Ile His		
195	200	205
Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn		
210	215	220
Glu Ser Ser Asn Leu Thr Thr His Lys Met Ile His Thr Gly Glu Lys		
225	230	235
Pro Tyr Lys Cys Asp Glu Cys Gly Lys Ala Phe Asn Arg Ser Ser Gln		
245	250	255

Leu Thr Ala His Lys Met Ile His Thr Gly Glu Lys Pro Tyr Lys Cys
 260 265 270
 Glu Glu Cys Gly Lys Ala Phe Asn Arg Ser Ser Thr His Thr Lys His
 275 280 285
 Lys Ile Thr His Thr Gly Glu Lys Ser Tyr Lys Trp Glu Glu Cys Gly
 290 295 300
 Lys Asp Phe Asn Gln Ser Leu Ser Leu Ile Lys Gln Asn Asn Ser Tyr
 305 310 315 320
 Trp Arg Glu Thr Leu Gln Met
 325

<210> 1965

<211> 217

<212> PRT

<213> Homo sapiens

<400> 1965

Met Lys Arg Arg His Ile Ala Lys Pro Phe Ser Met Glu Lys Leu Leu
 1 5 10 15
 Tyr Gln Ile Ala Gln Ala Glu Ala Lys Lys Glu Asn Gly Pro Thr Leu
 20 25 30
 Ser Thr Ile Ser Ala Leu Leu Asp Glu Leu Arg Asp Thr Glu Leu Arg
 35 40 45
 Gln Arg Arg Gln Leu Phe Glu Ala Gly Leu His Ser Ser Ala Arg Tyr
 50 55 60
 Gly Ser His Asp Gly Ser Ser Thr Val Ala Asp Gly Lys Lys Lys Pro
 65 70 75 80
 Arg Lys Trp Leu Gln Leu Glu Thr Ser Glu Arg Arg Cys Gln Ile Cys

	85		90		95
Gln His Leu Cys Tyr Leu Ser Met Val Ser Pro Pro Gly Pro Ala Gly					
	100		105		110
Ala Leu Ala Cys Ser Ala Trp Pro Glu Ser Ser Gly Val Ala Pro Arg					
	115		120		125
Arg Gly Arg Ala Leu Ser Ala Gln Glu Thr Cys Cys Ala Pro Ile Ser					
	130		135		140
Gly Ala Gly Cys Gly Thr Ser Ala Glu Leu Leu Ala Ala Gly Gly Gly					
	145		150		155
					160
Cys Leu Thr His Ser Asp Gln Ala Thr Gln Arg Leu Ser Leu Cys Ser					
	165		170		175
Ala His Ala Trp Pro Ser Leu Gly Pro Ala Val Arg Pro Ser Ser Leu					
	180		185		190
Gly Ser Arg Trp Pro Pro Ser Pro Pro Tyr Phe Val Thr Pro Ala Pro					
	195		200		205
Thr His Ser Ala Leu Thr His Ser Phe					
	210		215		

<210> 1966

<211> 402

<212> PRT

<213> Homo sapiens

<400> 1966

Met Asn Gln Glu Asn Arg Ser Ser Phe Phe Trp Leu Leu Val Ile Phe			
1	5	10	15
Thr Phe Leu Leu Lys Ile Thr Ala Ser Phe Ser Met Ser Ala Tyr Val			
20	25	30	

Thr Val Thr Tyr Tyr Asn Glu Thr Ser Asn Tyr Thr Ala Ile Glu Thr
 35 40 45
 Cys Glu Cys Gly Val Tyr Gly Leu Ala Ser Pro Val Ala Asn Ala Met
 50 55 60
 Gly Val Val Gly Ile Pro Lys Asn Asn Asn Tyr Gln Ala Cys Asp His
 65 70 75 80
 Asn Thr Glu Phe Ser Asn Thr Lys Lys Pro Trp Ile Ala Leu Ile Glu
 85 90 95
 Arg Gly Asn Cys Thr Phe Ser Glu Lys Ile Gln Thr Ala Gly Arg Arg
 100 105 110
 Asn Ala Asp Ala Val Val Ile Tyr Asn Ala Pro Glu Thr Gly Asn Gln
 115 120 125
 Thr Ile Gln Met Ala Asn Phe Gly Ala Val Asp Ile Val Ala Ile Met
 130 135 140
 Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile Gln Arg Gly
 145 150 155 160
 Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His Gly Pro Trp
 165 170 175
 Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe Phe Ile Ile
 180 185 190
 Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala Arg Arg Leu
 195 200 205
 Arg Asn Ala Arg Ala Gln Ser Arg Lys Gln Arg Gln Leu Lys Ala Asp
 210 215 220
 Ala Lys Lys Ala Ile Gly Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly
 225 230 235 240
 Asp Lys Glu Ile Gly Pro Asp Gly Asp Ser Cys Ala Val Cys Ile Glu
 245 250 255
 Leu Tyr Lys Pro Asn Asp Leu Val Arg Ile Leu Thr Cys Asn His Ile

260					265					270						
Phe	His	Lys	Thr	Cys	Val	Asp	Pro	Trp	Leu	Leu	Glu	His	Arg	Thr	Cys	
275					280					285						
Pro	Met	Cys	Lys	Cys	Asp	Ile	Leu	Lys	Ala	Leu	Gly	Ile	Glu	Val	Asp	
290					295					300						
Val	Glu	Asp	Gly	Ser	Val	Ser	Leu	Gln	Val	Pro	Val	Ser	Asn	Glu	Ile	
305					310					315					320	
Ser	Asn	Ser	Ala	Ser	Ser	His	Glu	Glu	Asp	Asn	Arg	Ser	Glu	Thr	Ala	
325					330					335						
Ser	Ser	Gly	Tyr	Ala	Ser	Val	Gln	Gly	Thr	Asp	Glu	Pro	Pro	Leu	Glu	
340					345					350						
Glu	His	Val	Gln	Ser	Thr	Asn	Glu	Ser	Leu	Gln	Leu	Val	Asn	His	Glu	
355					360					365						
Ala	Asn	Ser	Val	Ala	Val	Asp	Val	Ile	Pro	His	Val	Asp	Asn	Pro	Thr	
370					375					380						
Phe	Glu	Glu	Asp	Glu	Thr	Pro	Asn	Gln	Glu	Thr	Ala	Val	Arg	Glu	Ile	
385					390					395					400	
Lys		Ser														

<210> 1967

<211> 408

<212> PRT

<213> Homo sapiens

<400> 1967

Met Thr Met Thr Ala Asn Lys Asn Ser Ser Ile Thr His Gly Ala Gly
1 5 10 15

Gly Thr Lys Ala Pro Arg Gly Thr Leu Ser Arg Ser Gln Ser Val Ser
 20 25 30
 Pro Pro Pro Val Leu Ser Pro Pro Arg Ser Pro Ile Tyr Pro Leu Ser
 35 40 45
 Asp Ser Glu Thr Ser Ala Cys Arg Tyr Pro Ser His Ser Ser Ser Arg
 50 55 60
 Val Leu Leu Lys Asp Arg His Pro Pro Ala Pro Ser Pro Gln Asn Pro
 65 70 75 80
 Gln Asp Pro Ser Pro Asp Thr Ser Pro Pro Thr Cys Pro Phe Lys Thr
 85 90 95
 Ala Ser Phe Gly Tyr Leu Asp Arg Ser Pro Ser Ala Cys Lys Arg Asp
 100 105 110
 Ala Gln Lys Glu Ser Val Gln Gly Ala Ala Gln Asp Val Ala Gly Val
 115 120 125
 Ala Ala Cys Leu Pro Leu Ala Gln Ser Thr Pro Phe Pro Gly Pro Ala
 130 135 140
 Ala Gly Pro Arg Gly Val Leu Leu Thr Arg Thr Gly Thr Arg Ala His
 145 150 155 160
 Ser Leu Gly Ile Arg Glu Glu Ile Ser Ala Trp Glu Gly Arg Arg Glu
 165 170 175
 Ala Ser Pro Arg Met Ser Met Cys Gly Glu Lys Arg Glu Gly Ser Gly
 180 185 190
 Ser Glu Trp Ala Ala Ser Glu Gly Cys Pro Ser Leu Gly Cys Pro Ser
 195 200 205
 Val Val Pro Ser Pro Cys Ser Ser Glu Lys Thr Phe Asp Phe Lys Gly
 210 215 220
 Leu Arg Arg Met Ser Arg Thr Phe Ser Glu Cys Ser Tyr Pro Glu Thr
 225 230 235 240
 Glu Glu Glu Gly Glu Ala Leu Pro Val Arg Asp Ser Phe Tyr Arg Leu

245 250 255
Glu Lys Arg Leu Gly Arg Ser Glu Pro Ser Ala Phe Leu Arg Gly Arg
260 265 270
Gly Ser Arg Lys Glu Ser Ser Ala Val Leu Ser Arg Ile Gln Lys Ile
275 280 285
Glu Gln Val Leu Lys Glu Gln Pro Gly Arg Gly Leu Pro Gln Leu Pro
290 295 300
Ser Ser Cys Tyr Ser Val Asp Arg Gly Lys Arg Asn Thr Gly Thr Leu
305 310 315 320
Gly Ser Leu Glu Glu Pro Ala Gly Gly Ala Ser Val Ser Ala Gly Ser
325 330 335
Arg Ala Val Gly Val Ala Gly Val Ala Gly Glu Ala Gly Pro Pro Pro
340 345 350
Glu Arg Glu Gly Ser Gly Ser Thr Lys Pro Gly Thr Pro Gly Asn Ser
355 360 365
Pro Ser Ser Gln Arg Leu Pro Ser Lys Ser Ser Leu Asp Pro Ala Val
370 375 380
Asn Pro Ile Leu Gln Ala Ser Pro Pro Leu Pro Ser Ser Tyr Pro Arg
385 390 395 400
Ile Leu Phe Val Asn Asn Leu Leu
405

<210> 1968

<211> 159

<212> PRT

<213> Homo sapiens

<400> 1968

Met Trp Val Pro Ala Pro Ser Leu Ala Leu Ser Ile Ser Leu Ser Pro
 1 5 10 15
 Thr Arg Gly Pro Gln Cys Ser Lys Ser Cys Ser Ser Gly Thr Arg Arg
 20 25 30
 Arg Gln Val Ile Cys Ala Ile Gly Pro Pro Ser His Cys Gly Ser Leu
 35 40 45
 Gln His Ser Lys Pro Val Asp Val Glu Pro Cys Asn Thr Gln Pro Cys
 50 55 60
 His Leu Pro Gln Gly Lys Asp Arg Arg Ala Gly Arg Ser Pro Ala Ser
 65 70 75 80
 Asp Leu Ser Pro Thr Arg Tyr Lys Pro Ser Lys His Val Leu Pro Arg
 85 90 95
 Gly Leu Cys Leu His Cys Val Ile Pro Leu Asp Pro Thr Ser Pro Met
 100 105 110
 Ser Pro Pro Ala Glu Pro Phe Ala Ile Ser Lys Ala His Leu Val Cys
 115 120 125
 Ser Pro Pro Gly Ser Pro Ala Phe Leu His Ser Ala Val Ala Cys Pro
 130 135 140
 Cys Pro Ser Gly Pro His Ser Met Leu Ser Phe Leu Trp Asp Pro
 145 150 155

<210> 1969

<211> 517

<212> PRT

<213> Homo sapiens

<400> 1969

Met Thr Arg Leu Gly Thr Val Pro Arg Lys Ala Leu Glu Met Ser Cys

1	5	10	15
Ala Ile Gln Asn Gln Leu Ala Arg Ile Leu Ala Glu Phe Glu Met Thr			
20	25	30	
Leu Glu Arg Asp Val Leu Gln Pro Leu Ser Arg Leu Ser Glu Glu Glu			
35	40	45	
Leu Pro Ala Ile Leu Lys His Lys Lys Ser Leu Gln Lys Leu Val Ser			
50	55	60	
Asp Trp Asn Thr Leu Lys Ser Arg Leu Ser Gln Ala Thr Lys Asn Ser			
65	70	75	80
Gly Ser Ser Gln Gly Leu Gly Gly Ser Pro Gly Ser His Ser His Thr			
85	90	95	
Thr Met Ala Asn Lys Val Glu Thr Leu Lys Glu Glu Glu Glu Glu Leu			
100	105	110	
Lys Arg Lys Val Glu Gln Cys Arg Asp Glu Tyr Leu Ala Asp Leu Tyr			
115	120	125	
His Phe Val Thr Lys Glu Asp Ser Tyr Ala Asn Tyr Phe Ile Arg Leu			
130	135	140	
Leu Glu Ile Gln Ala Asp Tyr His Arg Arg Ser Leu Ser Ser Leu Asp			
145	150	155	160
Thr Ala Leu Ala Glu Leu Arg Glu Asn His Gly Gln Ala Asp His Ser			
165	170	175	
Pro Ser Met Thr Ala Thr His Phe Pro Arg Val Tyr Gly Val Ser Leu			
180	185	190	
Ala Thr His Leu Gln Glu Leu Gly Arg Glu Ile Ala Leu Pro Ile Glu			
195	200	205	
Ala Cys Val Met Met Leu Leu Ser Glu Gly Met Lys Glu Glu Gly Leu			
210	215	220	
Phe Arg Leu Ala Ala Gly Ala Ser Val Leu Lys Arg Leu Lys Gln Thr			
225	230	235	240

Met Ala Ser Asp Pro His Ser Leu Glu Glu Phe Cys Ser Asp Pro His
 245 250 255
 Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro
 260 265 270
 Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp Met Arg Ala Ala Ser Leu
 275 280 285
 Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu Gln Glu Val Cys Ser Arg
 290 295 300
 Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg Tyr Leu Met Lys Phe Leu
 305 310 315 320
 Ala Arg Leu Ala Glu Glu Gln Glu Val Asn Lys Met Thr Pro Ser Asn
 325 330 335
 Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Pro Pro Glu Lys Glu
 340 345 350
 Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser Val Ser Ser Ile Gln Val
 355 360 365
 Val Gly Val Val Glu Ala Leu Ile Gln Ser Ala Asp Thr Leu Phe Pro
 370 375 380
 Gly Asp Ile Asn Phe Asn Val Ser Gly Leu Phe Ser Ala Val Thr Leu
 385 390 395 400
 Gln Asp Thr Val Ser Asp Arg Leu Ala Ser Glu Glu Leu Pro Ser Thr
 405 410 415
 Ala Val Pro Thr Pro Ala Thr Thr Pro Ala Pro Ala Pro Ala Pro Ala
 420 425 430
 Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala Ala Thr Lys Glu Arg Thr
 435 440 445
 Glu Ser Glu Val Pro Pro Arg Pro Ala Ser Pro Lys Val Thr Arg Ser
 450 455 460
 Pro Pro Glu Thr Ala Ala Pro Val Glu Asp Met Ala Arg Arg Ser Pro

465 470 475 480
 Arg Gly Ala Thr Gly Arg Lys Glu Arg Phe Ala Cys Ser Tyr Gly Thr
 485 490 495
 Asp Ser Ser Leu Val Asp Met Phe Phe Val Arg Leu Val Asn Lys Leu
 500 505 510
 Phe Trp Thr Lys Leu
 515

<210> 1970

<211> 142

<212> PRT

<213> Homo sapiens

<400> 1970

Met Trp Met Asp Arg Met Arg Cys Gly Pro Ser Leu Ile Tyr Ile His
 1 5 10 15
 Val Tyr Leu Phe Ile Ser Gly Trp Ala Lys Leu Ser Gln Leu Ser Cys
 20 25 30
 Asp Leu Ser Leu Thr Ser Leu Ser Phe Pro Met Thr Cys Asp Gly Ile
 35 40 45
 Phe Ser Ala Ser Trp Val Pro Ala Val Leu Gly Ser Gly Ser Ser Gly
 50 55 60
 Trp Phe Ser Val Ser Trp Val Leu Ala Val Leu Gly Ser Val Ser Ser
 65 70 75 80
 Gly Trp Phe Ser Val Ser Trp Val Leu Thr Leu Leu Glu Ser Gly Ser
 85 90 95
 Asp Gly Trp Phe Ser Val Ser Trp Val Pro Thr Val Leu Glu Ser Ser
 100 105 110

Ser Gly Gly Trp Phe Ser Ala Ser Trp Val Pro Ala Val Leu Gly Ser
115 120 125
Gly Gly Ser Ser Trp Phe Gly Gly Pro Leu Cys Cys Pro Cys
130 135 140

<210> 1971

<211> 308

<212> PRT

<213> Homo sapiens

<400> 1971

Met Arg Glu Arg Arg Arg Glu Arg Trp Lys Ala Lys Gly Gly Lys Leu
1 5 10 15
Arg Gly Gly Gly Ser Arg Asn Arg Asp Trp Asp Arg Leu Pro Ser Ala
20 25 30
Lys Arg Thr Gln Asn Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Ser
35 40 45
Ser Arg Val Ala Ala Val Ala Ala Ala Ala Pro Pro Glu Gly Gly Ser
50 55 60
Glu Gly Arg Leu Ala Pro Pro Ser Thr Ser His Ser Ser Leu Leu Ala
65 70 75 80
Phe Phe Pro Thr Val Pro Arg Ser Ala Arg Leu Arg Pro Arg Ser Ala
85 90 95
His Ala Arg Pro His Ala Tyr Glu Cys Leu Arg Ala Arg Arg Trp Leu
100 105 110
Leu Pro Pro Thr Thr Thr Phe Gly Arg Pro Ala Arg Gln Pro Ala Arg
115 120 125
Thr Arg Ser Pro Thr Gly Thr Pro Ser Ser Ser Pro Ser Leu Pro Leu

130 135 140
Arg Pro Cys Gln Ala Gly Ala Gly Ala Gly Pro His Ala Tyr Leu Gln
145 150 155 160
Arg Arg Lys Pro Lys Pro Pro Pro Pro Pro Pro Pro Pro Pro Leu Leu
165 170 175
Ser Ser Pro Pro Phe Pro Ala Pro Thr Ala Thr Asn Arg Arg His Gly
180 185 190
Arg Arg Arg Arg Arg Gln Pro Pro Leu Pro Pro Ser Thr Pro Arg Ala
195 200 205
Cys Ala Ser His Asn Pro Pro Arg Gly Thr Val Pro Phe Leu Ser Ala
210 215 220
Ala Gly Ala Gly Glu Glu Gly Thr Gly Arg Ala Gly Arg Gly Leu Pro
225 230 235 240
Phe Asp Trp Asn Cys Gln Asn Gly Gly Pro Ser Pro Thr Thr Thr Tyr
245 250 255
Leu Pro Gly Leu Leu Ala Ala Ala Leu Arg Leu Ala Ser Leu Cys Ser
260 265 270
Ser Ser Ser Ala Gly Ser Arg Arg Ala Asp Arg Gly Leu Pro Ser Ala
275 280 285
Pro Leu Pro Thr Gly Gly Trp Arg Pro Arg Arg Leu Arg Val Glu Ser
290 295 300
Phe Pro Ala Gly
305

<210> 1972

<211> 134

<212> PRT

<213> Homo sapiens

<400> 1972

Met Gly Val Ser Gly Gln Glu Gly Arg Leu Lys Pro Ala Leu Thr Ala
 1 5 10 15
 Val Thr His Ser His Ser Lys Leu Cys Ile Trp Ala Ser Arg His Ser
 20 25 30
 Ala Ser Thr Trp Arg Phe Leu Thr Cys Ala Val Ser Arg Arg Asp Trp
 35 40 45
 Ala Cys Thr Phe His Ser Ile Val Lys Asn Ala His Pro Thr Leu Leu
 50 55 60
 Ala Lys Ala Pro Ser Phe Ser Val Leu Tyr Ala Ser Arg Cys Phe Arg
 65 70 75 80
 Ala Phe Ser Met Leu Met Gly Asp Leu Ser Thr Ser Ala His Val Ser
 85 90 95
 Thr Arg Ala His Leu Asp Ser Thr Ala Ala Thr Lys Tyr Arg Asn Pro
 100 105 110
 Cys Trp Gly His Met Ala Asn Gln Gly Ser Ser Gly Ala Glu Asp Ser
 115 120 125
 Leu Thr Ser Glu Ser Cys
 130

<210> 1973

<211> 137

<212> PRT

<213> Homo sapiens

<400> 1973

Met Met Ala Met Leu Met Leu Pro Leu Gln Gly Phe Leu Glu Asp Lys

1	5	10	15
Ala Arg Arg Ala Trp Glu Ala Leu Pro Pro Arg Cys Ser Gln Cys Ser			
20	25	30	
Phe Ile Pro Phe Leu Pro Cys Phe Leu Leu Pro Ser Ala Phe Ser Pro			
35	40	45	
Arg His Cys Leu Pro Pro Ser Pro Arg Pro Ala Ile Gln Thr Leu Thr			
50	55	60	
Leu Ala Leu Ser Ser Met Arg Pro Ser Glu Met Ala Leu Ala Ala Thr			
65	70	75	80
Ser Glu Gly Ala Ala Pro Ile His Leu Gln Ile Arg Ile Ser Gly His			
85	90	95	
Pro Leu Pro Gly Leu Ser Cys Cys Cys Phe Ile Ser Gln Glu Pro Arg			
100	105	110	
His Leu Phe Ser Asn Trp Val Glu Phe Leu Glu Leu Lys Ser Asn Ser			
115	120	125	
Ala Leu Arg Gly Met Arg Leu Trp Met			
130	135		

<210> 1974

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1974

Met Gly Asn Leu Arg Gly Lys Arg Gln Gly Pro Ala Cys Pro Ala Met			
1	5	10	15
Arg Gly Ile Pro Cys Pro Pro Ala Leu Cys Leu Pro Arg Trp Asn Val			
20	25	30	

Gly Pro Cys Ser Pro Ser Gly Cys Ala Val Ser Asp Leu Cys Leu His
 35 40 45
 Pro Arg Gly Val Ser Ala Ser Ser Pro Pro Arg Ser Gly Cys Gly Pro
 50 55 60
 Ala Ala Cys Cys Gly Val Leu Thr Cys Val Thr Thr Ala Pro Leu Ala
 65 70 75 80
 Pro Gly Gly Val Met Val Ser Ser Trp Met Leu Leu Leu Glu Ser Phe
 85 90 95
 Phe Leu Ile Asn Leu Leu Gln Leu Arg
 100 105

<210> 1975

<211> 413

<212> PRT

<213> Homo sapiens

<400> 1975

Met Glu Leu Met His Ala Glu Lys Leu Arg Lys Glu Lys Glu Glu Phe
 1 5 10 15
 Glu Lys Ala Ser Met Asp Val Glu Asn Pro Asp Tyr Ser Glu Glu Ile
 20 25 30
 Leu Lys Gly Glu Leu Ala Trp Ile Ile Tyr Lys Asn Ser Val Ser Ile
 35 40 45
 Ile Lys Gly Ala Glu Phe His Val Ser Leu Leu Ser Ile Ala Gln Leu
 50 55 60
 Phe Asp Phe Ala Lys Asp Leu Gln Lys Glu Ile Tyr Asp Asp Leu Gln
 65 70 75 80
 Ala Leu His Thr Asp Asp Pro Leu Thr Trp Asp Tyr Val Ala Arg Arg

	85		90		95
Glu Leu Glu Ile Glu Ser Gln Thr	Glu Glu Gln Pro Thr Thr Lys Gln				
100	105	110			
Ala Lys Ala Val Glu Val Gly Arg Lys Glu Glu Arg Cys Cys Ala Val					
115	120	125			
Tyr Glu Glu Ala Val Lys Thr Leu Pro Thr Glu Ala Met Trp Lys Cys					
130	135	140			
Tyr Ile Thr Phe Cys Leu Glu Arg Phe Thr Lys Lys Ser Asn Ser Gly					
145	150	155	160		
Phe Leu Arg Gly Lys Arg Leu Glu Arg Thr Met Thr Val Phe Arg Lys					
165	170	175			
Ala His Glu Leu Lys Leu Leu Ser Glu Cys Gln Tyr Lys Gln Leu Ser					
180	185	190			
Val Ser Leu Leu Cys Tyr Asn Phe Leu Arg Glu Ala Leu Glu Val Ala					
195	200	205			
Val Ala Gly Thr Glu Leu Phe Arg Asp Ser Gly Thr Met Trp Gln Leu					
210	215	220			
Lys Leu Gln Val Leu Ile Glu Ser Lys Ser Pro Asp Ile Ala Met Leu					
225	230	235	240		
Phe Glu Glu Ala Phe Val His Leu Lys Pro Gln Val Cys Leu Pro Leu					
245	250	255			
Trp Ile Ser Trp Ala Glu Trp Ser Glu Gly Ala Lys Ser Gln Glu Asp					
260	265	270			
Thr Glu Ala Val Phe Lys Lys Ala Leu Leu Ala Val Ile Gly Ala Asp					
275	280	285			
Ser Val Thr Leu Lys Asn Lys Tyr Leu Asp Trp Ala Tyr Arg Ser Gly					
290	295	300			
Gly Tyr Lys Lys Ala Arg Ala Val Phe Lys Ser Leu Gln Glu Ser Arg					
305	310	315	320		

出証特 2 0 0 4 - 3 0 5 9 6 6 1

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Ser Leu Gln Asp Lys Leu Pro Val Ala Asp Ile Lys Ala Val Val Thr
 305 310 315 320
 Gly Lys Asp Cys Pro His Met Lys Glu Lys Gly Ala Leu Lys Gln Asn
 325 330 335
 Lys Glu Val Leu Glu Leu Ala Phe Ser Ile Leu Tyr Asp Ser Asn Cys
 340 345 350
 Gln Leu Asn Phe Ile Ala Pro Asp Lys His Glu Tyr Cys Ile Trp Thr
 355 360 365
 Asp Gly Leu Asn Ala Leu Leu Gly Lys Asp Met Met Ser Asp Leu Thr
 370 375 380
 Arg Asn Asp Leu Asp Thr Leu Leu Ser Met Glu Ile Lys Leu Arg Leu
 385 390 395 400
 Leu Asp Leu Glu Asn Ile Gln Ile Pro Asp Ala Pro Pro Pro Ile Pro
 405 410 415
 Lys Glu Pro Ser Asn Tyr Asp Phe Val Tyr Asp Cys Asn
 420 425

<210> 1977

<211> 197

<212> PRT

<213> Homo sapiens

<400> 1977

Met Pro Arg Pro Leu Ala Ser Ser Leu Ser Ser Val Met Gly Gln Thr
 1 5 10 15
 Val Ser Gln Glu Ala Ala Pro Pro Pro Gly Ser Gln Gly Trp Phe Trp
 20 25 30
 Trp Ser Phe Ser Ile Pro Gly Leu Tyr Leu Leu Gly Val Asp Leu Val

35 40 45
Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe Phe Gln Val
50 55 60
Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr Leu Gln Arg
65 70 75 80
Leu Pro Lys Val Ile Arg Asn Gln Ser Leu Val Asn Glu Leu Ala Phe
85 90 95
Thr Ala Arg Lys Met Met Ala Asp Glu Ala Leu Gly Ser Gly Leu Val
100 105 110
Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu Asp Ala Ala Leu Ala
115 120 125
Leu Ala Ala Glu Ile Ser Ser Lys Ser Pro Val Ala Val Gln Ser Thr
130 135 140
Lys Val Asn Leu Leu Tyr Ser Arg Asp His Ser Val Ala Glu Ser Leu
145 150 155 160
Asn Tyr Val Ala Ser Trp Asn Met Ser Met Leu Gln Thr Gln Asp Leu
165 170 175
Val Lys Ser Val Gln Ala Thr Thr Glu Asn Lys Glu Leu Lys Thr Val
180 185 190
Thr Phe Ser Lys Leu
195

<210> 1978

<211> 310

<212> PRT

<213> Homo sapiens

<400> 1978

Met Glu Asp Leu Glu Glu Asp Val Arg Phe Ile Val Asp Glu Thr Leu
 1 5 10 15
 Asp Phe Gly Gly Leu Ser Pro Ser Asp Ser Arg Glu Glu Glu Asp Ile
 20 25 30
 Thr Val Leu Val Thr Pro Glu Lys Pro Leu Arg Arg Gly Leu Ser His
 35 40 45
 Arg Ser Asp Pro Asn Ala Val Ala Pro Ala Pro Gln Gly Val Arg Leu
 50 55 60
 Ser Leu Gly Pro Leu Ser Pro Glu Lys Leu Glu Glu Ile Leu Asp Glu
 65 70 75 80
 Ala Asn Arg Leu Ala Ala Gln Leu Glu Gln Cys Ala Leu Gln Asp Arg
 85 90 95
 Glu Ser Ala Gly Glu Gly Leu Gly Pro Arg Arg Val Lys Pro Ser Pro
 100 105 110
 Arg Arg Glu Thr Phe Val Leu Lys Asp Ser Pro Val Arg Asp Leu Leu
 115 120 125
 Pro Thr Val Asn Ser Leu Thr Arg Ser Thr Pro Ser Pro Ser Ser Leu
 130 135 140
 Thr Pro Arg Leu Arg Ser Asn Asp Arg Lys Gly Ser Val Arg Ala Leu
 145 150 155 160
 Arg Ala Thr Ser Gly Lys Arg Pro Ser Asn Met Lys Arg Glu Ser Pro
 165 170 175
 Thr Cys Asn Leu Phe Pro Ala Ser Lys Ser Pro Ala Ser Ser Pro Leu
 180 185 190
 Thr Arg Ser Thr Pro Pro Val Arg Gly Arg Ala Gly Pro Ser Gly Arg
 195 200 205
 Ala Ala Ala Ser Glu Glu Thr Arg Ala Ala Lys Leu Arg Ala Cys Gln
 210 215 220
 Pro Asn Ala Thr His Gln Pro Glu Cys Ala Thr Trp Gln Arg Cys Pro

225	230	235	240
Thr Ser Gly Phe Ser Val Asn Ser Lys Arg Ala Ser Lys Thr Lys His			
	245	250	255
Cys Arg Thr Gln Ser Ala Gly Lys Trp Thr Gln Gly Ser Cys Phe Pro			
	260	265	270
Ala Thr Lys Ser Ser Cys His Gly Cys His Ser Gln Gln Ser Ala Ala			
	275	280	285
Pro Gln Glu Ser Gly Ser Pro Arg Thr Tyr Gln Val Lys Arg Ser Gly			
	290	295	300
Gln Gln Ala Arg Leu Gln			
305	310		

<210> 1979

<211> 339

<212> PRT

<213> Homo sapiens

<400> 1979

Met Ser Gly Gln Leu Glu Arg Cys Glu Arg Glu Trp His Glu Leu Glu			
1	5	10	15
Gly Glu Phe Gln Glu Leu Gln Glu Thr His Arg Ile Tyr Lys Gln Lys			
	20	25	30
Leu Glu Glu Leu Ala Ala Leu Gln Thr Leu Cys Ser Ser Ser Ile Ser			
	35	40	45
Lys Gln Lys Lys His Leu Lys Asp Leu Lys Leu Thr Leu Gln Arg Cys			
	50	55	60
Lys Arg His Ala Ser Arg Glu Glu Ala Glu Leu Val Gln Gln Met Ala			
	65	70	75
			80

Ala Asn Ile Lys Glu Arg Gln Asp Val Phe Phe Asp Met Glu Ala Tyr			
	85	90	95
Leu Pro Lys Lys Asn Gly Leu Tyr Leu Asn Leu Val Leu Gly Asn Val			
	100	105	110
Asn Val Thr Leu Leu Ser Asn Gln Ala Lys Phe Ala Tyr Lys Asp Glu			
	115	120	125
Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu Leu Leu Gly Ala			
	130	135	140
Val Ala Cys Arg Phe Val Leu His Tyr Arg Val Thr Asp Glu Val Phe			
	145	150	155
Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser			
	165	170	175
Ile Leu Ile Ser Asn Gly Ser Arg Ile Lys Gly Trp Trp Val Ser His			
	180	185	190
His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu Thr Trp Pro Asn			
	195	200	205
Gly Pro Ile Tyr Gln Lys Phe Arg Asn Gln Phe Leu Ala Phe Ser Ile			
	210	215	220
Phe Gln Ser Cys Val Gln Phe Leu Gln Tyr Tyr Tyr Gln Arg Gly Cys			
	225	230	235
Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg Asn His Leu Asp Leu Thr			
	245	250	255
Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu Thr Phe Leu Leu			
	260	265	270
Pro Phe Leu Phe Cys Gly His Phe Trp Gln Leu Tyr Asn Ala Val Thr			
	275	280	285
Leu Phe Glu Leu Ser Ser His Glu Glu Cys Arg Glu Trp Gln Val Phe			
	290	295	300
Val Leu Ala Phe Thr Phe Leu Ile Leu Phe Leu Gly Asn Phe Leu Thr			

305 310 315 320
 Thr Leu Lys Val Val His Ala Lys Leu Gln Lys Asn Arg Gly Lys Thr
 325 330 335
 Lys Gln Pro

<210> 1980

<211> 109

<212> PRT

<213> Homo sapiens

<400> 1980

Met Arg Pro Pro Gln Pro Cys Gly Thr Asp Pro Cys Pro Leu Cys Asp
 1 5 10 15
 Glu Ala Lys Glu Val Leu Lys Pro Tyr Glu Asn Gly Gln Pro Tyr Lys
 20 25 30
 Asp Gln Lys Leu Pro Gly Thr Arg Arg Arg Arg Ser Pro Ser Ser Pro
 35 40 45
 Ser His Pro His Met Ala Ser Gln Ser Gly Lys Arg Tyr Asn Leu Thr
 50 55 60
 Leu Asn Gln Val Leu Ser Phe Asp Tyr Asp Met Gly Leu Asp Ala Pro
 65 70 75 80
 Lys Thr Ile Ser Ser Asp Cys Gly Ala Phe Tyr Cys Leu Arg Met Phe
 85 90 95
 Lys Ser Pro Asp Met Thr Cys Cys Phe Tyr Pro Lys Gln
 100 105

<210> 1981

<211> 454

<212> PRT

<213> Homo sapiens

<400> 1981

Met Lys Phe Ala Phe Glu Glu Phe His Leu Trp Tyr Gln Phe Ala Leu

1 5 10 15

Ser Leu Met Ala Ala Gly Lys Ser Ala Arg Ala Val Lys Val Leu Lys

20 25 30

Glu Cys Ile Arg Leu Lys Pro Asp Asp Ala Thr Ile Pro Leu Leu Ala

35 40 45

Ala Lys Leu Cys Met Gly Ser Leu His Trp Leu Glu Glu Ala Glu Lys

50 55 60

Phe Ala Lys Thr Val Val Asp Val Gly Glu Lys Thr Ser Glu Phe Lys

65 70 75 80

Ala Lys Gly Tyr Leu Ala Leu Gly Leu Thr Tyr Ser Leu Gln Ala Thr

85 90 95

Asp Ala Ser Leu Arg Gly Met Gln Glu Val Leu Gln Arg Lys Ala Leu

100 105 110

Leu Ala Phe Gln Arg Ala His Ser Leu Ser Pro Thr Asp His Gln Ala

115 120 125

Ala Phe Tyr Leu Ala Leu Gln Leu Ala Ile Ser Arg Gln Ile Pro Glu

130 135 140

Ala Leu Gly Tyr Val Arg Gln Ala Leu Gln Leu Gln Gly Asp Asp Ala

145 150 155 160

Asn Ser Leu His Leu Leu Ala Leu Leu Leu Ser Ala Gln Lys His Tyr

165 170 175

His Asp Ala Leu Asn Ile Ile Asp Met Ala Leu Ser Glu Tyr Pro Glu

180	185	190
Asn Phe Ile Leu Leu Phe Ser Lys Val Lys Leu Gln Ser Leu Cys Arg		
195	200	205
Gly Pro Asp Glu Ala Leu Leu Thr Cys Lys His Met Leu Gln Ile Trp		
210	215	220
Lys Ser Cys Tyr Asn Leu Thr Asn Pro Ser Asp Ser Gly Arg Gly Ser		
225	230	235
Ser Leu Leu Asp Arg Thr Ile Ala Asp Arg Arg Gln Leu Asn Thr Ile		
245	250	255
Thr Leu Pro Asp Phe Ser Asp Pro Glu Thr Gly Ser Val His Ala Thr		
260	265	270
Ser Val Ala Ala Ser Arg Val Glu Gln Ala Leu Ser Glu Val Ala Ser		
275	280	285
Ser Leu Gln Ser Ser Ala Pro Lys Gln Gly Pro Leu His Pro Trp Met		
290	295	300
Thr Leu Ala Gln Ile Trp Leu His Ala Ala Glu Val Tyr Ile Gly Ile		
305	310	315
Gly Lys Pro Ala Glu Ala Thr Ala Cys Thr Gln Glu Ala Ala Asn Leu		
325	330	335
Phe Pro Met Ser His Asn Val Leu Tyr Met Arg Gly Gln Ile Ala Glu		
340	345	350
Leu Arg Gly Ser Met Asp Glu Ala Arg Arg Trp Tyr Glu Glu Ala Leu		
355	360	365
Ala Ile Ser Pro Thr His Val Lys Ser Met Gln Arg Leu Ala Leu Ile		
370	375	380
Leu His Gln Leu Gly Arg Tyr Ser Leu Ala Glu Lys Ile Leu Arg Asp		
385	390	395
Ala Val Gln Val Asn Ser Thr Ala His Glu Val Trp Asn Gly Leu Gly		
405	410	415

Glu Val Leu Gln Ala Gln Gly Asn Asp Ala Ala Ala Thr Glu Cys Phe
 420 425 430
 Leu Thr Ala Leu Glu Leu Glu Ala Ser Ser Pro Ala Val Pro Phe Thr
 435 440 445
 Ile Ile Pro Arg Val Leu
 450

<210> 1982

<211> 391

<212> PRT

<213> Homo sapiens

<400> 1982

Met Lys Val Leu Gly His Arg Leu Glu Leu Leu Thr Gly Leu Leu Leu
 1 5 10 15
 His Asp Val Thr Met Ala Gly Leu Gln Glu Leu Arg Phe Pro Glu Glu
 20 25 30
 Lys Pro Leu Leu Arg Gly Gln Asp Ala Thr Glu Leu Glu Ser Ser Asp
 35 40 45
 Ala Phe Leu Leu Ala Ala Asp Thr Asp Trp Lys Glu His Asp Ile Glu
 50 55 60
 Thr Pro Tyr Gly Leu Leu His Val Val Ile Arg Gly Ser Pro Lys Gly
 65 70 75 80
 Asn Arg Pro Ala Ile Leu Thr Tyr His Asp Val Gly Leu Asn His Lys
 85 90 95
 Leu Cys Phe Asn Thr Phe Phe Asn Phe Glu Asp Met Gln Glu Ile Thr
 100 105 110
 Lys His Phe Val Val Cys His Val Asp Ala Pro Gly Gln Gln Val Gly

115 120 125
Ala Ser Gln Phe Pro Gln Gly Tyr Gln Phe Pro Ser Met Glu Gln Leu
130 135 140
Ala Ala Met Leu Pro Ser Val Val Gln His Phe Gly Phe Lys Tyr Val
145 150 155 160
Ile Gly Ile Gly Val Gly Ala Gly Ala Tyr Val Leu Ala Lys Phe Ala
165 170 175
Leu Ile Phe Pro Asp Leu Val Glu Gly Leu Val Leu Val Asn Ile Asp
180 185 190
Pro Asn Gly Lys Gly Trp Ile Asp Trp Ala Ala Thr Lys Leu Ser Gly
195 200 205
Leu Thr Ser Thr Leu Pro Asp Thr Val Leu Ser His Leu Phe Ser Gln
210 215 220
Glu Glu Leu Val Asn Asn Thr Glu Leu Val Gln Ser Tyr Arg Gln Gln
225 230 235 240
Ile Gly Asn Val Val Asn Gln Ala Asn Leu Gln Leu Phe Trp Asn Met
245 250 255
Tyr Asn Ser Arg Arg Asp Leu Asp Ile Asn Arg Pro Gly Thr Val Pro
260 265 270
Asn Ala Lys Thr Leu Arg Cys Pro Val Met Leu Val Val Gly Asp Asn
275 280 285
Ala Pro Ala Glu Asp Gly Val Val Glu Cys Asn Ser Lys Leu Asp Pro
290 295 300
Thr Thr Thr Thr Phe Leu Lys Met Ala Asp Ser Gly Gly Leu Pro Gln
305 310 315 320
Val Thr Gln Pro Gly Lys Leu Thr Glu Ala Phe Lys Tyr Phe Leu Gln
325 330 335
Gly Met Gly Tyr Met Pro Ser Ala Ser Met Thr Arg Leu Ala Arg Ser
340 345 350

Arg Thr Ala Ser Leu Thr Ser Ala Ser Ser Val Asp Gly Ser Arg Pro
 355 360 365
 Gln Ala Cys Thr His Ser Glu Ser Ser Glu Gly Leu Gly Gln Val Asn
 370 375 380
 His Thr Met Glu Val Ser Cys
 385 390

<210> 1983

<211> 440

<212> PRT

<213> Homo sapiens

<400> 1983

Met Asp Glu Ala Gly Ser Ser Ala Ser Gly Gly Gly Phe Arg Pro Gly
 1 5 10 15
 Val Asp Ser Leu Asp Glu Pro Pro Asn Ser Arg Ile Phe Leu Val Ile
 20 25 30
 Ser Lys Tyr Thr Pro Glu Ser Val Leu Arg Glu Arg Phe Ser Pro Phe
 35 40 45
 Gly Asp Ile Gln Asp Ile Trp Val Val Arg Asp Lys His Thr Lys Pro
 50 55 60
 Ile Lys Val Phe Ile Ala Gln Ser Arg Ser Ser Gly Ser His Arg Asp
 65 70 75 80
 Val Glu Asp Glu Glu Leu Thr Arg Ile Phe Val Met Ile Pro Lys Ser
 85 90 95
 Tyr Thr Glu Glu Asp Leu Arg Glu Lys Phe Lys Val Tyr Gly Asp Ile
 100 105 110
 Glu Tyr Cys Ser Ile Ile Lys Asn Lys Val Thr Gly Glu Ser Lys Gly

115	120	125
Leu Gly Tyr Val Arg Tyr Leu Lys Pro Ser Gln Ala Ala Gln Ala Ile		
130	135	140
Glu Asn Cys Asp Arg Ser Phe Arg Ala Ile Leu Ala Glu Pro Lys Asn		
145	150	155
Lys Ala Ser Glu Ser Ser Glu Gln Asp Tyr Tyr Ser Asn Met Arg Gln		
165	170	175
Glu Ala Leu Gly His Glu Pro Arg Val Asn Met Phe Pro Phe Glu Gln		
180	185	190
Gln Ser Glu Phe Ser Ser Phe Asp Lys Asn Asp Ser Arg Gly Gln Glu		
195	200	205
Ala Ile Ser Lys Arg Leu Ser Val Val Ser Arg Val Pro Phe Thr Glu		
210	215	220
Glu Gln Leu Phe Ser Ile Phe Asp Ile Val Pro Gly Leu Glu Tyr Cys		
225	230	235
Glu Val Gln Arg Asp Pro Tyr Ser Asn Tyr Gly His Gly Val Val Gln		
245	250	255
Tyr Phe Asn Val Ala Ser Ala Ile Tyr Ala Lys Tyr Lys Leu His Gly		
260	265	270
Phe Gln Tyr Pro Pro Gly Asn Arg Ile Gly Val Ser Phe Ile Asp Asp		
275	280	285
Gly Ser Asn Ala Thr Asp Leu Leu Arg Lys Met Ala Thr Gln Met Val		
290	295	300
Ala Ala Gln Leu Ala Ser Met Val Trp Asn Asn Pro Ser Gln Gln Gln		
305	310	315
Phe Met Gln Phe Gly Gly Ser Ser Gly Ser Gln Leu Pro Gln Ile Gln		
325	330	335
Thr Asp Val Val Leu Pro Ser Cys Lys Lys Lys Ala Pro Ala Glu Thr		
340	345	350

Pro Val Lys Glu Arg Leu Phe Ile Val Phe Asn Pro His Pro Leu Pro
 355 360 365
 Leu Asp Val Leu Glu Asp Ile Phe Cys Arg Phe Gly Asn Leu Ile Glu
 370 375 380
 Val Tyr Leu Val Ser Gly Lys Asn Val Gly Tyr Ala Lys Tyr Ala Asp
 385 390 395 400
 Arg Ile Ser Ala Asn Asp Ala Ile Ala Thr Leu His Gly Lys Ile Leu
 405 410 415
 Asn Gly Val Arg Leu Lys Val Met Leu Ala Asp Ser Pro Arg Glu Glu
 420 425 430
 Ser Asn Lys Arg Gln Arg Thr Tyr
 435 440

<210> 1984

<211> 135

<212> PRT

<213> Homo sapiens

<400> 1984

Met Arg Pro Arg Met Leu Pro Val Phe Phe Gly Glu Ser Ile Lys Val
 1 5 10 15
 Ser Pro Glu Pro Thr His Glu Ile Arg Cys Asn Ser Glu Val Lys Tyr
 20 25 30
 Ala Ser Glu Lys His Phe Gln Asp Lys Val Phe Tyr Ala Pro Val Pro
 35 40 45
 Thr Val Thr Ala Tyr Ser Glu Thr Ile Val Ala Ala Pro Asn Cys Thr
 50 55 60
 Trp Arg Asn Tyr Arg Ser Gln Leu Thr Leu Glu Pro Arg Pro Arg Ala

65 70 75 80
 Leu Arg Phe Arg Ser Thr Thr Ile Ile Phe Pro Lys His Ala Arg Ser
 85 90 95
 Thr Phe Arg Thr Thr Leu His Cys Ser Leu Gly Arg Pro Ser Arg Trp
 100 105 110
 Phe Thr Ala Ser Val Gln Leu Gln Leu Cys Gln Asp Pro Ala Pro Ser
 115 120 125
 Leu Leu Gly Pro Ala Thr Leu
 130 135

<210> 1985

<211> 113

<212> PRT

<213> Homo sapiens

<400> 1985

Met Glu Phe Val Met Lys Gln Ala Leu Gly Gly Ala Thr Lys Asp Met
 1 5 10 15
 Gly Lys Met Leu Gly Gly Asp Glu Glu Lys Asp Pro Asp Ala Ala Lys
 20 25 30
 Lys Glu Glu Glu Arg Gln Glu Ala Leu Arg Gln Gly Ile Arg Asp Lys
 35 40 45
 Tyr Gly Ile Lys Lys Lys Glu Glu Arg Glu Ala Glu Ala Gln Ala Ala
 50 55 60
 Met Glu Ala Asn Ser Glu Gly Ser Leu Thr Arg Pro Lys Lys Ala Ile
 65 70 75 80
 Pro Pro Gly Cys Gly Asp Glu Val Glu Glu Glu Asp Glu Ser Ile Leu
 85 90 95

Asp Thr Val Ile Lys Tyr Leu Pro Gly Pro Leu Gln Asp Met Leu Lys

100

105

110

Lys

<210> 1986

<211> 125

<212> PRT

<213> Homo sapiens

<400> 1986

Met Pro Thr Glu Asn Trp Asp Pro Ala Gln Ser Ala Gly Leu Val Ala

1

5

10

15

Glu Met Met Trp Gly Ala Gly Gln Ser Thr Trp Met Gln Arg Gly Arg

20

25

30

Ala Ala Arg Trp Ala Cys Pro Gln Asp Asn Ser Phe Leu Gly Ile Arg

35

40

45

Ala Pro Gly Thr Ala Arg Gln Pro Arg Glu Ala Cys Gln Leu Gln Lys

50

55

60

Arg Ala Ser Gly Val Leu Gly Asp Trp Leu Pro Gly Leu Gly Gln Glu

65

70

75

80

Leu Gly Thr Cys Thr Asp Lys Gly Arg Arg Asn Ser Ser Gln Glu Gly

85

90

95

Val Gln Ile His Thr Gly Met Tyr Phe Val Arg Lys Val Gly Phe His

100

105

110

Ser Cys Lys Gln Lys Thr Gly Ala Leu Asp Arg Trp Gly

115

120

125

<210> 1987

<211> 155

<212> PRT

<213> Homo sapiens

<400> 1987

Met Arg Cys Pro Leu Gln Pro Val Gln Ala Tyr Thr Gly Val Gln Pro

1 5 10 15

Gly Gly Tyr Ser Gln Gly Glu Pro Phe Ser His Arg Arg Ala Leu Gly

20 25 30

Cys Gly Ala Trp Gly Thr Gly Ser Gly Thr Ala Leu Ser Arg Ala Arg

35 40 45

Asn Glu Leu Ser Asp His Leu Asp Ala Met Asp Ser Asn Leu Asp Asn

50 55 60

Leu Gln Thr Met Leu Ser Ser His Gly Phe Ser Val Asp Thr Ser Ala

65 70 75 80

Leu Leu Asp Leu Phe Ser Pro Ser Val Thr Val Pro Asp Met Ser Leu

85 90 95

Pro Asp Leu Asp Ser Ser Leu Ala Ser Val Arg Arg Arg Ala Gly Gly

100 105 110

Glu Gly Glu Arg Gly Arg Glu Gln Gln Pro Gly Phe Arg Glu Ala Ala

115 120 125

Gly Ala Leu His Ser Ala Ala Ala Val Pro Ala Gly Pro Arg Leu Arg

130 135 140

Gly His Arg Glu Gln Arg Pro Ala Gly Ala Val

145 150 155

<210> 1988

<211> 236

<212> PRT

<213> Homo sapiens

<400> 1988

Met Leu Thr Pro Ser Ser Gln Val His Ala Tyr Ile Ile Ser Ser Leu

1 5 10 15

Lys Lys Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu

20 25 30

Leu Val Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His

35 40 45

Gln Ile Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu

50 55 60

Leu Gln Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu

65 70 75 80

Leu Asp Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met

85 90 95

Val Met Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys

100 105 110

Gly Gly Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr

115 120 125

Gly Glu Gly Ala Gly Glu Gly Ile Asp Asp Val Glu Trp Val Val Gly

130 135 140

Lys Asp Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val

145 150 155 160

Asn Gly Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser

165 170 175

Lys Leu Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val

180 185 190
 Asp Lys Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His
 195 200 205
 Leu Ile Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Pro Pro
 210 215 220
 Pro His Leu Val Pro Pro Ser Lys Arg Arg His Glu
 225 230 235

<210> 1989

<211> 105

<212> PRT

<213> Homo sapiens

<400> 1989

Met Pro Leu Thr Trp Leu Leu Ala Ser Gly Met Gly Pro Leu Met Phe
 1 5 10 15
 Leu Ser Phe His Ser Asn Phe Pro Phe Leu Cys Leu Ser Thr Leu Phe
 20 25 30
 Ser Trp Lys Phe Ser His Leu Tyr Leu Ser Asp Leu Leu Leu Arg Phe
 35 40 45
 Ser Phe Leu Val Ala Phe Phe Leu Val Gly Gly Gly Gly Leu Thr Ile
 50 55 60
 Ser His Arg Leu Glu His Ser Gly Ala Ile Ile Ala Tyr Cys Asn Leu
 65 70 75 80
 Glu Leu Leu Gly Ser Ser Asp Pro Leu Ala Ser Ala Ser Gln Val Ser
 85 90 95
 Gly Thr Ala Gly Met Cys His Cys Thr
 100 105

<210> 1990

<211> 240

<212> PRT

<213> Homo sapiens

<400> 1990

Met Thr Lys Glu Thr Tyr Val Glu Ser Ile Leu Glu Gly Ile Lys Gln
 1 5 10 15
 Ser Lys Gln Glu Asn Leu Asp Thr Asp Val Arg Tyr Leu Ile Ala Val
 20 25 30
 Asp Arg Arg Gly Gly Pro Leu Val Ala Lys Glu Thr Val Lys Leu Ala
 35 40 45
 Glu Glu Phe Phe Leu Ser Thr Glu Gly Thr Val Leu Gly Leu Asp Leu
 50 55 60
 Ser Gly Asp Pro Thr Val Gly Gln Ala Lys Asp Phe Leu Glu Pro Leu
 65 70 75 80
 Leu Glu Ala Lys Lys Ala Gly Leu Lys Leu Ala Leu His Leu Ser Glu
 85 90 95
 Ile Pro Asn Gln Lys Lys Glu Thr Gln Ile Leu Leu Asp Leu Leu Pro
 100 105 110
 Asp Arg Ile Gly His Gly Thr Phe Leu Asn Ser Gly Glu Gly Gly Ser
 115 120 125
 Leu Asp Leu Val Asp Phe Val Arg Gln His Arg Ile Pro Leu Glu Leu
 130 135 140
 Cys Leu Thr Ser Asn Val Lys Ser Gln Thr Val Pro Ser Tyr Asp Gln
 145 150 155 160
 His His Phe Gly Phe Trp Tyr Ser Ile Ala His Pro Ser Val Ile Cys

	165		170		175										
Thr	Asp	Asp	Lys	Gly	Val	Phe	Ala	Thr	His	Leu	Ser	Gln	Glu	Tyr	Gln
	180		185		190										
Leu	Ala	Ala	Glu	Thr	Phe	Asn	Leu	Thr	Gln	Ser	Gln	Val	Trp	Asp	Leu
	195		200		205										
Ser	Tyr	Glu	Ser	Ile	Asn	Tyr	Ile	Phe	Ala	Ser	Asp	Ser	Thr	Arg	Ser
	210		215		220										
Glu	Leu	Arg	Lys	Lys	Trp	Asn	His	Leu	Lys	Pro	Arg	Val	Leu	His	Ile
	225		230		235										

<210> 1991

<211> 423

<212> PRT

<213> Homo sapiens

<400> 1991

Met	Ala	Ala	Val	Gln	Ala	Ala	Glu	Val	Lys	Val	Asp	Gly	Ser	Glu	Pro
1			5						10					15	
Lys	Leu	Ser	Lys	Asn	Glu	Leu	Lys	Arg	Arg	Leu	Lys	Ala	Glu	Lys	Lys
			20						25					30	
Val	Ala	Glu	Lys	Glu	Ala	Lys	Gln	Lys	Glu	Leu	Ser	Glu	Lys	Gln	Leu
			35						40					45	
Ser	Gln	Ala	Thr	Ala	Ala	Ala	Thr	Asn	His	Thr	Thr	Asp	Asn	Gly	Val
			50						55					60	
Gly	Pro	Glu	Glu	Glu	Ser	Val	Asp	Pro	Asn	Gln	Tyr	Tyr	Lys	Ile	Arg
			65						70					75	
Ser	Gln	Ala	Ile	His	Leu	His	Phe	Gly	Leu	Lys	Asp	Lys	Glu	Thr	Arg
									85					90	
															95

Tyr Arg Gln Arg Tyr Leu Asp Leu Ile Leu Asn Asp Phe Val Arg Gln
100 105 110
Lys Phe Ile Ile Arg Ser Lys Ile Ile Thr Tyr Ile Arg Ser Phe Leu
115 120 125
Asp Glu Leu Gly Phe Leu Glu Ile Glu Thr Pro Met Met Asn Ile Ile
130 135 140
Pro Glu Gly Ala Val Ala Lys Pro Phe Ile Thr Tyr His Asn Glu Leu
145 150 155 160
Asp Met Asn Leu Tyr Met Arg Ile Ala Pro Glu Leu Tyr His Lys Met
165 170 175
Leu Val Val Gly Gly Ile Asp Arg Val Tyr Glu Ile Gly Arg Gln Phe
180 185 190
Arg Asn Glu Gly Ile Asp Leu Thr His Asn Pro Glu Phe Thr Thr Cys
195 200 205
Glu Phe Tyr Met Ala Tyr Ala Asp Tyr His Asp Leu Met Glu Ile Thr
210 215 220
Glu Lys Met Val Ser Gly Met Val Lys Leu Pro Glu Thr Asn Leu Phe
225 230 235 240
Glu Thr Glu Glu Thr Arg Lys Ile Leu Asp Asp Ile Cys Val Ala Lys
245 250 255
Ala Val Glu Cys Pro Pro Pro Arg Thr Thr Ala Arg Leu Leu Asp Lys
260 265 270
Leu Val Gly Glu Phe Leu Glu Val Thr Cys Ile Asn Pro Thr Phe Ile
275 280 285
Cys Asp His Pro Gln Ile Met Ser Pro Leu Ala Lys Trp His Arg Ser
290 295 300
Lys Glu Gly Leu Thr Glu Arg Phe Glu Leu Phe Val Met Lys Lys Glu
305 310 315 320
Ile Cys Asn Ala Tyr Thr Glu Leu Asn Asp Pro Met Arg Gln Arg Gln

	325		330		335
Leu Phe Glu Glu Gln Ala Lys Ala Lys Ala Ala Gly Asp Asp Glu Ala					
	340		345		350
Met Phe Ile Asp Glu Asn Phe Cys Thr Ala Leu Glu Tyr Gly Leu Pro					
	355		360		365
Pro Thr Ala Gly Trp Gly Met Gly Ile Asp Arg Val Ala Met Phe Leu					
	370		375		380
Thr Asp Ser Asn Asn Ile Lys Glu Val Leu Leu Phe Pro Ala Met Lys					
385		390		395	400
Pro Glu Asp Lys Lys Glu Asn Val Ala Thr Thr Asp Thr Leu Glu Ser					
	405		410		415
Thr Thr Val Gly Thr Ser Val					
	420				

<210> 1992

<211> 157

<212> PRT

<213> Homo sapiens

<400> 1992

Met Ala Val Asp Ala Leu Glu Tyr Asp Glu Ser Ala Glu Asp Ala Asn			
1	5	10	15
Pro Ala Gly Ala Leu Glu Glu Ile Leu Glu Asn Pro Glu Arg Leu Lys			
20	25	30	
Asp Leu Asp Leu Asp Ala Phe Ala Glu Glu Leu Glu Arg Gln Gly Tyr			
35	40	45	
Gly Asp Lys His Ile Thr Leu Tyr Asp Ile Arg Ala Glu Leu Ser Cys			
50	55	60	

Arg Tyr Lys Asp Leu Arg Thr Ala Tyr Arg Ser Pro Asn Thr Glu Glu
65 70 75 80
Ile Phe Asn Met Leu Thr Lys Glu Thr Pro Glu Thr Phe Tyr Ile Gly
85 90 95
Lys Leu Ile Ile Cys Asn Val Thr Gly Ile Ala His Arg Arg Pro Gln
100 105 110
Gly Glu Ser Tyr Asp Gln Ala Ile Arg Asn Asp Glu Thr Gly Leu Trp
115 120 125
Gln Cys Pro Phe Cys Gln Gln Asp Asn Phe Pro Glu Leu Ser Glu Val
130 135 140
Cys Ala Ala Ala Leu Ser Cys Ser Val Asp Phe Leu Gly
145 150 155

<210> 1993

<211> 257

<212> PRT

<213> Homo sapiens

<400> 1993

Met Ala His Tyr Ile Thr Phe Leu Cys Met Val Leu Val Leu Leu Leu
1 5 10 15
Gln Asn Ser Val Leu Ala Glu Asp Gly Glu Val Arg Ser Ser Cys Arg
20 25 30
Thr Ala Pro Thr Asp Leu Val Phe Ile Leu Asp Gly Ser Tyr Ser Val
35 40 45
Gly Pro Glu Asn Phe Glu Ile Val Lys Lys Trp Leu Val Asn Ile Thr
50 55 60
Lys Asn Phe Asp Ile Gly Pro Lys Phe Ile Gln Val Gly Val Val Gln

65	70	75	80
Tyr Ser Asp Tyr Pro Val Leu Glu Ile Pro Leu Gly Ser Tyr Asp Ser			
	85	90	95
Gly Glu His Leu Thr Ala Ala Val Glu Ser Ile Leu Tyr Leu Gly Gly			
	100	105	110
Asn Thr Lys Thr Gly Lys Ala Ile Gln Phe Ala Leu Asp Tyr Leu Phe			
	115	120	125
Ala Lys Ser Ser Arg Phe Leu Thr Lys Ile Ala Val Val Leu Thr Asp			
	130	135	140
Gly Lys Ser Gln Asp Asp Val Lys Asp Ala Ala Gln Ala Ala Arg Asp			
145	150	155	160
Ser Lys Ile Thr Leu Phe Ala Ile Gly Val Gly Ser Glu Thr Glu Asp			
	165	170	175
Ala Glu Leu Arg Ala Ile Ala Asn Lys Pro Ser Ser Thr Tyr Val Phe			
	180	185	190
Tyr Val Glu Gly Tyr Ile Ala Ile Ser Lys Ile Arg Glu Val Met Lys			
	195	200	205
Gln Lys Leu Cys Glu Glu Ser Val Cys Pro Thr Arg Ile Pro Val Ala			
	210	215	220
Ala Arg Asp Glu Arg Gly Phe Asp Ile Leu Leu Gly Leu Asp Val Asn			
225	230	235	240
Lys Lys Val Lys Lys Arg Ile Gln Leu Ser Pro Lys Lys Asp Lys Arg			
	245	250	255
Ile			

<210> 1994

<211> 106

<212> PRT

<213> Homo sapiens

<400> 1994

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Met Thr Ser Gly Phe Phe Ile Gly Gly Pro Ser Asn Met Ile Ser Ser
  1           5           10           15
Ala Ile Ser Ala Asp Leu Gly Arg Gln Glu Leu Ile Gln Arg Ser Ser
          20           25           30
Glu Ala Leu Ala Thr Val Thr Gly Ile Val Asp Gly Ser Gly Ser Ile
          35           40           45
Gly Ala Ala Val Gly Gln Tyr Leu Val Ser Leu Ile Arg Asp Lys Leu
          50           55           60
Gly Trp Met Trp Val Phe Tyr Phe Phe Ile Leu Met Thr Ser Cys Thr
          65           70           75           80
Ile Val Phe Ile Ser Pro Leu Ile Val Arg Glu Ile Phe Ser Leu Val
          85           90           95
Leu Arg Arg Gln Ala His Ile Leu Arg Glu
          100          105

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<210> 1995

<211> 114

<212> PRT

<213> Homo sapiens

<400> 1995

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Met Ser Pro Ala Pro Val Pro Leu Leu Ser Leu His Ala Leu His Trp
  1           5           10           15
Gly Glu Asn Gly Arg Cys Ser Cys Trp Pro Trp Val Gly Ala Gly Ser

```

20 25 30
 Pro Gly Glu Thr Pro Val Arg Trp Thr Ile Leu Pro Ala Trp Gly Ile
 35 40 45
 Pro Phe Pro Thr Ser Val Leu Cys His Cys Cys Ser Ala Ser Phe Gln
 50 55 60
 Cys Val Ser Ala Trp Gly Glu Gly Arg Ser Thr Pro Ser Ala Pro Leu
 65 70 75 80
 Asn Leu Thr Lys Ser His Gly Cys Cys Ser Pro Leu Cys Met Met Gln
 85 90 95
 Met Leu Lys Cys Thr Lys Ser Thr Met Thr Thr Lys Lys Lys Thr Leu
 100 105 110
 Tyr Ser

<210> 1996

<211> 419

<212> PRT

<213> Homo sapiens

<400> 1996

Met Asp Gln Thr Cys Glu Leu Pro Arg Arg Asn Cys Leu Leu Pro Phe
 1 5 10 15
 Ser Asn Pro Val Asn Leu Asp Ala Pro Glu Asp Lys Asp Ser Pro Phe
 20 25 30
 Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro Leu Asn Gly Cys Thr Met
 35 40 45
 Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
 50 55 60

Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65 70 75 80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
85 90 95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
100 105 110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
115 120 125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
130 135 140
Thr Ile Lys Asn Gly Leu Leu His Phe Glu Asn Phe Thr Cys Val Asp
145 150 155 160
Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
165 170 175
Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
180 185 190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
195 200 205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
210 215 220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
225 230 235 240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
245 250 255
Pro Phe Ser Leu Gly Asp Thr Asn Ile Thr Ile Glu Glu Gln Leu Asn
260 265 270
Ser Ile Asn Leu Ser Phe Gln Asp Asp Pro Asp Ser Ser Thr Ser Thr
275 280 285
Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser Ser Thr Ser

290	295	300
Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr Pro Leu Lys		
305	310	315
Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg Arg Pro Trp		
	325	330
		335
Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr His Ser Lys		
	340	345
		350
Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr Val Glu Ala		
	355	360
		365
Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys Ala Ile Val		
	370	375
		380
Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val Leu Arg Arg		
385	390	395
		400
Glu Glu Arg Lys Lys Glu Arg Lys Arg Lys Arg Lys Glu Lys Glu Arg		
	405	410
		415
Lys Lys Glu		

<210> 1997

<211> 103

<212> PRT

<213> Homo sapiens

<400> 1997

Met Glu Gly Ser Ser His Pro Thr Ala Trp Leu Pro Ser Gly Leu Phe
1 5 10 15
Ser Leu Leu Leu Ser Val Ser Phe Ser Val Ser Pro Leu Leu Ile Met
20 25 30

Ala His Cys Ser Leu Asp Leu Pro Arg Leu Ser Asp Pro Leu Ala Ser
 35 40 45
 Ala Ser Gln Val Ala Glu Thr Thr Gly Val Arg His His Thr Trp Leu
 50 55 60
 Ile Phe Ile Phe Ile Phe Val Glu Thr Gly Leu Ala Leu Phe Pro Arg
 65 70 75 80
 Leu Val Ser Asn Ser Trp Ala Gln Ala Ile Pro Leu Pro Leu Pro Pro
 85 90 95
 Lys Val Leu Gly Leu Gln Ala
 100

<210> 1998

<211> 193

<212> PRT

<213> Homo sapiens

<400> 1998

Met Glu Ser Leu Ser Leu Leu Leu His Thr Leu Pro Met Ser Pro Glu
 1 5 10 15
 Glu Glu Gly Gly Arg Asp Gly Gly Val Gln Glu Arg Ala Pro Gly Ala
 20 25 30
 Leu Ser Ala Arg Gly Lys Gly Val Leu Asp Leu Arg Arg Arg Gly Lys
 35 40 45
 Gly Phe Leu Lys Ile Phe Cys Ser Ser Phe Pro Glu Asn Glu Arg Arg
 50 55 60
 Met Gly Glu Gly Gly Lys His Leu Thr Gly Thr Arg Pro Thr Ser Thr
 65 70 75 80
 Asn Val Ser Ala Leu Pro Pro Pro Gly Glu Lys Pro Phe Arg Cys Glu

	85		90		95										
Phe	Glu	Gly	Cys	Glu	Arg	Arg	Phe	Ala	Asn	Ser	Ser	Asp	Arg	Lys	Lys
	100						105					110			
His	Ser	His	Val	His	Thr	Ser	Asp	Lys	Pro	Tyr	Thr	Cys	Lys	Val	Arg
	115						120					125			
Gly	Cys	Asp	Lys	Cys	Tyr	Thr	His	Pro	Ser	Ser	Leu	Arg	Lys	His	Met
	130						135					140			
Lys	Val	His	Gly	Arg	Ser	Pro	Pro	Pro	Ser	Ser	Gly	Tyr	Asp	Ser	Ala
	145						150					155			160
Thr	Pro	Ser	Ala	Leu	Val	Ser	Pro	Ser	Ser	Asp	Cys	Gly	His	Lys	Ser
							165					170			175
Gln	Val	Ala	Ser	Ser	Ala	Ala	Val	Ala	Ala	Arg	Thr	Ala	Asp	Leu	Ser
							180					185			190
Glu															

<210> 1999

<211> 118

<212> PRT

<213> Homo sapiens

<400> 1999

Met	Arg	Arg	Leu	Ile	Pro	Phe	Leu	Phe	Ser	Phe	Gly	Ser	Ile	Ser	Ala
1				5					10					15	
Leu	Leu	Ser	Gly	Arg	Ile	Tyr	Val	Gly	Leu	Leu	Pro	Arg	Arg	Lys	Leu
				20					25					30	
Gln	Ala	Gln	Lys	Arg	Gly	Cys	Val	Ile	Arg	Cys	His	Leu	Ser	Gly	Cys
				35					40					45	

Leu Cys Cys Tyr Leu Ser Val Ala Leu Pro Leu Pro Arg Ser Leu Pro
 50 55 60
 Leu Pro Ala Asn Gln Phe Tyr Leu Pro Phe Thr Pro Gln Ser Phe Ile
 65 70 75 80
 Ser Val Ala Arg Ile Leu Ile Ser Tyr Gln Arg Lys Thr Thr Thr Ala
 85 90 95
 Leu Leu Pro Gly Pro Leu Leu Leu Ser Asn Val Pro Gln Thr Gly Ile
 100 105 110
 Arg Arg Pro Glu Glu Ser
 115

<210> 2000

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2000

Met Glu Thr Val Ile Met Ile Thr Tyr Trp Asp Leu Ile Ser His Ser
 1 5 10 15
 Glu Met Phe Ser Asp Ser Tyr Met Ser Gln Glu Ile Ala Asp Gly Leu
 20 25 30
 Arg Leu Glu Val Glu Gly Lys Ile Val Ser Arg Thr Glu Gly Asn Ile
 35 40 45
 Phe Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly
 50 55 60
 Lys Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp Ser Val Met Asn
 65 70 75 80
 His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala Tyr Asn Lys Cys

	85		90		95
Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg					
	100		105		110
Pro Lys Arg Val Lys Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys					
	115		120		125
His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Lys Thr					
	130		135		140

<210> 2001

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2001

Met Pro Leu Pro Gly Thr Pro Gly Pro Val Thr Thr Ser Pro Gln Thr			
1	5	10	15
Pro Thr Pro Arg Pro Leu Thr Thr Asp Trp Arg Ile Leu Ser Gly Lys			
	20	25	30
Gly Ser Gly Gly Ser Ala Arg Ala Val Ser Lys Leu Arg Ser Ser Ser			
	35	40	45
Ser Gly Asn Ser Leu Leu Arg Ile Arg Asp Leu Gly Val Arg Lys Ser			
	50	55	60
Gln Glu Glu Ala Ala Pro Pro Ser Pro Arg Pro Gln Ser Arg Ala His			
65	70	75	80
Ala Gln Thr Thr Asn Pro Tyr Trp Ala Asp Thr Asn Thr Arg Pro Gly			
	85	90	95
Ala His Pro Pro Glu His Gly Gly Val Ala Ala Leu Pro Ala Gln Val			
	100	105	110

Val Gly Gln Cys His Gln Glu Ala Thr Glu Asp

115

120

<210> 2002

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2002

Met Ser Val Leu Pro Ala His Ser Cys His Pro Gln Leu Pro Ser Tyr

1

5

10

15

Ser Leu Pro Leu Arg Thr Arg Asn Phe Gln Pro Val Ala Lys Gly Lys

20

25

30

Arg Gln Arg Gln Arg Arg Arg Pro Trp Glu Thr Ile Glu Lys His Lys

35

40

45

Glu Thr Gly Val Cys Val Trp Gly Gly Ser Gly Asp Lys Lys Gly Val

50

55

60

Gly Thr Asn Thr Lys Ile Phe Ile Cys Phe Leu His Gly Thr Cys Ser

65

70

75

80

Pro Leu Cys Pro Leu Gly Ser Leu Lys Glu Gly Pro Leu Leu Cys Leu

85

90

95

Thr His Leu Leu Ser Pro Ser Pro Val Leu Ser Lys Thr Asp Gln Arg

100

105

110

Asn

<210> 2003

<211> 197

<212> PRT

<213> Homo sapiens

<400> 2003

Met Phe Leu His Ser Leu Asn Glu Thr Lys Ser Thr Ser Leu Thr Lys

1 5 10 15

Leu Met Cys Ser Pro Ser Asp Ile Thr His Ser Thr Thr Gly Gly Ile

20 25 30

Ser Asp Ser Leu Arg Gln Leu Ser Phe Gln Gly Ala Trp Ala Gln Gly

35 40 45

Trp Trp Ser Asp Pro Ser Ala Ala Ile Cys Cys His Ile Leu Leu Met

50 55 60

Gly Ser Arg Pro Gln Thr Glu Gly Met Gly Ala Ile Asn Lys His Ser

65 70 75 80

Cys Arg Gly Leu Ala Ile Asn Ala Gln Ala Pro Arg Val Leu Gly Arg

85 90 95

Pro Val Ser Arg Val Arg Gln Ser Gln Lys Gly Thr Lys Thr Glu Asp

100 105 110

Leu Ser Gln Trp Trp Gln Arg Lys Gly His Ser Ser Leu Gly Lys Gln

115 120 125

Glu Gly Trp Arg Gln Ala Thr Ser Met Val Ala Trp Pro Pro Gly His

130 135 140

Thr Gly Gly Trp Gly Thr Val Gln Met Ser Leu Thr Cys Gly Leu Lys

145 150 155 160

Leu Leu Leu Cys Ser Gln Leu Asp Met Val Trp Leu Tyr Pro His Pro

165 170 175

Asn Leu Ile Leu Asn Cys Ser Ser His Asn Ser His Val Leu Trp Glu

180 185 190

Gly Pro Gly Gly Arg

195

<210> 2004

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2004

Met Leu Pro Glu Val Thr Ile Asn Glu Glu Thr Ala Leu Ala Glu Val

1 5 10 15

Asn Leu Lys Lys Lys Ser Tyr Leu Asn Ile Arg Thr His Pro Val Ala

20 25 30

Thr Ser Phe Ala Val Phe Asp Asp Thr Leu Leu Ile Val Asp Pro Thr

35 40 45

Gly Glu Glu Glu His Leu Ala Thr Gly Thr Leu Thr Ile Val Met Asp

50 55 60

Glu Glu Gly Lys Leu Cys Cys Leu His Lys Pro Gly Gly Ser Gly Leu

65 70 75 80

Thr Gly Ala Lys Leu Gln Asp Cys Met Ser Arg Ala Val Thr Arg His

85 90 95

Lys Glu Val Lys Lys Leu Met Asp Glu Val Ile Lys Ser Met Lys Pro

100 105 110

Lys

<210> 2005

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2005

Met Asp Gly Gly Arg Gln Arg Glu Asn Glu Glu Asp Val Lys Ala Glu

1 5 10 15

Thr Ser Asp Asn Ile Ile Arg Ser Arg Glu Thr Tyr Cys His Lys Asn

20 25 30

Asn Thr Gly Lys Thr Arg Leu His Asn Ser Val Ile Ser His Trp Val

35 40 45

Pro Pro Thr Thr Arg Gly Asn Tyr Gly Ser Tyr Lys Met Arg Phe Gly

50 55 60

Trp Gly Tyr Arg Ala Lys Pro Tyr Leu Ser Ala Pro Gly Pro Ser Gln

65 70 75 80

Ile Ser Tyr Leu His Ile Ser Lys Pro Ile Met Pro Ser Gln Gln Ser

85 90 95

Pro Lys Val Ser Thr Leu Phe Ser Ile Asn Pro Lys Ile Gln Val Gln

100 105 110

Ser Leu Ile

115

<210> 2006

<211> 210

<212> PRT

<213> Homo sapiens

<400> 2006

Met His Gly Asn Val His Val Cys Thr Val Cys Gly Val Tyr Ala Trp
 1 5 10 15
 Cys Val His Val Cys Thr Val Cys Gly Val Tyr Ala Trp Cys Val His
 20 25 30
 Met Cys Thr Val Tyr Ala Trp Cys Val His Val Cys Thr Val Tyr Ala
 35 40 45
 Trp Cys Val His Val Cys Thr Val Trp Cys Val Cys Met Val Cys Ala
 50 55 60
 His Val His Cys Val Cys Met Val Met Cys Thr Arg Ala Leu Cys Val
 65 70 75 80
 Cys Met Val Met Cys Thr Cys Ala Leu Cys Val Val Cys Met His Gly
 85 90 95
 Val Cys Thr Cys Ala Leu Cys Met His Gly Asn Val His Val Cys Thr
 100 105 110
 Val Trp Cys Val Cys Met Val Cys Ala Arg Val His Cys Val Cys Ile
 115 120 125
 Val Cys Ala Arg Val His Cys Val Trp Met His Gly Asn Val His Val
 130 135 140
 Cys Thr Val Cys Gly Val Tyr Ala Trp Cys Val His Val Cys Thr Val
 145 150 155 160
 Cys Gly Val Tyr Ala Trp Cys Val His Val Cys Thr Val Cys Met Arg
 165 170 175
 Val Trp Cys Val Cys Met Tyr Ala Trp Cys Val His Thr Cys Ala Ala
 180 185 190
 Ala Pro Gly Pro Ile Ser Ser Ala Gln Gln His His Thr His Phe Gly
 195 200 205
 Ala Leu
 210

<210> 2007

<211> 118

<212> PRT

<213> Homo sapiens

<400> 2007

Met Lys Asn Arg Asn Leu Phe Pro Thr Val Leu Lys Val Gly Gly Ser

1 5 10 15

Pro Lys Ser Arg Leu Gln Gln Ile Gln Cys Leu Ile Ser Cys Pro Leu

20 25 30

Leu Ser Arg Trp Ser Leu Val Ser Val Ser Ser Leu Gly Arg Arg Asn

35 40 45

Glu Leu Ala Pro Leu Ser Pro Tyr Ile Lys Ser Leu Ile Leu Ser Ile

50 55 60

Arg Val Glu Leu Val Trp Pro Asn His Leu Met Lys Ala Pro Pro Leu

65 70 75 80

Tyr Phe Leu Phe Leu Val Glu Met Glu Ser His Cys Val Ala Gln Ala

85 90 95

Gly Val Lys Phe Leu Gly Ser Ser Asp Pro Ser Ala Trp Ala Ser Lys

100 105 110

Val Leu Trp Leu Gln Val

115

<210> 2008

<211> 126

<212> PRT

<213> Homo sapiens

<400> 2008

Met	Glu	Arg	Leu	Arg	Val	Asp	Pro	Arg	Asp	Gly	His	Glu	Pro	Pro	Glu
1				5						10				15	
Ser	His	Phe	Ile	Val	Ser	Lys	Ala	Ser	Thr	Asn	Thr	Ile	Ser	Pro	Leu
			20					25					30		
Val	Leu	Asn	Ala	Ala	Arg	Glu	Val	Lys	Gly	Gly	Gly	Val	Trp	Gly	Glu
		35					40					45			
His	Phe	Cys	Val	His	Pro	Phe	Cys	Asp	Ser	Glu	Lys	Asp	Ser	Lys	Val
	50					55					60				
Glu	Leu	Gln	Ser	Gln	Glu	Val	Ala	Glu	Asp	Phe	Asn	Arg	Leu	Leu	Gly
65					70					75				80	
Gly	Glu	Glu	Gly	Ala	Ser	Glu	Ala	Arg	Met	Tyr	Pro	Ser	Gln	Lys	Ser
			85					90					95		
Glu	Asp	His	Ser	Leu	Pro	Ser	Val	Ile	Arg	Arg	Ala	Pro	Asp	Leu	Arg
			100					105					110		
Gly	Cys	Trp	Gly	Gln	Pro	Val	Arg	Gly	Thr	Arg	Leu	Gly	Leu		
		115					120					125			

<210> 2009

<211> 233

<212> PRT

<213> Homo sapiens

<400> 2009

Met	Leu	Thr	Leu	Asn	Leu	Val	Lys	Gln	His	Thr	Gly	Lys	Pro	Glu	Ser
1				5					10					15	
Thr	Leu	Glu	Thr	Ser	Val	Asn	Gln	Asp	Thr	Gly	Val	Gly	Gly	Phe	His

20	25	30
Thr Cys Phe Tyr Asn Leu Asn Ser Thr Thr Ile Thr Leu Thr Ile Ser		
35	40	45
Asn Ser Glu Ser Ile His Gln Ser Leu Glu Thr Gln Glu Val Leu Glu		
50	55	60
Val Thr Ser Ser Tyr Leu Ala Asn Pro Asn Phe Thr Ser Asn Ser Met		
65	70	75
Glu Ile Lys Ser Ala Gln Glu Asn Pro Phe Leu Phe Ser Thr Ile Lys		
85	90	95
Gln Thr Val Glu Glu Leu Asn Thr Asn Lys Glu Ser Val Ile Ala Ile		
100	105	110
Phe Val Pro Ala Lys Asn Ser Lys Leu Ser Val Asn Ser Phe Ile Ser		
115	120	125
Ala Gln Lys Glu Thr Thr Glu Val Glu Asp Ile Asp Ile Glu Asp Ser		
130	135	140
Leu Tyr Lys Asp Val Asp Tyr Gly Thr Glu Val Leu Gln Ile Glu His		
145	150	155
Ser Tyr Cys Arg Gln Asp Ile Asn Lys Glu His Leu Trp Gln Lys Val		
165	170	175
Ser Lys Leu His Ser Lys Ile Thr Leu Leu Glu Phe Lys Glu Gln Gln		
180	185	190
Thr Leu Gly Arg Leu Lys Ser Leu Glu Ala Leu Ile Arg Gln Leu Lys		
195	200	205
Gln Glu Asn Trp Leu Ser Glu Glu Asn Val Lys Ile Ile Glu Asn Arg		
210	215	220
Phe Thr Thr Tyr Glu Val Thr Met Ile		
225	230	

<210> 2010

<211> 638

<212> PRT

<213> Homo sapiens

<400> 2010

Met Glu Gly Gln Ser Ser Arg Gly Ser Arg Arg Pro Gly Thr Arg Ala

1 5 10 15

Gly Leu Gly Ser Leu Pro Met Pro Gln Gly Val Ala Gln Thr Gly Ala

20 25 30

Pro Ser Lys Val Asp Ser Ser Phe Gln Leu Pro Ala Lys Lys Asn Ala

35 40 45

Ala Leu Gly Pro Ser Glu Pro Arg Ile Thr Val Val Thr Trp Asn Val

50 55 60

Gly Thr Ala Met Pro Pro Asp Asp Val Thr Ser Leu Leu His Leu Gly

65 70 75 80

Gly Gly Asp Asp Ser Asp Gly Ala Asp Met Ile Ala Ile Gly Leu Gln

85 90 95

Glu Val Asn Ser Met Leu Asn Lys Arg Leu Lys Asp Ala Leu Phe Thr

100 105 110

Asp Gln Trp Ser Glu Leu Phe Met Asp Ala Leu Gly Pro Phe Asn Phe

115 120 125

Val Leu Val Ser Ser Val Arg Met Gln Gly Val Ile Leu Leu Leu Phe

130 135 140

Ala Lys Tyr Tyr His Leu Pro Phe Leu Arg Asp Val Gln Thr Asp Cys

145 150 155 160

Thr Arg Thr Gly Leu Gly Gly Tyr Trp Gly Asn Lys Gly Gly Val Ser

165 170 175

Val Arg Leu Ala Ala Phe Gly His Met Leu Cys Phe Leu Asn Cys His

180	185	190
Leu Pro Ala His Met Asp Lys	Ala Glu Gln Arg Lys Asp Asn Phe Gln	
195	200	205
Thr Ile Leu Ser Leu Gln Gln Phe	Gln Gly Pro Gly Ala Gln Gly Ile	
210	215	220
Leu Asp His Asp Leu Val Phe Trp	Phe Gly Asp Leu Asn Phe Arg Ile	
225	230	235
Glu Ser Tyr Asp Leu His Phe Val	Lys Phe Ala Ile Asp Ser Asp Gln	
245	250	255
Leu His Gln Leu Trp Glu Lys Asp	Gln Leu Asn Met Ala Lys Asn Thr	
260	265	270
Trp Pro Ile Leu Lys Gly Phe Gln	Glu Gly Pro Leu Asn Phe Ala Pro	
275	280	285
Thr Phe Lys Phe Asp Ala Gly Thr	Asn Lys Tyr Asp Thr Ser Ala Lys	
290	295	300
Lys Arg Lys Pro Ala Trp Thr Asp	Arg Ile Leu Trp Lys Val Lys Ala	
305	310	315
Pro Gly Gly Gly Pro Ser Pro Ser	Gly Arg Lys Ser His Arg Leu Gln	
325	330	335
Val Thr Gln His Ser Tyr Arg Ser	His Met Glu Tyr Thr Val Ser Asp	
340	345	350
His Lys Pro Val Ala Ala Gln Phe	Leu Leu Gln Phe Ala Phe Arg Asp	
355	360	365
Asp Met Pro Leu Val Arg Leu Glu	Val Ala Asp Glu Trp Val Arg Pro	
370	375	380
Glu Gln Ala Val Val Arg Tyr Arg	Met Glu Thr Val Phe Ala Arg Ser	
385	390	395
Ser Trp Asp Trp Ile Gly Leu Tyr	Arg Val Gly Phe Arg His Cys Lys	
405	410	415

Asp Tyr Val Ala Tyr Val Trp Ala Lys His Glu Asp Val Asp Gly Asn
420 425 430

Thr Tyr Gln Val Thr Phe Ser Glu Glu Ser Leu Pro Lys Gly His Gly
435 440 445

Asp Phe Ile Leu Gly Tyr Tyr Ser His Asn His Ser Ile Leu Ile Gly
450 455 460

Ile Thr Glu Pro Phe Gln Ile Ser Leu Pro Ser Ser Glu Leu Ala Ser
465 470 475 480

Ser Ser Thr Asp Ser Ser Gly Thr Ser Ser Glu Gly Glu Asp Asp Ser
485 490 495

Thr Leu Glu Leu Leu Ala Pro Lys Ser Arg Ser Pro Ser Pro Gly Lys
500 505 510

Ser Lys Arg His Arg Ser Arg Ser Pro Gly Leu Ala Arg Phe Pro Gly
515 520 525

Leu Ala Leu Arg Pro Ser Ser Arg Glu Arg Arg Gly Ala Ser Arg Ser
530 535 540

Pro Ser Pro Gln Ser Arg Arg Leu Ser Arg Val Ala Pro Asp Arg Ser
545 550 555 560

Ser Asn Gly Ser Ser Arg Gly Ser Ser Glu Glu Gly Pro Ser Gly Leu
565 570 575

Pro Gly Pro Trp Ala Phe Pro Pro Ala Val Pro Arg Ser Leu Gly Leu
580 585 590

Leu Pro Ala Leu Arg Leu Glu Thr Val Asp Pro Gly Gly Gly Gly Ser
595 600 605

Trp Gly Pro Asp Arg Glu Ala Leu Ala Pro Asn Ser Leu Ser Pro Ser
610 615 620

Pro Gln Gly His Arg Gly Leu Glu Glu Gly Gly Leu Gly Pro
625 630 635

<210> 2011

<211> 111

<212> PRT

<213> Homo sapiens

<400> 2011

Met Pro Leu His Ser Ser Leu Gly Thr Gln Ser Glu Thr Cys Leu Lys

1 5 10 15

Lys Arg Glu Ile Lys Lys Glu Thr Thr Leu Leu Ile His Gln Ser Val

20 25 30

Phe Cys Phe Ile Ile Gln Gly Ser Lys Ser Ser Leu Thr Leu Phe Pro

35 40 45

Lys Lys Leu Thr Ser Ile Ser Lys Pro Leu Asn Phe Val Leu Leu Ser

50 55 60

Leu Gly Leu Trp Lys Leu His Lys Thr Tyr Arg Leu Thr Cys Lys Glu

65 70 75 80

Tyr Leu Ser Arg Ile Trp Val Ala Lys Phe Leu Leu Asp Ser Phe Arg

85 90 95

Val Phe Phe Val Arg Ile Leu Tyr Ser Trp Ala Phe Cys Ser Phe

100 105 110

<210> 2012

<211> 119

<212> PRT

<213> Homo sapiens

<400> 2012

Met Leu Thr Thr Ser Pro Ile Pro Ala Thr Ser Ser Pro Leu Trp Glu
 1 5 10 15
 Lys Ala Arg Cys Pro Ala Pro Trp Gly Arg Val Arg Val Leu Arg Gly
 20 25 30
 Trp Tyr Val Pro Arg Lys Ser Lys Ile Phe Ser Trp Trp Ser Arg Pro
 35 40 45
 Glu Val Ala Met Tyr Leu Val Arg Glu Glu Gly Ser Ile Asn Met Ser
 50 55 60
 Val Asn Gly Phe Thr Lys Gln Ala Val Ala Lys Ser Arg His Gln Val
 65 70 75 80
 Trp Leu Gly Arg Lys Arg Leu Ile Val Ile Thr Thr Ala Ile Thr Leu
 85 90 95
 Asn Thr Pro Gln Ala Ser Ser Gln Leu Ser Cys Thr Gln Leu Ile Leu
 100 105 110
 Phe Leu Phe Pro Phe Lys Arg
 115

<210> 2013

<211> 182

<212> PRT

<213> Homo sapiens

<400> 2013

Met Glu Arg Glu Glu Glu Gly Gly Thr Gly Thr Val Ile Leu Pro Ser
 1 5 10 15
 Arg Lys Cys Leu Ser Ser Thr Ser Pro Lys Leu Ala Ser Gly Cys Cys
 20 25 30
 Pro Trp Pro Ser Arg Met Arg Ala Cys Pro Cys Trp Asp Ala Gly Ile

35 40 45
 Gln Leu Leu Val Leu Val Ser Gly Gly Arg Cys Arg Glu Gly Ser Gln
 50 55 60
 Gly Leu Phe Ile Asp Pro Arg Gly Gly Arg Trp Trp Cys Pro Val Thr
 65 70 75 80
 Glu Pro Leu Leu Ala Lys Pro Val Ser Leu Gln Ser Gln Leu Leu Ala
 85 90 95
 Gln Trp Ile Glu Gln Pro Tyr Leu Lys His Phe His Phe Ser Val Leu
 100 105 110
 Ile Trp His Val Pro Pro Pro Ser Leu Pro Pro Ser Leu Ser Pro Ser
 115 120 125
 Leu Pro Phe Ser Leu Pro Pro Phe Leu Pro Pro Ser Leu Ser Pro Leu
 130 135 140
 Leu Asn Ser Lys Lys Trp Gly Pro Thr Phe Phe Leu Gln Leu Glu Asp
 145 150 155 160
 Ser Leu Leu Phe Ile Thr Val Glu Ser Gln Val Ser Gln Gly Phe Ser
 165 170 175
 Gln Ala Val Gln Gln Ala
 180

<210> 2014

<211> 488

<212> PRT

<213> Homo sapiens

<400> 2014

Met Leu Ala Ala Val Thr Gly Gln Leu Ala Leu Val Gln Leu Leu Val
 1 5 10 15

Glu Arg His Ala Asp Val Asp Lys Gln Asp Ser Val His Gly Trp Thr
 20 25 30
 Ala Leu Met Gln Ala Thr Tyr His Gly Asn Lys Glu Ile Val Lys Tyr
 35 40 45
 Leu Leu Asn Gln Gly Ala Asp Val Thr Leu Arg Ala Lys Asn Gly Tyr
 50 55 60
 Thr Ala Phe Asp Leu Val Met Leu Leu Asn Asp Pro Asp Thr Glu Leu
 65 70 75 80
 Val Arg Leu Leu Ala Ser Val Cys Met Gln Val Asn Lys Asp Lys Gly
 85 90 95
 Arg Pro Ser His Gln Pro Pro Leu Pro His Ser Lys Val Arg Gln Pro
 100 105 110
 Trp Ser Ile Pro Val Leu Pro Asp Asp Lys Gly Gly Leu Lys Ser Trp
 115 120 125
 Trp Asn Arg Met Ser Asn Arg Phe Arg Lys Leu Lys Leu Met Gln Thr
 130 135 140
 Leu Pro Arg Gly Leu Ser Ser Asn Gln Pro Leu Pro Phe Ser Asp Glu
 145 150 155 160
 Pro Glu Pro Ala Leu Asp Ser Thr Met Arg Ala Ala Pro Gln Asp Lys
 165 170 175
 Thr Ser Arg Ser Ala Leu Pro Asp Ala Ala Pro Val Thr Lys Asp Asn
 180 185 190
 Gly Pro Gly Ser Thr Arg Gly Glu Lys Glu Asp Thr Leu Leu Thr Thr
 195 200 205
 Met Leu Arg Asn Gly Ala Pro Leu Thr Arg Leu Pro Ser Asp Lys Leu
 210 215 220
 Lys Ala Val Ile Pro Pro Phe Leu Pro Pro Ser Ser Phe Glu Leu Trp
 225 230 235 240
 Ser Ser Asp Arg Ser Arg Thr Arg His Asn Gly Lys Ala Asp Pro Met

	245		250		255
Lys Thr Ala Leu Pro Gln Arg Ala Ser Arg Gly His Pro Val Gly Gly					
	260		265		270
Gly Gly Thr Asp Thr Thr Pro Val Arg Pro Val Lys Phe Pro Ser Leu					
	275		280		285
Pro Arg Ser Pro Ala Ser Ser Ala Asn Ser Gly Asn Phe Asn His Ser					
	290		295		300
Pro His Ser Ser Gly Gly Ser Ser Gly Ile Gly Val Ser Arg His Gly					
305		310		315	320
Gly Glu Leu Leu Asn Arg Ser Gly Gly Ser Ile Asp Asn Val Leu Ser					
	325		330		335
Gln Ile Ala Ala Gln Arg Lys Lys Ala Ala Gly Leu Leu Glu Gln Lys					
	340		345		350
Pro Ser His Arg Ser Ser Pro Val Gly Pro Ala Pro Gly Ser Ser Pro					
	355		360		365
Ser Glu Leu Pro Ala Ser Pro Ala Gly Gly Ser Ala Pro Val Gly Lys					
	370		375		380
Lys Leu Glu Thr Ser Lys Arg Pro Pro Ser Gly Thr Ser Thr Thr Ser					
385		390		395	400
Lys Ser Thr Ser Pro Thr Leu Thr Pro Ser Pro Ser Pro Lys Gly His					
	405		410		415
Thr Ala Glu Ser Ser Val Ser Ser Ser Ser Ser His Arg Gln Ser Lys					
	420		425		430
Ser Ser Gly Gly Ser Ser Ser Gly Thr Ile Thr Asp Glu Asp Glu Leu					
	435		440		445
Thr Gly Ile Leu Lys Lys Leu Ser Leu Glu Lys Tyr Gln Pro Ile Phe					
	450		455		460
Glu Glu Gln Glu Ser Val Ser Val Ser Cys Val Val Arg Glu Met Arg					
465		470		475	480

Trp Thr Trp Lys Arg Ser Ser His

485

<210> 2015

<211> 169

<212> PRT

<213> Homo sapiens

<400> 2015

Met Val Pro Arg Ala Pro Pro Cys Ala Trp Leu Arg Pro Gly Arg Arg

1 5 10 15

Ala Gln Ala Gly Glu Gly Pro Arg Asp Pro Gly Asn Ala Ala Trp Arg

20 25 30

Thr Arg Arg Thr Gly Phe Pro Glu Ala Thr Gly Pro Ala Arg His Leu

35 40 45

Gln Leu Leu Tyr Val Asp Phe Gly Arg Trp Thr His Gly Arg Pro Val

50 55 60

Pro Leu Cys Arg Ala Gly Trp Arg Pro Arg Cys Pro Gly Ala Ala Ala

65 70 75 80

Ala Leu Gly Leu Ala Gly Leu Gly Asp His Ile Trp Pro Pro Gly Arg

85 90 95

Thr Val Pro Gln Asp Pro Pro Ala Trp Ala Pro Pro Ser Ser Leu Ala

100 105 110

His Ser Leu Gly Ala Pro Val Gly Ala Gly Ala Ala Gly Cys Pro Cys

115 120 125

Gly Pro Ala Ile His Arg Pro Ala His Ala Ala Ser Pro Ser Thr Cys

130 135 140

Leu Pro Thr Pro Pro Gln Pro Pro Thr Ser His Leu Glu Glu Thr Met

145 150 155 160
Gly Pro Ala Pro Pro Ala Pro Gly Cys
165

<210> 2016

<211> 309

<212> PRT

<213> Homo sapiens

<400> 2016

Met Ser Ala Leu Gly Thr Leu Arg Cys Gly Pro Ser Ile Pro Ser Val
1 5 10 15
Phe Pro Ser Val Leu Gly Ser Leu Arg Cys Gly Pro Ser Thr Pro Ser
20 25 30
Val Phe Pro Ser Val Leu Arg Met Leu Arg Cys Gly Pro Ser Ser Pro
35 40 45
Ser Val Phe Ser Ser Val Leu Gly Met Leu Lys Cys Gly Pro Ser Ile
50 55 60
Pro Ser Val Phe Pro Ser Val Leu Arg Met Leu Arg Cys Gly Pro Ser
65 70 75 80
Ser Pro Ser Val Phe Ser Ser Val Leu Gly Met Leu Arg Cys Gly Pro
85 90 95
Ser Ser Pro Ser Val Phe Pro Ser Val Leu Arg Met Leu Arg Cys Gly
100 105 110
Pro Ser Leu Pro Ser Val Phe Ser Ser Val Leu Gly Met Leu Ser Cys
115 120 125
Gly Pro Ser Ile Pro Ser Val Phe Ser Ser Val Leu Arg Met Leu Arg
130 135 140

Cys Gly Pro Ser Ile Pro Ser Val Phe Ser Ser Val Leu Arg Met Leu
145 150 155 160
Arg Cys Gly Pro Ser Ile Pro Ser Val Phe Ser Ser Val Leu Gly Met
165 170 175
Pro Ile Pro Leu Val Phe Tyr Leu Gln Leu Ser Leu Phe Phe Val Ser
180 185 190
Ser Leu Pro Thr Gln Val Glu Arg Gly Gly Asp Pro Ile Ala Cys Glu
195 200 205
Glu Asp Thr Ala Pro Gly Trp Thr Leu Gln Ile Val Lys Phe Lys Ser
210 215 220
Gln Leu Leu Gly Arg Ser Leu Cys Val Lys Ile Met Gly Val Arg Gln
225 230 235 240
Ile Gln Gly Pro His Ser Ala Leu Leu Cys Thr Ser Glu Cys Arg Ser
245 250 255
Ser Cys Leu Val Thr Arg Thr Leu Arg Arg Ser Met Asp Pro Ala Arg
260 265 270
Gly Asp Arg Val Ser Pro Val Ser Trp Asp Leu Arg Leu Pro Gly Trp
275 280 285
Ser Pro Ser Pro Asp Leu Val Ile Arg Leu Pro Leu Ser Pro Lys Val
290 295 300
Leu Gly Leu Gln Ala
305

<210> 2017

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2017

Met Glu Val Pro Cys Asp Lys Pro Phe Ser Glu Glu Gln Ala Arg Leu
 1 5 10 15
 Tyr Leu Arg Asp Val Ile Leu Gly Leu Glu Tyr Cys Glu Cys Gly Ala
 20 25 30
 Ala Cys Pro Leu Gly Leu Gly Leu Gly Asp Leu Ala Gly Gly Arg Ala
 35 40 45
 Gln Ala Glu Gln Thr Leu Ser Ser Ser Arg Gln Ser Glu Leu Thr Cys
 50 55 60
 Gln Ser Ala Ser Val Gly Val Gly His Ala Arg Val Ala Gly Pro Lys
 65 70 75 80
 Ala Phe Leu Trp Gly Gly Ala Gly Gly Gly Leu His Trp Ala Cys Ala
 85 90 95
 Arg Ser Phe Val Val Ser Gly Pro Val Gly Leu Ser Pro Gly Cys Ser
 100 105 110
 Val Ser Phe Phe Cys
 115

<210> 2018

<211> 180

<212> PRT

<213> Homo sapiens

<400> 2018

Met Glu Leu Ala Ala Leu Gly Leu Ser Pro Cys Pro Arg Leu Leu His
 1 5 10 15
 Ala Glu Leu Leu Pro Gly Leu Leu Thr Val Phe Ser Leu Arg Phe Leu
 20 25 30

Gln Asp Tyr Gly Gly Tyr Leu Ser Thr Tyr Ile Leu Pro Ala Lys Gly
35 40 45
Glu Asn Gln Gly Gln Thr Phe Thr Cys Gly Ser Ala Leu Ser Pro Ile
50 55 60
Thr Asp Phe Lys Leu Tyr Ala Ser Ala Phe Ser Glu Arg Tyr Leu Gly
65 70 75 80
Leu His Gly Leu Asp Asn Arg Ala Tyr Glu Met Thr Lys Val Ala His
85 90 95
Arg Val Ser Ala Leu Glu Glu Gln Gln Phe Leu Ile Ile His Pro Thr
100 105 110
Ala Asp Glu Lys Ile His Phe Gln His Thr Ala Glu Leu Ile Thr Gln
115 120 125
Leu Ile Arg Gly Lys Ala Asn Tyr Ser Leu Gln Val Gln Tyr Ala Cys
130 135 140
Tyr Ser Val Leu Asn Leu Glu Gln Asp Ile Pro Phe Met Glu Lys Asp
145 150 155 160
Leu Thr Gly Val Gln Gly Leu Leu Leu Gln Gln Thr Arg Leu Cys Cys
165 170 175
Gly Gly Arg Cys
180

<210> 2019

<211> 892

<212> PRT

<213> Homo sapiens

<400> 2019

Met His Gly Phe Arg Arg Thr Leu Arg Asn Ala Val Leu Thr Gln Lys

1	5	10	15
Gln Asp Ser Leu Arg Ile Ile Ser Ile Gln Pro Val Ala Gly Thr Asn			
20	25	30	
Gln Leu Asp Met Leu Phe Ala Val Glu Met His Ser Ser Glu Phe Tyr			
35	40	45	
Lys Pro Ala Tyr Leu Ile Gln Lys Leu Ser Asn Ala Arg Arg His Leu			
50	55	60	
Glu Asn Ile Met Arg Ile Ser Ala Ile Leu Glu Lys Asn Cys Ser Gly			
65	70	75	80
Leu Asp Cys Gln Glu Gln His Cys Glu Gln Gly Leu Ser Leu Asp Ser			
85	90	95	
His Ala Leu Met Thr Tyr Ser Thr Ala Arg Ile Ser Phe Val Cys Pro			
100	105	110	
Arg Phe Tyr Arg Asn Val Arg Cys Thr Cys Asn Gly Gly Leu Cys Pro			
115	120	125	
Gly Ser Asn Asp Pro Cys Val Glu Lys Pro Cys Pro Gly Asp Met Gln			
130	135	140	
Cys Val Gly Tyr Glu Ala Ser Arg Arg Pro Phe Leu Cys Gln Cys Pro			
145	150	155	160
Pro Gly Lys Leu Gly Glu Cys Ser Gly His Thr Ser Leu Ser Phe Ala			
165	170	175	
Gly Asn Ser Tyr Ile Lys Tyr Arg Leu Ser Glu Asn Ser Lys Glu Glu			
180	185	190	
Asp Phe Lys Leu Ala Leu Arg Leu Arg Thr Leu Gln Ser Asn Gly Ile			
195	200	205	
Ile Met Tyr Thr Arg Ala Asn Pro Cys Ile Ile Leu Lys Ile Val Asp			
210	215	220	
Gly Lys Leu Trp Phe Gln Leu Asp Cys Gly Ser Gly Pro Gly Ile Leu			
225	230	235	240

Gly Ile Ser Gly Arg Ala Val Asn Asp Gly Ser Trp His Ser Val Phe
245 250 255
Leu Glu Leu Asn Arg Asn Phe Thr Ser Leu Ser Leu Asp Asp Ser Tyr
260 265 270
Val Glu Arg Arg Arg Ala Pro Leu Tyr Phe Gln Thr Leu Ser Thr Glu
275 280 285
Ser Ser Ile Tyr Phe Gly Ala Leu Val Gln Ala Asp Asn Ile Arg Ser
290 295 300
Leu Thr Asp Thr Arg Val Thr Gln Val Leu Ser Gly Phe Gln Gly Cys
305 310 315 320
Leu Asp Ser Val Ile Leu Asn Asn Asn Glu Leu Pro Leu Gln Asn Lys
325 330 335
Arg Ser Ser Phe Ala Glu Val Val Gly Leu Thr Glu Leu Lys Leu Gly
340 345 350
Cys Val Leu Tyr Pro Asp Ala Cys Lys Arg Ser Pro Cys Gln His Gly
355 360 365
Gly Ser Cys Thr Gly Leu Pro Ser Gly Gly Tyr Gln Cys Thr Cys Leu
370 375 380
Ser Gln Phe Thr Gly Arg Asn Cys Glu Ser Glu Ile Thr Ala Cys Phe
385 390 395 400
Pro Asn Pro Cys Arg Asn Gly Gly Ser Cys Asp Pro Ile Gly Asn Thr
405 410 415
Phe Ile Cys Asn Cys Lys Ala Gly Leu Thr Gly Val Thr Cys Glu Glu
420 425 430
Asp Ile Asn Glu Cys Glu Arg Glu Glu Cys Glu Asn Gly Gly Ser Cys
435 440 445
Val Asn Val Phe Gly Ser Phe Leu Cys Asn Cys Thr Pro Gly Tyr Val
450 455 460
Gly Gln Tyr Cys Gly Leu Arg Pro Val Val Val Pro Asn Ile Gln Ala

465 470 475 480
Gly His Ser Tyr Val Gly Lys Glu Glu Leu Ile Gly Ile Ala Val Val
 485 490 495
Leu Phe Val Ile Phe Ile Leu Val Val Leu Phe Ile Val Phe Arg Lys
 500 505 510
Lys Val Phe Arg Lys Asn Tyr Ser Arg Asn Asn Ile Thr Leu Val Gln
 515 520 525
Asp Pro Ala Thr Ala Ala Leu Leu Asn Lys Ser Asn Gly Ile Pro Phe
 530 535 540
Arg Asn Leu Arg Gly Ser Gly Asp Gly Arg Asn Val Tyr Gln Glu Val
545 550 555 560
Gly Pro Pro Gln Val Pro Val Arg Pro Met Ala Tyr Thr Pro Cys Phe
 565 570 575
Gln Ser Asp Ser Arg Ser Asn Leu Asp Lys Ile Val Asp Gly Leu Gly
 580 585 590
Gly Glu His Gln Glu Met Thr Thr Phe His Pro Glu Ser Pro Arg Ile
 595 600 605
Leu Thr Ala Arg Arg Gly Val Val Val Cys Ser Val Ala Pro Asn Leu
 610 615 620
Pro Ala Val Ser Pro Cys Arg Ser Asp Cys Asp Ser Ile Arg Lys Asn
625 630 635 640
Gly Trp Asp Ala Gly Thr Glu Asn Lys Gly Val Asp Asp Pro Gly Glu
 645 650 655
Val Thr Cys Phe Ala Gly Ser Asn Lys Gly Ser Asn Ser Glu Val Gln
 660 665 670
Ser Leu Ser Ser Phe Gln Ser Asp Ser Gly Asp Asp Asn Ala Tyr His
 675 680 685
Trp Asp Thr Ser Asp Trp Met Pro Gly Ala Arg Leu Ser Asp Ile Glu
 690 695 700

Glu Val Pro Asn Tyr Glu Asn Gln Asp Gly Gly Ser Ala His Gln Gly
705 710 715 720
Ser Thr Arg Glu Leu Glu Ser Asp Tyr Tyr Leu Gly Gly Tyr Asp Ile
725 730 735
Asp Ser Glu Tyr Pro Pro Pro His Glu Glu Glu Phe Leu Ser Gln Asp
740 745 750
Gln Leu Pro Pro Pro Leu Pro Glu Asp Phe Pro Asp Gln Tyr Glu Ala
755 760 765
Leu Pro Pro Ser Gln Pro Val Ser Leu Ala Ser Thr Leu Ser Pro Asp
770 775 780
Cys Arg Arg Arg Pro Gln Phe His Pro Ser Gln Tyr Leu Pro Pro His
785 790 795 800
Pro Phe Pro Asn Glu Thr Asp Leu Val Gly Pro Pro Ala Ser Cys Glu
805 810 815
Phe Ser Thr Phe Ala Val Ser Met Asn Gln Gly Thr Glu Pro Thr Gly
820 825 830
Pro Ala Asp Ser Val Ser Leu Ser Leu His Asn Ser Arg Gly Thr Ser
835 840 845
Ser Ser Asp Val Ser Ala Asn Cys Gly Phe Asp Asp Ser Glu Val Ala
850 855 860
Met Ser Asp Tyr Glu Ser Val Gly Glu Leu Ser Leu Ala Ser Leu His
865 870 875 880
Ile Pro Phe Val Glu Ala Gln His Gln Thr Gln Val
885 890

<210> 2020

<211> 932

<212> PRT

<213> Homo sapiens

<400> 2020

Met	Ile	Gln	Glu	Lys	Lys	Glu	Gln	Ala	Glu	Met	Lys	Arg	Lys	Val	Gln
1				5					10					15	
Glu	Glu	Glu	Leu	Arg	Glu	Asn	His	Pro	Tyr	Phe	Asp	Lys	Pro	Leu	Phe
			20					25					30		
Ile	Val	Gly	Arg	Glu	His	Arg	Phe	Arg	Asn	Phe	Cys	Arg	Val	Val	Val
		35					40					45			
Arg	Ala	Arg	Phe	Asn	Ala	Ser	Lys	Thr	Asp	Pro	Val	Thr	Gly	Ala	Val
	50					55					60				
Lys	Asn	Thr	Lys	Tyr	His	Gln	Leu	Tyr	Asp	Leu	Leu	Gly	Leu	Val	Thr
65				70					75					80	
Tyr	Leu	Asp	Trp	Val	Met	Ile	Ile	Val	Thr	Ile	Cys	Ser	Cys	Ile	Ser
			85						90					95	
Met	Met	Phe	Glu	Ser	Pro	Phe	Arg	Arg	Val	Met	His	Ala	Pro	Thr	Leu
		100						105					110		
Gln	Ile	Ala	Glu	Tyr	Val	Phe	Val	Ile	Phe	Met	Ser	Ile	Glu	Leu	Asn
		115						120					125		
Leu	Lys	Ile	Met	Ala	Asp	Gly	Leu	Phe	Phe	Thr	Pro	Thr	Ala	Val	Ile
	130						135						140		
Arg	Asp	Phe	Gly	Gly	Val	Met	Asp	Ile	Phe	Ile	Tyr	Leu	Val	Ser	Leu
145				150					155					160	
Ile	Phe	Leu	Cys	Trp	Met	Pro	Gln	Asn	Val	Pro	Ala	Glu	Ser	Gly	Ala
			165						170					175	
Gln	Leu	Leu	Met	Val	Leu	Arg	Cys	Leu	Arg	Pro	Leu	Arg	Ile	Phe	Lys
		180							185					190	
Leu	Val	Pro	Gln	Met	Arg	Lys	Val	Val	Arg	Glu	Leu	Phe	Ser	Gly	Phe
		195						200						205	

Lys Glu Ile Phe Leu Val Ser Ile Leu Leu Leu Thr Leu Met Leu Val
210 215 220
Phe Ala Ser Phe Gly Val Gln Leu Phe Ala Gly Lys Leu Ala Lys Cys
225 230 235 240
Asn Asp Pro Asn Ile Ile Arg Arg Glu Asp Cys Asn Gly Ile Phe Arg
245 250 255
Ile Asn Val Ser Val Ser Lys Asn Leu Asn Leu Lys Leu Arg Pro Gly
260 265 270
Glu Lys Lys Pro Gly Phe Trp Val Pro Arg Val Trp Ala Asn Pro Arg
275 280 285
Asn Phe Asn Phe Asp Asn Val Gly Asn Ala Met Leu Ala Leu Phe Glu
290 295 300
Val Leu Ser Leu Lys Gly Trp Val Glu Val Arg Asp Val Ile Ile His
305 310 315 320
Arg Val Gly Pro Ile His Gly Ile Tyr Ile His Val Phe Val Phe Leu
325 330 335
Gly Cys Met Ile Gly Leu Thr Leu Phe Val Gly Val Val Ile Ala Asn
340 345 350
Phe Asn Glu Asn Lys Gly Thr Ala Leu Leu Thr Val Asp Gln Arg Arg
355 360 365
Trp Glu Asp Leu Lys Ser Arg Leu Lys Ile Ala Gln Pro Leu His Leu
370 375 380
Pro Pro Arg Pro Asp Asn Asp Gly Phe Arg Ala Lys Met Tyr Asp Ile
385 390 395 400
Thr Gln His Pro Phe Phe Lys Arg Thr Ile Ala Leu Leu Val Leu Ala
405 410 415
Gln Ser Val Leu Leu Ser Val Lys Trp Asp Val Glu Asp Pro Val Thr
420 425 430
Val Pro Leu Ala Thr Met Ser Val Val Phe Thr Phe Ile Phe Val Leu

435 440 445
Glu Val Thr Met Lys Ile Ile Ala Met Ser Pro Ala Gly Phe Trp Gln
450 455 460
Ser Arg Arg Asn Arg Tyr Asp Leu Leu Val Thr Ser Leu Gly Val Val
465 470 475 480
Trp Val Val Leu His Phe Ala Leu Leu Asn Ala Tyr Thr Tyr Met Met
485 490 495
Gly Ala Cys Val Ile Val Phe Arg Phe Phe Ser Ile Cys Gly Lys His
500 505 510
Val Thr Leu Lys Met Leu Leu Leu Thr Val Val Val Ser Met Tyr Lys
515 520 525
Ser Phe Phe Ile Ile Val Gly Met Phe Leu Leu Leu Leu Cys Tyr Ala
530 535 540
Phe Ala Gly Val Val Leu Phe Gly Thr Val Lys Tyr Gly Glu Asn Ile
545 550 555 560
Asn Arg His Ala Asn Phe Ser Ser Ala Gly Lys Ala Ile Thr Val Leu
565 570 575
Phe Arg Ile Val Thr Gly Glu Asp Trp Asn Lys Ile Met Arg Asp Cys
580 585 590
Met Val Gln Pro Pro Phe Cys Thr Pro Asp Glu Phe Thr Tyr Trp Ala
595 600 605
Thr Asp Cys Gly Asn Tyr Ala Gly Ala Leu Met Tyr Phe Cys Ser Phe
610 615 620
Tyr Val Ile Ile Ala Tyr Ile Met Leu Asn Leu Leu Val Ala Ile Ile
625 630 635 640
Val Glu Asn Phe Ser Leu Phe Tyr Ser Thr Glu Glu Asp Gln Leu Leu
645 650 655
Ser Tyr Asn Asp Leu Arg His Phe Gln Ile Ile Trp Asn Met Val Asp
660 665 670

Asp Lys Arg Glu Gly Val Ile Pro Thr Phe Arg Val Lys Phe Leu Leu
675 680 685
Arg Leu Leu Arg Gly Arg Leu Glu Val Asp Leu Asp Lys Asp Lys Leu
690 695 700
Leu Phe Lys His Met Cys Tyr Glu Met Glu Arg Leu His Asn Gly Gly
705 710 715 720
Asp Val Thr Phe His Asp Val Leu Ser Met Leu Ser Tyr Arg Ser Val
725 730 735
Asp Ile Arg Lys Ser Leu Gln Leu Glu Glu Leu Leu Ala Arg Glu Gln
740 745 750
Leu Glu Tyr Thr Ile Glu Glu Glu Val Ala Lys Gln Thr Ile Arg Met
755 760 765
Trp Leu Lys Lys Cys Leu Lys Arg Ile Arg Ala Lys Gln Gln Gln Ser
770 775 780
Cys Ser Ile Ile His Ser Leu Arg Glu Ser Gln Gln Gln Glu Leu Ser
785 790 795 800
Arg Phe Leu Asn Pro Pro Ser Ile Glu Thr Thr Gln Pro Ser Glu Asp
805 810 815
Thr Asn Ala Asn Ser Gln Asp Asn Ser Met Gln Pro Glu Thr Ser Ser
820 825 830
Gln Gln Gln Leu Leu Ser Pro Thr Leu Ser Asp Arg Gly Gly Ser Arg
835 840 845
Gln Asp Ala Ala Asp Ala Gly Lys Pro Gln Arg Lys Phe Gly Gln Trp
850 855 860
Arg Leu Pro Ser Ala Pro Lys Pro Ile Ser His Ser Val Ser Ser Val
865 870 875 880
Asn Leu Arg Phe Gly Gly Arg Thr Thr Met Lys Ser Val Val Cys Lys
885 890 895
Met Asn Pro Met Thr Asp Ala Ala Ser Cys Gly Ser Glu Val Lys Lys

900 905 910
Trp Trp Thr Arg Gln Leu Thr Val Glu Ser Asp Glu Ser Gly Asp Asp
915 920 925
Leu Leu Asp Ile
930

<210> 2021

<211> 1060

<212> PRT

<213> Homo sapiens

<400> 2021

Met Leu Gly Glu Gly Leu Gly Pro Glu Trp Gly Pro Arg Pro Glu His
1 5 10 15
Leu Pro Leu Ala Trp Leu Cys Val Ser Ala Ser Pro Gly Gly Ser Gly
20 25 30
Arg Cys Glu Leu Arg Gln Cys Ser Val Leu Ile Pro Cys Arg Met Ala
35 40 45
Ser Cys Gly Gln Gly Ser Val Arg Leu Trp Arg Leu Arg Gly Gly Val
50 55 60
Leu Arg Ser Cys Pro Val Asp Leu Gly Glu His His Ala Leu Gln Phe
65 70 75 80
Thr Asp Leu Ala Phe Lys Gln Ala Arg Asp Gly Cys Pro Glu Pro Ser
85 90 95
Ala Ala Met Leu Phe Val Cys Ser Arg Ser Gly His Ile Leu Glu Ile
100 105 110
Asp Cys Gln Arg Met Val Val Arg His Ala Arg Arg Leu Leu Pro Thr
115 120 125

Arg Thr Pro Gly Gly Pro His Pro Gln Lys Gln Thr Phe Ser Ser Gly
 130 135 140
 Pro Gly Ile Ala Ile Ser Ser Leu Ser Val Ser Pro Ala Met Cys Ala
 145 150 155 160
 Val Gly Ser Glu Asp Gly Phe Leu Arg Leu Trp Pro Leu Asp Phe Ser
 165 170 175
 Ser Val Leu Leu Glu Ala Glu His Glu Gly Pro Val Ser Ser Val Cys
 180 185 190
 Val Ser Pro Asp Gly Leu Arg Val Leu Ser Ala Thr Ser Ser Gly His
 195 200 205
 Leu Gly Phe Leu Asp Thr Leu Ser Arg Val Tyr His Met Leu Ala Arg
 210 215 220
 Ser His Thr Ala Pro Val Leu Ala Leu Ala Met Glu Gln Arg Arg Gly
 225 230 235 240
 Gln Leu Ala Thr Val Ser Gln Asp Arg Thr Val Arg Ile Trp Asp Leu
 245 250 255
 Ala Thr Leu Gln Gln Leu Tyr Asp Phe Thr Ser Ser Glu Asp Ala Pro
 260 265 270
 Cys Ala Val Thr Phe His Pro Thr Arg Pro Thr Phe Phe Cys Gly Phe
 275 280 285
 Ser Ser Gly Ala Val Arg Ser Phe Ser Leu Glu Ala Ala Glu Val Leu
 290 295 300
 Val Glu His Thr Cys His Arg Gly Ala Val Thr Gly Leu Thr Ala Thr
 305 310 315 320
 Pro Asp Gly Arg Leu Leu Phe Ser Ser Cys Ser Gln Gly Ser Leu Ala
 325 330 335
 Gln Tyr Ser Cys Ala Asp Pro Gln Trp His Val Leu Arg Val Ala Ala
 340 345 350
 Asp Met Val Cys Pro Asp Ala Pro Ala Ser Pro Ser Ala Leu Ala Val

355	360	365
Ser Arg Asp Gly Arg Leu Leu Ala Phe Val Gly Pro Ser Arg Cys Thr		
370	375	380
Val Thr Val Met Gly Ser Ala Ser Leu Asp Glu Leu Leu Arg Val Asp		
385	390	395
Ile Gly Thr Leu Asp Leu Ala Ser Ser Arg Leu Asp Ser Ala Met Ala		
405	410	415
Val Cys Phe Gly Pro Ala Ala Leu Gly His Leu Leu Val Ser Thr Ser		
420	425	430
Ser Asn Arg Val Val Val Leu Asp Ala Val Ser Gly Arg Ile Ile Arg		
435	440	445
Glu Leu Pro Gly Val His Pro Glu Pro Cys Pro Ser Leu Thr Leu Ser		
450	455	460
Glu Asp Ala Arg Phe Leu Leu Ile Ala Ala Gly Arg Thr Ile Lys Val		
465	470	475
Trp Asp Tyr Ala Thr Gln Ala Ser Pro Gly Pro Gln Val Tyr Ile Gly		
485	490	495
His Ser Glu Pro Val Gln Ala Val Ala Phe Ser Pro Asp Gln Gln Gln		
500	505	510
Val Leu Ser Ala Gly Asp Ala Val Phe Leu Trp Asp Val Leu Ala Pro		
515	520	525
Thr Glu Ser Asp Gln Ser Phe Pro Gly Ala Pro Pro Ala Cys Lys Thr		
530	535	540
Gly Pro Gly Ala Gly Pro Leu Glu Asp Ala Ala Ser Arg Ala Ser Glu		
545	550	555
Leu Pro Arg Gln Gln Val Pro Lys Pro Cys Gln Ala Ser Pro Pro Arg		
565	570	575
Leu Gly Val Cys Ala Arg Pro Pro Glu Gly Gly Asp Gly Ala Arg Asp		
580	585	590

Thr Arg Asn Ser Gly Ala Pro Arg Thr Thr Tyr Leu Ala Ser Cys Lys
595 600 605
Ala Phe Thr Pro Ala Arg Val Ser Cys Ser Pro His Ser Ala Lys Gly
610 615 620
Thr Cys Pro Pro Pro Ala Ser Gly Gly Trp Leu Arg Leu Lys Ala Val
625 630 635 640
Val Gly Tyr Ser Gly Asn Gly Arg Ala Asn Met Val Trp Arg Pro Asp
645 650 655
Thr Gly Phe Phe Ala Tyr Thr Cys Gly Arg Leu Val Val Val Glu Asp
660 665 670
Leu His Ser Gly Ala Gln Gln His Trp Ser Gly His Ser Ala Glu Ile
675 680 685
Ser Thr Leu Ala Leu Ser His Ser Ala Gln Val Leu Ala Ser Ala Ser
690 695 700
Gly Arg Ser Ser Thr Thr Ala His Cys Gln Ile Arg Val Trp Asp Val
705 710 715 720
Ser Gly Gly Leu Cys Gln His Leu Ile Phe Pro His Ser Thr Thr Val
725 730 735
Leu Ala Leu Ala Phe Ser Pro Asp Asp Arg Leu Leu Val Thr Leu Gly
740 745 750
Asp His Asp Gly Arg Thr Leu Ala Leu Trp Gly Thr Ala Thr Tyr Asp
755 760 765
Leu Val Ser Ser Thr Arg Leu Pro Glu Pro Val His Gly Val Ala Phe
770 775 780
Asn Pro Trp Asp Ala Gly Glu Leu Thr Cys Val Gly Gln Gly Thr Val
785 790 795 800
Thr Phe Trp Leu Leu Gln Gln Arg Gly Ala Asp Ile Ser Leu Gln Val
805 810 815
Arg Arg Glu Pro Val Pro Glu Ala Val Gly Ala Gly Glu Leu Thr Ser

820	825	830
Leu Cys Tyr Gly Ala Pro Pro	Leu Leu Tyr Cys Gly Thr	Ser Ser Gly
835	840	845
Gln Val Cys Val Trp Asp Thr	Arg Ala Gly Arg Cys Phe	Leu Ser Trp
850	855	860
Glu Ala Asp Asp Gly Gly Ile Gly	Leu Leu Leu Phe Ser Gly	Ser Arg
865	870	875
880		
Leu Val Ser Gly Ser Ser Thr	Gly Arg Leu Arg Leu Trp	Ala Val Gly
885	890	895
Ala Val Ser Glu Leu Arg Cys Lys	Gly Ser Gly Ala Ser Ser	Val Phe
900	905	910
Met Glu His Glu Leu Val Leu Asp	Gly Ala Val Val Ser Ala	Ser Phe
915	920	925
Asp Asp Ser Val Asp Met Gly Val	Val Gly Thr Thr Ala Gly	Thr Leu
930	935	940
Trp Phe Val Ser Trp Ala Glu Gly	Thr Ser Thr Arg Leu Ile	Ser Gly
945	950	955
960		
His Arg Ser Lys Val Arg Asp Phe	Gln Pro Gly Gln Arg Arg	Gly Ser
965	970	975
Arg Thr Trp Cys Pro Pro Cys Leu	Pro Ala Pro Ser Pro Pro	Ala Gln
980	985	990
Met Ile Pro Ser Pro Ala Val Thr	Gly Ser Gln Arg Pro Pro	Trp Gly
995	1000	1005
Ser Gln Arg Gly Ser Leu Gly Cys	Ala Arg Pro Leu Lys Ala	Val Pro
1010	1015	1020
Val Val Ser Ala Gln Ala Ser Arg	Leu Ala Gly Leu Ala Gly	Leu Leu
1025	1030	1035
1040		
Lys Leu Ser Phe Pro Cys Tyr Cys	Phe Ala Phe Phe Cys Leu	Phe Val
1045	1050	1055

Phe Cys Phe Leu

1060

<210> 2022

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2022

Met Arg Leu Val Pro Asn Gly Gly Gly Ser Leu Arg Gly Phe Leu Thr

1

5

10

15

Pro Arg Arg Ala Glu Gln Ile Thr Gly His Asn Ser Pro Pro Gln Gly

20

25

30

His Thr Ala Pro Ser Thr Leu Val Gly Gly Ser Val Leu Ser Thr Val

35

40

45

Ser Cys Ser Leu Asn Thr Ser Ser Trp Asn Asn Arg Thr Ala Ala Phe

50

55

60

Val Gln Thr His Ser Phe Phe Phe Phe Asn Lys Lys Thr Ala Leu Pro

65

70

75

80

Arg Arg Lys His Met Ser Tyr Asn Ser Ala Ala Val Leu Arg Gln Arg

85

90

95

Leu Cys Leu Pro Pro Pro Cys Phe Ser Ile Gly Ala Leu Ala Ala Ser

100

105

110

<210> 2023

<211> 701

<212> PRT

<213> Homo sapiens

<400> 2023

Met Gly Ser Ala Ala Asp Val Arg Phe Ser Leu Gly Thr Thr Thr His
1 5 10 15
Ala Pro Pro Gly Val His Arg Arg Tyr Ser Ala Leu Arg Glu Glu Ser
20 25 30
Ala Lys Asp Trp Glu Thr Ser Pro Leu Pro Gly Met Leu Ala Pro Ala
35 40 45
Ala Gly Pro Ala Phe Asp Ser Asp Pro Glu Ile Ser Asp Val Asp Glu
50 55 60
Asp Glu Pro Gly Gly Leu Val Gly Ser Ala Asp Val Val Ser Pro Ser
65 70 75 80
Gly His Ser Asp Ala Gln Thr Leu Ala Met Met Leu Gln Glu Gln Leu
85 90 95
Asp Ala Ile Asn Glu Glu Ile Arg Met Ile Gln Glu Glu Lys Glu Ser
100 105 110
Thr Glu Leu Arg Ala Glu Glu Ile Glu Thr Arg Val Thr Ser Gly Ser
115 120 125
Met Glu Ala Leu Asn Leu Lys Gln Leu Arg Lys Arg Gly Ser Ile Pro
130 135 140
Thr Ser Leu Thr Ala Leu Ser Leu Ala Ser Ala Ser Pro Pro Leu Ser
145 150 155 160
Gly Arg Ser Thr Pro Lys Leu Thr Ser Arg Ser Ala Ala Gln Asp Leu
165 170 175
Asp Arg Met Gly Val Met Thr Leu Pro Ser Asp Leu Arg Lys His Arg
180 185 190
Arg Lys Leu Leu Ser Pro Val Ser Arg Glu Glu Asn Arg Glu Asp Lys
195 200 205

Ala Thr Ile Lys Cys Glu Thr Ser Pro Pro Ser Ser Pro Arg Thr Leu
210 215 220
Arg Leu Glu Lys Leu Gly His Pro Ala Leu Ser Gln Glu Glu Gly Lys
225 230 235 240
Ser Ala Leu Glu Asp Gln Gly Ser Asn Pro Ser Ser Ser Asn Ser Ser
245 250 255
Gln Asp Ser Leu His Lys Gly Ala Lys Arg Lys Gly Ile Lys Ser Ser
260 265 270
Ile Gly Arg Leu Phe Gly Lys Lys Glu Lys Gly Arg Leu Ile Gln Leu
275 280 285
Ser Arg Asp Gly Ala Thr Gly His Val Leu Leu Thr Asp Ser Glu Phe
290 295 300
Ser Met Gln Glu Pro Met Val Pro Ala Lys Leu Gly Thr Gln Ala Glu
305 310 315 320
Lys Asp Arg Arg Leu Lys Lys Lys His Gln Leu Leu Glu Asp Ala Arg
325 330 335
Arg Lys Gly Met Pro Phe Ala Gln Trp Asp Gly Pro Thr Val Val Ser
340 345 350
Trp Leu Glu Leu Trp Val Gly Met Pro Ala Trp Tyr Val Ala Ala Cys
355 360 365
Arg Ala Asn Val Lys Ser Gly Ala Ile Met Ser Ala Leu Ser Asp Thr
370 375 380
Glu Ile Gln Arg Glu Ile Gly Ile Ser Asn Ala Leu His Arg Leu Lys
385 390 395 400
Leu Arg Leu Ala Ile Gln Glu Met Val Ser Leu Thr Ser Pro Ser Ala
405 410 415
Pro Pro Thr Ser Arg Thr Ser Ser Gly Asn Val Trp Val Thr His Glu
420 425 430
Glu Met Glu Thr Leu Glu Thr Ser Thr Lys Thr Asp Ser Glu Glu Gly

435	440	445
Ser Trp Ala Gln Thr Leu	Ala Tyr Gly Asp Met Asn His Glu Trp Ile	
450	455	460
Gly Asn Glu Trp Leu Pro Ser Leu Gly Leu Pro Gln Tyr Arg Ser Tyr		
465	470	475
Phe Met Glu Cys Leu Val Asp Ala Arg Met Leu Asp His Leu Thr Lys		
485	490	495
Lys Asp Leu Arg Val His Leu Lys Met Val Asp Ser Phe His Arg Thr		
500	505	510
Ser Leu Gln Tyr Gly Ile Met Cys Leu Lys Arg Leu Asn Tyr Asp Arg		
515	520	525
Lys Glu Leu Glu Lys Arg Arg Glu Glu Ser Gln His Glu Ile Lys Asp		
530	535	540
Val Leu Val Trp Thr Asn Asp Gln Val Val His Trp Val Gln Ser Ile		
545	550	555
Gly Leu Arg Asp Tyr Ala Gly Asn Leu His Glu Ser Gly Val His Gly		
565	570	575
Ala Leu Leu Ala Leu Asp Glu Asn Phe Asp His Asn Thr Leu Ala Leu		
580	585	590
Ile Leu Gln Ile Pro Thr Gln Asn Thr Gln Ala Arg Gln Val Met Glu		
595	600	605
Arg Glu Phe Asn Asn Leu Leu Ala Leu Gly Thr Asp Arg Lys Leu Asp		
610	615	620
Asp Gly Asp Asp Lys Val Phe Arg Arg Ala Pro Ser Trp Arg Lys Arg		
625	630	635
Phe Arg Pro Arg Glu His His Gly Arg Gly Gly Met Leu Ser Ala Ser		
645	650	655
Ala Glu Thr Leu Pro Ala Gly Phe Arg Val Ser Thr Leu Gly Thr Leu		
660	665	670

Gln Pro Pro Pro Ala Pro Pro Lys Lys Ile Met Pro Glu Ala His Ser

675

680

685

His Tyr Leu Tyr Gly His Met Leu Ser Ala Phe Arg Asp

690

695

700

<210> 2024

<211> 291

<212> PRT

<213> Homo sapiens

<400> 2024

Met Gly Pro Phe Ser Ser Val Asn Ser Leu Val Leu Asn Glu Ala Ser

1

5

10

15

Thr Leu Ala Lys Arg Leu Ser Thr Phe Thr Thr Phe Ile Arg Pro Phe

20

25

30

Ser Ser Met Lys Ser Pro Val Leu Asn Glu Ala Arg Ala Leu Ser Lys

35

40

45

Arg Phe Ala Thr Phe Thr Ala Leu Ile Arg Ser Cys Ala Ser Met Asn

50

55

60

Ser Pro Val Leu Asn Glu Val Arg Phe Ala Gly Lys Gly Phe Ser Thr

65

70

75

80

Phe Thr Ala Phe Ile Gly Ser Phe Ser Ser Val Asn Ser Leu Val Leu

85

90

95

Asn Gln Asp Lys Phe Ala Ala Lys Gly Phe Leu Thr Phe Thr Ala Leu

100

105

110

Ile Arg Pro Ile Thr Ser Val Asn Ala Ala Val Ser Asn Glu Val Arg

115

120

125

Glu Leu Ser Lys Gly Phe Pro Thr Phe Ser Ala Phe Ile Arg Ser Phe

130 135 140
Ser Thr Val Asn Ser Leu Val Leu Asn Glu Phe Arg Phe Ala Ala Lys
145 150 155 160
Arg Phe Pro Thr Ile Thr Ala Leu Ile Arg His Phe Ser Ser Val Asn
165 170 175
Ser Ser Met Ser Asn Glu Ile Glu Asp Leu Ser Lys Gly Phe Pro Thr
180 185 190
Leu Thr Ala Leu Ile Arg Pro Phe Ser Arg Val Asn Ser Leu Val Ser
195 200 205
Lys Lys Ala Arg Ala Leu Ser Lys Gly Phe Pro Ala Leu Ala Thr Phe
210 215 220
Ile Arg Pro Phe Ser Ser Val Asn Ser Leu Val Phe Asn Glu Val Arg
225 230 235 240
Phe Val Ala Lys Gly Phe Pro Thr Phe Thr Thr Leu Met Thr His Ser
245 250 255
Ser Ser Val Thr Ser Leu Val Val Asn Glu Phe Arg Phe Met Asp Lys
260 265 270
Gly Phe Leu Thr Ile Thr Ala Phe Ile Arg Pro Phe Ser Ser Val Asn
275 280 285
Tyr Leu Val
290

<210> 2025

<211> 167

<212> PRT

<213> Homo sapiens

<400> 2025

Met Cys Ser Leu Phe His Ala Phe Ile Phe Ala Gln Leu Trp Thr Val
1 5 10 15
Tyr Cys Glu Gln Ser Ala Val Ala Thr Asn Leu Gln Asn Gln Asn Glu
20 25 30
Phe Ser Phe Thr Ala Ile Leu Thr Ala Leu Glu Phe Trp Ser Arg Val
35 40 45
Thr Pro Ser Ile Leu Gln Leu Met Ala His Asn Lys Val Met Val Glu
50 55 60
Met Val Cys Leu His Val Ile Ser Leu Met Glu Ala Leu Gln Glu Cys
65 70 75 80
Asn Ser Thr Ile Phe Val Lys Leu Ile Pro Met Trp Leu Pro Met Ile
85 90 95
Gln Ser Asn Ile Lys His Leu Ser Ala Gly Leu Gln Leu Arg Leu Gln
100 105 110
Ala Ile Gln Asn His Val Asn His His Ser Leu Arg Thr Leu Pro Gly
115 120 125
Ser Gly Gln Ser Ser Ala Gly Leu Ala Ala Leu Arg Lys Trp Leu Gln
130 135 140
Cys Thr Gln Phe Lys Met Ala Gln Val Glu Ile Gln Ser Ser Glu Ala
145 150 155 160
Ala Ser Gln Phe Tyr Pro Leu
165

<210> 2026

<211> 121

<212> PRT

<213> Homo sapiens

<400> 2026

Met Arg Trp Ala Thr Trp Gly Ala Pro His Glu Ala Lys Gly Gly Pro
 1 5 10 15
 Trp Gly Arg Val Ser Phe Gly Gly Ile Val Trp Arg Gly Arg Gln Leu
 20 25 30
 Ala Pro Thr Ala Gly Ser Gly Gly Ile Pro Ala Leu Pro Ile Pro Ala
 35 40 45
 Lys Leu Gly Leu Cys Val Asp Leu Gly Val Asn Ser Cys Phe Leu Leu
 50 55 60
 Cys Phe Cys His Ala Ser Lys Gln Gln Leu Leu His Pro Pro Leu Asn
 65 70 75 80
 Lys Tyr Ala Ser His Glu Val Met Tyr Ala Cys Ser Leu Arg Leu Gln
 85 90 95
 Ser Arg Val Ser Leu Val Gly Val Gly Ala Ala Pro Ala Gly Tyr Thr
 100 105 110
 Leu Pro Phe Pro Tyr Ser Trp Ile Asn
 115 120

<210> 2027

<211> 148

<212> PRT

<213> Homo sapiens

<400> 2027

Met Glu Gly Tyr Leu Gly Arg Lys His Asp Leu Glu Gly Pro Asn Lys
 1 5 10 15
 Lys Ala Ser Asn Arg Ser Trp Asn Asn Leu Tyr Cys Val Leu Arg Asn
 20 25 30

Ser Glu Leu Thr Phe Tyr Lys Asp Ala Lys Asp Leu Ala Leu Gly Met
 35 40 45
 Pro Tyr His Gly Glu Glu Pro Leu Ala Leu Arg His Ala Ile Cys Glu
 50 55 60
 Ile Ala Ala Asn Tyr Lys Lys Lys Lys His Val Phe Lys Leu Arg Leu
 65 70 75 80
 Ser Asn Gly Ser Glu Trp Leu Phe His Gly Lys Asp Glu Glu Glu Met
 85 90 95
 Leu Ser Trp Leu Gln Gly Val Ser Thr Ala Ile Asn Glu Ser Gln Ser
 100 105 110
 Ile Arg Val Lys Ala Gln Ser Leu Pro Leu Pro Ser Leu Ser Gly Pro
 115 120 125
 Asp Ala Ser Leu Gly Lys Lys Asp Lys Glu Lys Arg Phe Ser Phe Phe
 130 135 140
 Pro Lys Lys Lys
 145

<210> 2028

<211> 191

<212> PRT

<213> Homo sapiens

<400> 2028

Met Pro Gly Ala Ile Asp Asp His Cys Pro Ala Gln Pro Gly Glu Glu
 1 5 10 15
 Gly Thr Ala Phe Asn Val Thr Met Gly Tyr Arg Tyr Pro Pro Leu Cys
 20 25 30
 Leu Arg His Ala Thr Arg Cys Ile His Leu Glu Thr Gln Val Trp Ala

35 40 45
Ala Tyr Leu Leu Glu Arg Leu Ala Thr Gly Lys Trp Gly His Leu Val
50 55 60
Ser Gly Leu Ser Leu Cys Pro Leu Arg Gln Met Lys Arg Gly Val Ile
65 70 75 80
Gly Asp Thr Pro Tyr Phe Gln Tyr Lys Pro Val Gly Lys Leu Cys Pro
85 90 95
Lys Asn Phe Glu Gly Pro Ser Lys Thr Leu Ile Trp Gly Asp Cys Val
100 105 110
Asn Ser His Ala Val Val Leu Lys Asn Asp Ser Tyr Ala Leu Val Ile
115 120 125
Asp Trp Ala Pro Lys Gly Tyr Leu Lys Asn Thr Cys Ser Ser Gly Gly
130 135 140
Gly Glu Phe Leu Glu Ala Thr Tyr Phe Ile Ser Tyr Trp Glu Asp Glu
145 150 155 160
Asp His His Pro Thr Leu His Arg Trp Phe Gly Ser Phe Phe Thr Leu
165 170 175
Lys Trp Glu Asp Lys Asp Ile Thr Leu His Pro Gln Gly Leu Val
180 185 190

<210> 2029

<211> 156

<212> PRT

<213> Homo sapiens

<400> 2029

Met Pro Pro Ile Ile Leu Pro Thr Leu Tyr Lys Pro Ile Thr Ala Ile
1 5 10 15

Thr Pro Leu Ile Gln Asn Tyr Lys Ser Thr Phe Arg Val Thr Ala Gln
 20 25 30
 Tyr Pro Gly Ser Arg Gln Leu Trp Asp Lys Glu Arg Gly Lys Ile Cys
 35 40 45
 Arg Ser Leu Glu Arg Leu Lys His Lys Thr Gly Ala Gly Thr Phe Phe
 50 55 60
 Ser Thr Leu Ser Trp Gly Ala Phe Gln Thr Thr Ser Ala Leu Arg Gly
 65 70 75 80
 Leu His Ala His Thr Thr Leu Thr Pro Thr Leu Lys Glu Arg Ser Pro
 85 90 95
 Phe Ser Ser Glu Ser Trp Leu Ile Leu Arg Ser Ile Trp Leu Phe Ser
 100 105 110
 Val Phe Arg Ser Trp His Cys Phe Arg Val Ser Cys Ser Arg Met Gln
 115 120 125
 Ala Ala Ser Ser Ala Val Ser Ser Gly Thr Val Gly Ser Ala Gly Tyr
 130 135 140
 His Pro Trp Glu Lys Leu Glu Asn Leu Arg Glu Ser
 145 150 155

<210> 2030

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2030

Met Glu Val Ser Arg Gly Arg Arg Arg Gly Ala Pro His Ala Gln Thr
 1 5 10 15
 Ser Gly Gly Cys Ala Cys Gly Trp Arg Arg Ser Trp Arg Arg Trp Ala

20 25 30
 Pro Ser Ser Ser Ser Glu Arg Arg Ala Arg Arg Cys Arg Ala Pro Ala
 35 40 45
 Thr Ala Leu Ala Arg Arg Arg Thr Phe Cys Gly Ser Ser Ala Ala Cys
 50 55 60
 Cys Gly Ser Cys Thr Ala Arg Ile Ala Arg Ser Ala Ala Gly Met Ala
 65 70 75 80
 Arg Leu Arg Phe Gly Asn Pro Val Pro Asp Cys Ala Cys Cys Ala Phe
 85 90 95
 Ser Ala Gln Ser Ser Lys Pro Pro Ala Ser Cys Ala Ser Ala Leu Cys
 100 105 110
 Trp Ile Arg Val Leu Gly His Pro Leu Val Lys Gly
 115 120

<210> 2031

<211> 1016

<212> PRT

<213> Homo sapiens

<400> 2031

Met Leu Glu Met Arg Asp Val Tyr Met Glu Glu Asp Val Tyr Gln Leu
 1 5 10 15
 Gln Glu Leu Arg Gln Gln Leu Asp Gln Ala Ser Lys Thr Cys Arg Ile
 20 25 30
 Leu Gln Tyr Arg Leu Arg Lys Ala Glu Arg Arg Ser Leu Arg Ala Ala
 35 40 45
 Gln Thr Gly Gln Val Asp Gly Glu Leu Ile Arg Gly Leu Glu Gln Asp
 50 55 60

Val Lys Val Ser Lys Asp Ile Ser Met Arg Leu His Lys Glu Leu Glu
65 70 75 80
Val Val Glu Lys Lys Arg Ala Arg Leu Glu Glu Glu Asn Glu Glu Leu
85 90 95
Arg Gln Arg Leu Ile Glu Thr Glu Leu Ala Lys Gln Val Leu Gln Thr
100 105 110
Glu Leu Glu Arg Pro Arg Glu His Ser Leu Lys Lys Arg Gly Thr Arg
115 120 125
Ser Leu Gly Lys Ala Asp Lys Lys Thr Leu Val Gln Glu Asp Ser Ala
130 135 140
Asp Leu Lys Cys Gln Leu His Phe Ala Lys Glu Glu Ser Ala Leu Met
145 150 155 160
Cys Lys Lys Leu Thr Lys Leu Ala Lys Glu Asn Asp Ser Met Lys Glu
165 170 175
Glu Leu Leu Lys Tyr Arg Ser Leu Tyr Gly Asp Leu Asp Ser Ala Leu
180 185 190
Ser Ala Glu Glu Leu Ala Asp Ala Pro His Ser Arg Glu Thr Glu Leu
195 200 205
Lys Val His Leu Lys Leu Val Glu Glu Glu Ala Asn Leu Leu Ser Arg
210 215 220
Arg Ile Val Glu Leu Glu Val Glu Asn Arg Gly Leu Arg Ala Glu Met
225 230 235 240
Asp Asp Met Lys Asp His Gly Gly Gly Cys Gly Gly Pro Glu Ala Arg
245 250 255
Leu Ala Phe Ser Ala Leu Gly Gly Gly Glu Cys Gly Glu Ser Leu Ala
260 265 270
Glu Leu Arg Arg His Leu Gln Phe Val Glu Glu Glu Ala Glu Leu Leu
275 280 285
Arg Arg Ser Ser Ala Glu Leu Glu Asp Gln Asn Lys Leu Leu Leu Asn

290 295 300
Glu Leu Ala Lys Phe Arg Ser Glu His Glu Leu Asp Val Ala Leu Ser
305 310 315 320
Glu Asp Ser Cys Ser Val Leu Ser Glu Pro Ser Gln Glu Glu Leu Ala
325 330 335
Ala Ala Lys Leu Gln Ile Gly Glu Leu Ser Gly Lys Val Lys Lys Leu
340 345 350
Gln Tyr Glu Asn Arg Val Leu Leu Ser Asn Leu Gln Arg Cys Asp Leu
355 360 365
Ala Ser Cys Gln Ser Thr Arg Pro Met Leu Glu Thr Asp Ala Glu Ala
370 375 380
Gly Asp Ser Ala Gln Cys Val Pro Ala Pro Leu Gly Glu Thr His Glu
385 390 395 400
Ser His Ala Val Arg Leu Cys Arg Ala Arg Glu Ala Glu Val Leu Pro
405 410 415
Gly Leu Arg Glu Gln Ala Ala Leu Val Ser Lys Ala Ile Asp Val Leu
420 425 430
Val Ala Asp Ala Asn Gly Phe Thr Ala Gly Leu Arg Leu Cys Leu Asp
435 440 445
Asn Glu Cys Ala Asp Phe Arg Leu His Glu Ala Pro Asp Asn Ser Glu
450 455 460
Gly Pro Arg Asp Thr Lys Leu Ile His Ala Ile Leu Val Arg Leu Ser
465 470 475 480
Val Leu Gln Gln Glu Leu Asn Ala Phe Thr Arg Lys Ala Asp Ala Val
485 490 495
Leu Gly Cys Ser Val Lys Glu Gln Gln Glu Ser Phe Ser Ser Leu Pro
500 505 510
Pro Leu Gly Ser Gln Gly Leu Ser Lys Glu Ile Leu Leu Ala Lys Asp
515 520 525

Leu Gly Ser Asp Phe Gln Pro Pro Asp Phe Arg Asp Leu Pro Glu Trp
530 535 540
Glu Pro Arg Ile Arg Glu Ala Phe Arg Thr Gly Asp Leu Asp Ser Lys
545 550 555 560
Pro Asp Pro Ser Arg Ser Phe Arg Pro Tyr Arg Ala Glu Asp Asn Asp
565 570 575
Ser Tyr Ala Ser Glu Ile Lys Glu Leu Gln Leu Val Leu Ala Glu Ala
580 585 590
His Asp Ser Leu Arg Gly Leu Gln Glu Gln Leu Ser Gln Glu Arg Gln
595 600 605
Leu Arg Lys Glu Glu Ala Asp Asn Phe Asn Gln Lys Met Val Gln Leu
610 615 620
Lys Glu Asp Gln Gln Arg Ala Leu Leu Arg Arg Glu Phe Glu Leu Gln
625 630 635 640
Ser Leu Ser Leu Gln Arg Arg Leu Glu Gln Lys Phe Trp Ser Gln Glu
645 650 655
Lys Asn Met Leu Val Gln Glu Ser Gln Gln Phe Lys His Asn Phe Leu
660 665 670
Leu Leu Phe Met Lys Leu Arg Trp Phe Leu Lys Arg Trp Arg Gln Gly
675 680 685
Lys Val Leu Pro Ser Glu Gly Asp Asp Phe Leu Glu Val Asn Ser Met
690 695 700
Lys Glu Leu Tyr Leu Leu Met Glu Glu Glu Glu Ile Asn Ala Gln His
705 710 715 720
Ser Asp Asn Lys Ala Cys Thr Gly Asp Ser Trp Thr Gln Asn Thr Pro
725 730 735
Asn Glu Tyr Ile Lys Thr Leu Ala Asp Met Lys Val Thr Leu Lys Glu
740 745 750
Leu Cys Trp Leu Leu Arg Asp Glu Arg Arg Gly Leu Thr Glu Leu Gln

755 760 765
Gln Gln Phe Ala Lys Ala Lys Ala Thr Trp Glu Thr Glu Arg Ala Glu
770 775 780
Leu Lys Gly His Thr Ser Gln Met Glu Leu Lys Thr Gly Lys Gly Ala
785 790 795 800
Gly Glu Arg Ala Gly Pro Asp Trp Lys Ala Ala Leu Gln Arg Glu Arg
805 810 815
Glu Glu Gln Gln His Leu Leu Ala Glu Ser Tyr Ser Ala Val Met Glu
820 825 830
Leu Thr Arg Gln Leu Gln Ile Ser Glu Arg Asn Trp Ser Gln Glu Lys
835 840 845
Leu Gln Leu Val Glu Arg Leu Gln Gly Glu Lys Gln Gln Val Glu Gln
850 855 860
Gln Val Lys Glu Leu Gln Asn Arg Leu Ser Gln Leu Gln Lys Ala Ala
865 870 875 880
Asp Pro Trp Val Leu Lys His Ser Glu Leu Glu Lys Gln Asp Asn Ser
885 890 895
Trp Lys Glu Thr Arg Ser Glu Lys Ile His Asp Lys Glu Ala Val Ser
900 905 910
Glu Val Glu Leu Gly Gly Asn Gly Leu Lys Arg Thr Lys Ser Val Ser
915 920 925
Ser Met Ser Glu Phe Glu Ser Leu Leu Asp Cys Ser Pro Tyr Leu Ala
930 935 940
Gly Gly Asp Ala Arg Gly Lys Lys Leu Pro Asn Asn Pro Ala Phe Gly
945 950 955 960
Phe Val Ser Ser Glu Pro Gly Asp Pro Glu Lys Asp Thr Lys Glu Lys
965 970 975
Pro Gly Leu Ser Ser Arg Asp Cys Asn His Leu Gly Ala Leu Ala Cys
980 985 990

Gln Asp Pro Pro Gly Arg Gln Lys Leu Pro Phe Leu Leu Ile Leu Ala
 995 1000 1005
 Pro Pro Gln Pro Pro Pro Ile Leu
 1010 1015

<210> 2032

<211> 251

<212> PRT

<213> Homo sapiens

<400> 2032

Met Gln Pro Gly Gly Thr Ala Gly Pro Glu Glu Ala Pro Met Arg Glu
 1 5 10 15
 Ala Glu Ala Gly Pro Pro Gln Val Gly Leu Ser Arg Pro Thr Cys Ser
 20 25 30
 Leu Pro Ala Ser Ser Pro Gly Pro Ala Leu Pro Pro Gly Cys Val Ser
 35 40 45
 Arg Pro Asp Ser Gly Leu Pro Thr Thr Ser Leu Asp Ser Ala Pro Ala
 50 55 60
 Gln Leu Pro Ala Ala Leu Val Asp Pro Gln Leu Pro Glu Ala Lys Leu
 65 70 75 80
 Pro Arg Pro Ser Ser Gly Leu Thr Val Ala Ser Pro Gly Ser Ala Pro
 85 90 95
 Ala Leu Arg Trp His Leu Gln Ala Pro Asn Gly Leu Arg Ser Val Gly
 100 105 110
 Ser Ser Arg Pro Ser Leu Gly Leu Pro Ala Ala Ser Ala Gly Pro Lys
 115 120 125
 Arg Pro Glu Val Gly Leu Ser Arg Pro Ser Ser Gly Leu Pro Ala Ala

130	135	140
Phe Ala Gly Pro Ser Arg Pro Gln Val Gly Leu Glu Leu Gly Leu Glu		
145	150	155
Glu Gln Gln Val Ser Leu Ser Gly Pro Ser Ser Ile Leu Ser Ala Ala		
165	170	175
Ser Pro Gly Ala Lys Leu Pro Arg Val Ser Leu Ser Arg Pro Ser Ser		
180	185	190
Ser Cys Leu Pro Leu Ala Ser Phe Ser Pro Ala Gln Pro Ser Ser Trp		
195	200	205
Leu Ser Ala Ala Phe Pro Gly Pro Ala Phe Asp Phe Trp Arg Pro Leu		
210	215	220
Gln Ala Gln Asn Leu Pro Ser Ser Gly Pro Leu Gln Ala Arg Pro Arg		
225	230	235
Pro Arg Pro His Ser Gly Leu Ser Thr Pro Ser		
245	250	

<210> 2033

<211> 173

<212> PRT

<213> Homo sapiens

<400> 2033

Met Gly Phe Ser Ile Gln His Ala Gln Ala Gly Gln Arg Pro Pro Thr
1 5 10 15
Gln Ala Thr Leu Ser Gly Asn Arg Val Ser Arg Glu Cys Phe Leu Ala
20 25 30
Arg Ser Val Ser Gly Pro Ala Ser Arg Thr Cys Ala His Cys Lys Gly
35 40 45

His Pro Ser Ser Arg Pro Phe Leu Arg Gly Phe Gly Glu Ala Ser Gly
 50 55 60
 Arg Thr Pro Ser Gly Gly Pro Ala Cys Gln His Gly Leu Cys Gln Gly
 65 70 75 80
 Val Leu Ser Phe Leu Gln Val Cys Ile Val Ser Ser Thr Pro Ser Glu
 85 90 95
 Leu Pro Pro Tyr Cys Leu Asp His Thr Lys Leu Trp Gly Cys Gly Gln
 100 105 110
 Pro Val His Phe Pro Asp Leu Val Cys Arg Trp Arg Gln Trp Gln Cys
 115 120 125
 Pro Ser Arg Ala Ala Ala Ser Leu Ser Val Lys Ala Gly Arg His Trp
 130 135 140
 Arg Ala Ala Val Cys Lys Phe Val Ala Thr Ser Lys Gly Ala Gly Gly
 145 150 155 160
 Pro Ser Pro Pro Leu Glu Val Arg Met Ser Tyr Pro Lys
 165 170

<210> 2034

<211> 205

<212> PRT

<213> Homo sapiens

<400> 2034

Met Lys His Pro Arg Leu Glu Asp Gly Asp Trp Leu Phe His Leu Val
 1 5 10 15
 Ile Pro Ala His Ser Ala Val Leu Ser Gln Leu Arg Val Ser Pro Ser
 20 25 30
 Leu Tyr Val Gly Leu Pro Phe Leu Pro Phe Cys Leu Phe Cys His Pro

35 40 45
Ala Ala Val Pro His His Met Pro Gln Leu Pro Pro Cys Pro Ala Ser
50 55 60
Leu Leu His Ser Pro Phe His Ala Leu His Leu Pro Thr Leu Pro Gln
65 70 75 80
Gly Cys Pro Phe Pro Leu Pro Ala Leu Tyr Pro Pro Gln Pro Phe Pro
85 90 95
Ala Leu Trp Pro Gly Arg Gly Ala Pro Leu Cys Cys His Pro Leu Asp
100 105 110
Leu His Gly Phe Ala Leu Pro Pro Val Ser Pro Pro Ala Leu Pro Pro
115 120 125
Pro Asp Leu Leu Ile Ser Thr Leu Leu Pro Phe Ser Ser Leu Cys Val
130 135 140
Val Val Ser Ile Ser Cys Leu Cys Gly Arg Leu Ser Leu Leu Phe Val
145 150 155 160
Pro Leu Leu Val Ser Phe Ser Leu Cys Leu Ser Cys Leu Phe Ser Val
165 170 175
Ala Ser Val Gln Cys Thr Tyr Ala Asp Phe Gly Met Gly Asp Ala Gly
180 185 190
Gly Trp Gly Ala Leu Pro Trp Gly Val Val Phe His Leu
195 200 205

<210> 2035

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2035

Met Lys Ala Gln Leu Leu Gly Ala Gly Ser Ala His His Leu Cys Asp
 1 5 10 15
 Gly Cys Asn Ser His Gln Thr Pro Thr Arg Pro Arg Leu Trp Ser Asp
 20 25 30
 Arg Glu Gly Pro Gly Glu Asp Ser Thr Thr Leu Ser Pro Arg Gln Glu
 35 40 45
 Gly Thr Cys Ser Ser Pro Pro Ala Pro Leu Arg Pro Glu Leu Pro Ser
 50 55 60
 Gln Ser His Pro Glu Tyr Leu Lys Ala Leu Gly Phe Pro Arg Leu Leu
 65 70 75 80
 Pro Gln Arg Ser His Glu His His Val Ser Ser Ser Ser Lys Ser Ser
 85 90 95
 Ala Cys Gly Ala Gly Pro Gly Val Gly Ala Ala Lys Gly Ala Leu Cys
 100 105 110
 Arg Thr Arg Thr Gln His Gly His Ser Glu Cys Gly Pro Gly Ile Pro
 115 120 125
 Lys Pro Pro Ser Arg Glu Ser Glu Ala Glu Gly Asp Gly Gly Arg Gln
 130 135 140
 Glu Ala Trp Leu Cys Val Leu Gly Lys Leu Arg Phe Leu Thr Leu Ser
 145 150 155 160
 Leu Asn Val Gln Ala Gly Val Lys Ser Val Thr Ala Gly Ala Arg Arg
 165 170 175
 Leu Leu Cys Glu Phe His Gly Ala Ser Ala Gly Ala Val Leu Phe Asn
 180 185 190
 Ala Arg Thr Cys Ser Val Trp Ala Ser Leu Gly Leu Trp Ala Leu Pro
 195 200 205
 Ala Leu Gly His Arg Pro Gly Arg Leu Tyr Leu Asn Ala His Val Val
 210 215 220
 Pro Gly Pro Pro Gln Ser Ser Arg Pro Arg Pro

225

230

235

<210> 2036

<211> 162

<212> PRT

<213> Homo sapiens

<400> 2036

Met Gln Gly His Ser Val His Thr Gly Pro Thr Val Leu Pro Gly Ser

1

5

10

15

Glu Asp Gly Ala Pro Ser Pro Ala Val Gly Pro Ala Ala Lys Ala Ala

20

25

30

Val Pro Cys Pro Cys Arg Arg Arg Arg Gly Trp Arg Trp Trp Pro Pro

35

40

45

Ala Gly Thr Pro Ala Ala Ala Ala Gly Arg Thr Val Glu Gly Ala Gly

50

55

60

Ser Asp Arg Asp Pro Lys Gly Arg Thr Ala Ser Ala Pro Gln His Ala

65

70

75

80

Arg Gly Gln Gly His Val Pro His Gly Tyr Leu Val Leu Pro Gly Asn

85

90

95

Leu Cys Gln Ala Pro Thr Pro Arg Glu Pro Arg Thr Pro Pro Pro Pro

100

105

110

Gln Asn Pro Trp Pro Gln Val Gln Gly Leu Trp Leu Leu Cys Pro Ala

115

120

125

Gln Pro Leu Ser Val Gly Pro Trp Ala Gly Leu Gly Ser Pro Pro Leu

130

135

140

Pro Pro Ser Leu Gly Gln Pro Arg His Pro Gln Val Gly Thr Asn Pro

145

150

155

160

Cys Ser

<210> 2037

<211> 312

<212> PRT

<213> Homo sapiens

<400> 2037

Met Asn Ile Leu Gly Leu Val Leu Phe Ala Leu Val Leu Gly Val Ala

1

5

10

15

Leu Lys Lys Leu Gly Ser Glu Gly Glu Asp Leu Ile Arg Phe Phe Asn

20

25

30

Ser Leu Asn Glu Ala Thr Met Val Leu Val Ser Trp Ile Met Trp Tyr

35

40

45

Val Pro Val Gly Ile Met Phe Leu Val Gly Ser Lys Ile Val Glu Met

50

55

60

Lys Asp Ile Ile Val Leu Val Thr Ser Leu Gly Lys Tyr Ile Phe Ala

65

70

75

80

Ser Ile Leu Gly His Val Ile His Gly Gly Ile Val Leu Pro Leu Ile

85

90

95

Tyr Phe Val Phe Thr Arg Lys Asn Pro Phe Arg Phe Leu Leu Gly Leu

100

105

110

Leu Ala Pro Phe Ala Thr Ala Phe Ala Thr Cys Ser Ser Ser Ala Thr

115

120

125

Leu Pro Ser Met Met Lys Cys Ile Glu Glu Asn Asn Gly Val Asp Lys

130

135

140

Arg Ile Ser Arg Phe Ile Leu Pro Ile Gly Ala Thr Val Asn Met Asp

145 150 155 160
Gly Ala Ala Ile Phe Gln Cys Val Ala Ala Val Phe Ile Ala Gln Leu
 165 170 175
Asn Asn Val Glu Leu Asn Ala Gly Gln Ile Phe Thr Ile Leu Val Thr
 180 185 190
Ala Thr Ala Ser Ser Val Gly Ala Ala Gly Val Pro Ala Gly Gly Val
 195 200 205
Leu Thr Ile Ala Ile Ile Leu Glu Ala Ile Gly Leu Pro Thr His Asp
 210 215 220
Leu Pro Leu Ile Leu Ala Val Asp Trp Ile Val Asp Arg Thr Thr Thr
225 230 235 240
Val Val Asn Val Glu Gly Asp Ala Leu Gly Ala Gly Ile Leu His His
 245 250 255
Leu Asn Gln Lys Ala Thr Lys Lys Gly Glu Gln Glu Leu Ala Glu Val
 260 265 270
Lys Val Glu Ala Ile Pro Asn Cys Lys Ser Glu Glu Glu Thr Ser Pro
 275 280 285
Leu Val Thr His Gln Asn Pro Ala Gly Pro Val Ala Ser Ala Pro Glu
 290 295 300
Leu Glu Ser Lys Glu Ser Val Leu
305 310

<210> 2038

<211> 249

<212> PRT

<213> Homo sapiens

<400> 2038

Met Arg Ala Ser Gly His Pro Val Thr Leu Pro Thr Pro Glu Gly Gln
 1 5 10 15
 Val His His Pro Glu Ser Cys Leu Ile Ser Leu Gln Thr His Cys His
 20 25 30
 Asn Asp Ile Val Asn Pro Leu Leu Asp Cys Gly Ala Asp Val Asn Lys
 35 40 45
 Cys Ser Asp Glu Gly Leu Thr Ala Leu Ser Met Cys Phe Leu Leu His
 50 55 60
 Tyr Pro Ala Gln Ser Phe Lys Pro Asn Val Ala Glu Arg Thr Ile Pro
 65 70 75 80
 Glu Pro Gln Glu Pro Pro Lys Phe Pro Val Val Pro Ile Leu Ser Ser
 85 90 95
 Ser Phe Met Asp Thr Asn Leu Glu Ser Leu Tyr Tyr Glu Val Asn Val
 100 105 110
 Pro Ser Gln Gly Ser Tyr Glu Leu Arg Pro Pro Pro Ala Pro Leu Leu
 115 120 125
 Leu Pro Arg Val Ser Gly Ser His Glu Gly Gly His Phe Gln Asp Thr
 130 135 140
 Gly Gln Cys Gly Gly Ser Met Asp His Arg Ser Ser Ser Leu Lys Gly
 145 150 155 160
 Asp Ser Pro Leu Val Lys Gly Ser Leu Gly His Val Glu Ser Gly Leu
 165 170 175
 Glu Asp Val Leu Gly Asn Thr Asp Arg Gly Ser Leu Cys Ser Ala Glu
 180 185 190
 Thr Lys Phe Glu Ser Asn Val Cys Val Cys Asp Phe Ser Ile Glu Leu
 195 200 205
 Ser Gln Ala Met Leu Glu Arg Ser Ala Gln Ser His Ser Leu Leu Lys
 210 215 220
 Met Ala Ser Pro Ser Pro Cys Thr Ser Ser Phe Asp Lys Gly Thr Met

225 230 235 240
Arg Arg Met Ala Leu Ser Met Ile Glu
245

<210> 2039

<211> 110

<212> PRT

<213> Homo sapiens

<400> 2039

Met Thr Phe Ile Thr Glu Ile Glu Glu Ile Ile Leu Lys Phe Met Trp
1 5 10 15
Ser His Lys Arg His Arg Ile Ala Lys Ala Ile Leu Ser Lys Lys Asn
20 25 30
Lys Thr Glu Gly Ile Thr Leu Pro Phe Phe Lys Leu Tyr Tyr Ser Ala
35 40 45
Ile Val Thr Glu Lys Ala Trp Tyr Cys His Lys Asn Arg His Val Asp
50 55 60
Gln Trp Asn Thr Ile Glu Asn Pro Glu Thr Asn Pro Tyr Thr Tyr Ser
65 70 75 80
Glu Leu Ile Phe Asp Lys Gly Ala Lys Ser Ile His Trp Arg Lys Glu
85 90 95
Gly Leu Phe Asn Lys Ser Cys Trp Glu His Trp Ile Ser Ile
100 105 110

<210> 2040

<211> 185

<212> PRT

<213> Homo sapiens

<400> 2040

Met Ser Leu Pro Glu Val Gln Lys Asp Lys Tyr Pro Glu Glu Phe Ser

1 5 10 15

Leu Leu Lys Leu Gln Thr Lys Asp Gly His Arg Pro Glu Trp Thr Phe

20 25 30

Tyr Pro Arg Phe Ser Ser Asn Ile His Thr Tyr His Val Gly Lys Gln

35 40 45

Cys Phe Phe Asn Gly Val Phe Leu Gly Asn Lys Arg Ser Leu Ser Glu

50 55 60

Arg Thr Val Asp Lys Cys Phe Gly Arg Lys Lys Tyr Asp Ile Asp Pro

65 70 75 80

Arg Asn Gly Ile Pro Lys Leu Thr Pro Gly Asp Asn Pro Tyr Met Tyr

85 90 95

Pro Glu Gln Ser Lys Gly Phe His Lys Ala Gly Ser Met Leu Pro Pro

100 105 110

Val Asn Phe Ser Ile Val Pro Tyr Glu Lys Lys Phe Asp Thr Phe Ile

115 120 125

Pro Leu Glu Pro Leu Pro Gln Ile Pro Asn Leu Pro Phe Trp Val Lys

130 135 140

Glu Lys Ala Asn Ser Leu Lys Asn Glu Ile Gln Glu Val Glu Glu Leu

145 150 155 160

Asp Asn Trp Gln Pro Ala Val Pro Leu Met His Met Leu His Leu Ser

165 170 175

Gly Ala Leu Asp Phe Pro Arg Gln Ser

180 185

<210> 2041

<211> 165

<212> PRT

<213> Homo sapiens

<400> 2041

Met Gly Cys Phe Tyr Lys Val Gly Lys Phe Ser Arg Glu Ser Glu Gly

1 5 10 15

Gly Ile Leu Tyr Gly Val Glu Arg Glu Gly Gly Gly Pro Gly Gly Gly

20 25 30

Thr Val Ala Pro Gln Arg Ala Ala Ser Gly Leu Gln Arg Ala Ser Arg

35 40 45

Val Ala Gly Gly Arg Ala Gly Arg Gly Ala Cys Asp Ala Gly Gly Pro

50 55 60

Pro Phe Pro Arg Gly Pro Lys Gly Leu Gln Leu Pro Trp Ser Gly Ala

65 70 75 80

Arg Ala Thr Arg Cys Pro Arg Arg Val Gly Asn Gly Ala Pro Arg Val

85 90 95

Leu Leu Thr Tyr Val Glu Arg Ser Ala Gln Gly Arg Arg Ile Leu His

100 105 110

Val Gly Ala Arg Phe Ser Thr Thr Arg Gln Pro Trp Ala Ser Ala Gly

115 120 125

Ala Gln Pro Ser Pro Pro Pro Gln Glu Ala Pro Ala Pro Arg Pro Pro

130 135 140

Gly Pro Ser Ala Arg Thr Trp Glu Asp Leu Val Leu Asn Ala Pro Ser

145 150 155 160

Leu Val Arg Pro Arg

165

<210> 2042

<211> 141

<212> PRT

<213> Homo sapiens

<400> 2042

Met Cys His Pro Phe Phe Phe Leu Ser Arg Ser Val Ala Gln Ala Gly

1 5 10 15

Val Arg Trp Cys Asp Leu Cys Ser Leu Gln Ala Pro Pro Pro Gly Tyr

20 25 30

Thr Pro Phe Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Tyr Gly Arg

35 40 45

Pro Pro Arg Arg Pro Ala Asp Phe Leu Tyr Phe Leu Val Glu Thr Gly

50 55 60

Phe His Arg Ala Ser Gln Asp Gly Leu Asp Leu Leu Thr Thr Trp Ser

65 70 75 80

Ala Arg Ile Ser Leu Gln Ser Ala Gly Ile Thr Gly Val Ser His Cys

85 90 95

Ala Pro Ala Trp Ala Thr Glu Trp Asp Ser Val Ser Asn Lys Thr Lys

100 105 110

Gln Lys Asn Ser Tyr Lys Asn Thr Gly Lys Met Phe Gln Val Ile Arg

115 120 125

Ile Phe Trp His Trp Ser Met Arg Val Gly Ser Cys Leu

130 135 140

<210> 2043

<211> 1034

<212> PRT

<213> Homo sapiens

<400> 2043

Met Val Asp Ala Thr Thr Arg Met Gly Tyr Thr Pro Leu His Val Ala

1 5 10 15

Ser His Tyr Gly Asn Ile Lys Leu Val Lys Phe Leu Leu Gln His Gln

20 25 30

Ala Asp Val Asn Ala Lys Thr Lys Leu Gly Tyr Ser Pro Leu His Gln

35 40 45

Ala Ala Gln Gln Gly His Thr Asp Ile Val Thr Leu Leu Leu Lys Asn

50 55 60

Gly Ala Ser Pro Asn Glu Val Ser Ser Asp Gly Thr Thr Pro Leu Ala

65 70 75 80

Ile Ala Lys Arg Leu Gly Tyr Ile Ser Val Thr Asp Val Leu Lys Val

85 90 95

Val Thr Asp Glu Thr Ser Phe Val Leu Val Ser Asp Lys His Arg Met

100 105 110

Ser Phe Pro Glu Thr Val Asp Glu Ile Leu Asp Val Ser Glu Asp Glu

115 120 125

Gly Thr Ala His Ile Thr Ile Met Gly Glu Glu Leu Ile Ser Phe Lys

130 135 140

Ala Glu Arg Arg Asp Ser Arg Asp Val Asp Glu Glu Lys Glu Leu Leu

145 150 155 160

Asp Phe Val Pro Lys Leu Asp Gln Val Val Glu Ser Pro Ala Ile Pro

165 170 175

Arg Ile Pro Cys Ala Met Pro Glu Thr Val Val Ile Arg Ser Glu Glu

180 185 190

Gln Glu Gln Ala Ser Lys Glu Tyr Asp Glu Asp Ser Leu Ile Pro Ser
195 200 205

Ser Pro Ala Thr Glu Thr Ser Asp Asn Ile Ser Pro Val Ala Ser Pro
210 215 220

Val His Thr Gly Phe Leu Val Ser Phe Met Val Asp Ala Arg Gly Gly
225 230 235 240

Ser Met Arg Gly Ser Arg His Asn Gly Leu Arg Val Val Ile Pro Pro
245 250 255

Arg Thr Cys Ala Ala Pro Thr Arg Ile Thr Cys Arg Leu Val Lys Pro
260 265 270

Gln Lys Leu Ser Thr Pro Pro Pro Leu Ala Glu Glu Glu Gly Leu Ala
275 280 285

Ser Arg Ile Ile Ala Leu Gly Pro Thr Gly Ala Gln Phe Leu Ser Pro
290 295 300

Val Ile Val Glu Ile Pro His Phe Ala Ser His Gly Arg Gly Asp Arg
305 310 315 320

Glu Leu Val Val Leu Arg Ser Glu Asn Gly Ser Val Trp Lys Glu His
325 330 335

Arg Ser Arg Tyr Gly Glu Ser Tyr Leu Asp Gln Ile Leu Asn Gly Met
340 345 350

Asp Glu Glu Leu Gly Ser Leu Glu Glu Leu Glu Lys Lys Arg Val Cys
355 360 365

Arg Ile Ile Thr Thr Asp Phe Pro Leu Tyr Phe Val Ile Met Ser Arg
370 375 380

Leu Cys Gln Asp Tyr Asp Thr Ile Gly Pro Glu Gly Gly Ser Leu Lys
385 390 395 400

Ser Lys Leu Val Pro Leu Val Gln Ala Thr Phe Pro Glu Asn Ala Val
405 410 415

Thr Lys Arg Val Lys Leu Ala Leu Gln Ala Gln Pro Val Pro Asp Glu

420 425 430
Leu Val Thr Lys Leu Leu Gly Asn Gln Ala Thr Phe Ser Pro Ile Val
435 440 445
Thr Val Glu Pro Arg Arg Arg Lys Phe His Arg Pro Ile Gly Leu Arg
450 455 460
Ile Pro Leu Pro Pro Ser Trp Thr Asp Asn Pro Arg Asp Ser Gly Glu
465 470 475 480
Gly Asp Thr Thr Ser Leu Arg Leu Leu Cys Ser Val Ile Gly Gly Thr
485 490 495
Asp Gln Ala Gln Trp Glu Asp Ile Thr Gly Thr Thr Lys Leu Val Tyr
500 505 510
Ala Asn Glu Cys Ala Asn Phe Thr Thr Asn Val Ser Ala Arg Phe Trp
515 520 525
Leu Ser Asp Cys Pro Arg Thr Ala Glu Ala Val Asn Phe Ala Thr Leu
530 535 540
Leu Tyr Lys Glu Leu Thr Ala Val Pro Tyr Met Ala Lys Phe Val Ile
545 550 555 560
Phe Ala Lys Met Asn Asp Pro Arg Glu Gly Arg Leu Arg Cys Tyr Cys
565 570 575
Met Thr Asp Asp Lys Val Asp Lys Thr Leu Glu Gln His Glu Asn Phe
580 585 590
Val Glu Val Ala Arg Ser Arg Asp Ile Glu Val Leu Glu Gly Met Ser
595 600 605
Leu Phe Ala Glu Leu Ser Gly Asn Leu Val Pro Val Lys Lys Ala Ala
610 615 620
Gln Gln Arg Ser Phe His Phe Gln Ser Phe Arg Glu Asn Arg Leu Ala
625 630 635 640
Met Pro Val Lys Val Arg Asp Ser Ser Arg Glu Pro Gly Gly Ser Leu
645 650 655

Ser Phe Leu Arg Lys Ala Met Lys Tyr Glu Asp Thr Gln His Ile Leu
 660 665 670
 Cys His Leu Asn Ile Thr Met Pro Pro Cys Ala Lys Gly Ser Gly Ala
 675 680 685
 Glu Asp Arg Arg Arg Thr Pro Thr Pro Leu Ala Leu Arg Tyr Ser Ile
 690 695 700
 Leu Ser Glu Ser Thr Pro Gly Ser Leu Ser Gly Thr Glu Gln Ala Glu
 705 710 715 720
 Met Lys Met Ala Val Ile Ser Glu His Leu Gly Leu Ser Trp Ala Glu
 725 730 735
 Leu Ala Arg Glu Leu Gln Phe Ser Val Glu Asp Ile Asn Arg Ile Arg
 740 745 750
 Val Glu Asn Pro Asn Ser Leu Leu Glu Gln Ser Val Ala Leu Leu Asn
 755 760 765
 Leu Trp Val Ile Arg Glu Gly Gln Asn Ala Asn Met Glu Asn Leu Tyr
 770 775 780
 Thr Ala Leu Gln Ser Ile Asp Arg Gly Glu Ile Val Asn Met Leu Glu
 785 790 795 800
 Gly Ser Gly Arg Gln Ser Arg Asn Leu Lys Pro Asp Arg Arg His Thr
 805 810 815
 Asp Arg Asp Tyr Ser Leu Ser Pro Ser Gln Met Asn Gly His Gln Arg
 820 825 830
 Gly Gln Ala Arg Ile Thr His Ser Pro Thr Val Ser Gln Val Thr Glu
 835 840 845
 Arg Ser Gln Asp Arg Leu Gln Asp Trp Asp Ala Asp Gly Ser Ile Val
 850 855 860
 Ser Tyr Leu Gln Asp Ala Ala Gln Gly Ser Trp Gln Glu Glu Val Thr
 865 870 875 880
 Gln Gly Pro His Ser Phe Gln Gly Thr Ser Thr Met Thr Glu Gly Leu

885 890 895
Glu Pro Gly Gly Ser Gln Glu Tyr Glu Lys Val Leu Val Ser Val Ser
900 905 910
Glu His Thr Trp Thr Glu Gln Pro Glu Ala Glu Ser Ser Gln Ala Asp
915 920 925
Arg Asp Arg Arg Gln Gln Gly Gln Glu Glu Gln Val Gln Glu Ala Lys
930 935 940
Asn Thr Phe Thr Gln Val Val Gln Gly Asn Glu Phe Gln Asn Ile Pro
945 950 955 960
Gly Glu Gln Val Thr Glu Glu Gln Phe Thr Asp Glu Gln Gly Asn Ile
965 970 975
Val Thr Lys Lys Ile Ile Arg Lys Val Val Arg Gln Ile Asp Leu Ser
980 985 990
Ser Ala Asp Ala Ala Gln Glu His Glu Glu Val Glu Leu Arg Gly Ser
995 1000 1005
Gly Leu Gln Pro Asp Leu Ile Glu Gly Arg Lys Gly Ala Gln Ile Val
1010 1015 1020
Lys Arg Ala Ser Leu Lys Arg Gly Lys Gln
1025 1030

<210> 2044

<211> 496

<212> PRT

<213> Homo sapiens

<400> 2044

Met Val Glu Pro His Gln Glu Pro Arg His Ser Lys Val Gly Leu Gln

1

5

10

15

Asp Asn Pro Trp Phe Cys Asp Cys His Ile Ser Lys Met Ile Glu Leu
 20 25 30
 Ser Lys Val Val Asp Pro Ala Ile Val Leu Leu Asp Pro Leu Met Thr
 35 40 45
 Cys Ser Glu Pro Glu Arg Leu Thr Gly Ile Leu Phe Gln Arg Ala Glu
 50 55 60
 Leu Glu His Cys Leu Lys Pro Ser Val Met Thr Ser Ala Thr Lys Ile
 65 70 75 80
 Met Ser Ala Leu Gly Ser Asn Val Leu Leu Arg Cys Asp Ala Thr Gly
 85 90 95
 Phe Pro Thr Pro Gln Ile Thr Trp Thr Arg Ser Asp Ser Ser Pro Val
 100 105 110
 Asn Tyr Thr Val Ile Gln Glu Ser Pro Glu Glu Gly Val Arg Trp Ser
 115 120 125
 Ile Met Ser Leu Thr Gly Ile Ser Ser Lys Asp Ala Gly Asp Tyr Lys
 130 135 140
 Cys Lys Ala Lys Asn Leu Ala Gly Leu Ser Glu Ala Val Val Thr Val
 145 150 155 160
 Thr Val Leu Gly Ile Thr Thr Thr Pro Ile Pro Pro Asp Thr Ser Glu
 165 170 175
 Arg Thr Gly Asp His Pro Glu Trp Asp Val Gln Pro Gly Ser Gly Arg
 180 185 190
 Ser Thr Ser Val Ser Ser Ala Ser Ser Tyr Leu Trp Ser Ser Ser Phe
 195 200 205
 Ser Pro Thr Ser Ser Phe Ser Ala Ser Thr Leu Ser Pro Pro Ser Thr
 210 215 220
 Ala Ser Phe Ser Leu Ser Pro Phe Ser Ser Ser Thr Val Ser Ser Thr
 225 230 235 240
 Thr Thr Leu Ser Thr Ser Ile Ser Ala Ser Thr Thr Met Ala Asn Lys

245	250	255
Arg Ser Phe Gln Leu His Gln Gly Gly Lys Arg Asn Leu Lys Val Ala		
260	265	270
Lys Asn Gly Ser Lys Leu Pro Pro Ala Ser Thr Ser Lys Lys Glu Glu		
275	280	285
Leu Ala Leu Leu Asp Gln Thr Met Leu Thr Glu Thr Asn Ala Ala Ile		
290	295	300
Glu Asn Leu Arg Val Val Ser Glu Thr Lys Glu Ser Val Thr Leu Thr		
305	310	315
320		
Trp Asn Met Ile Asn Thr Thr His Asn Ser Ala Val Thr Val Leu Tyr		
325	330	335
Ser Lys Tyr Gly Gly Lys Asp Leu Leu Leu Leu Asn Ala Asp Ser Ser		
340	345	350
Lys Asn Gln Val Thr Ile Asp Gly Leu Glu Pro Gly Gly Gln Tyr Met		
355	360	365
Ala Cys Val Cys Pro Lys Gly Val Pro Pro Gln Lys Asp Gln Cys Ile		
370	375	380
Thr Phe Ser Thr Glu Arg Val Glu Gly Asp Asp Ser Gln Trp Ser Leu		
385	390	395
400		
Leu Leu Val Val Thr Ser Thr Ala Cys Val Val Ile Leu Pro Leu Ile		
405	410	415
Cys Phe Leu Leu Tyr Lys Val Cys Lys Leu Gln Cys Lys Ser Glu Pro		
420	425	430
Phe Trp Glu Asp Asp Leu Ala Lys Glu Thr Tyr Ile Gln Phe Glu Thr		
435	440	445
Leu Phe Pro Arg Ser Gln Ser Val Gly Glu Leu Trp Thr Arg Ser His		
450	455	460
Arg Asp Asp Ser Glu Lys Leu Leu Leu Cys Ser Arg Ser Ser Val Glu		
465	470	475
480		

Ser Gln Val Thr Phe Lys Ser Glu Gly Ser Arg Pro Glu Tyr Tyr Cys

485

490

495

<210> 2045

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2045

Met Thr Phe Val Phe Val Phe Val Phe Cys Phe Ser Arg Gln Gly Leu

1

5

10

15

Ala Leu Ser Ser Gly Met Glu Cys Ser Gly Val Ile Ser Ala His Cys

20

25

30

Gly Phe Arg His Pro Val Ser Ser Asp Pro Pro Thr Ala Thr Ser Gln

35

40

45

Val Ala Gly Arg Ser Gly Ala Arg His His Val Trp Leu Val Phe Val

50

55

60

Phe Phe Val Glu Thr Glu Phe Pro His Val Ala Gln Ala Ala Leu Arg

65

70

75

80

Leu Leu Ser Ser Ser Asp Leu Pro Pro Ala Trp Pro Ser Gln Ser Ser

85

90

95

Gly Ile Thr Gly Val Ser His Cys Ala Trp Pro Gly

100

105

<210> 2046

<211> 404

<212> PRT

<213> Homo sapiens

<400> 2046

Met Thr Val Ser Ala Ala Thr Arg Val Met Leu Leu Phe Ser Val Ala
 1 5 10 15
 Gly Trp Gly His Leu Ser Leu Ala Gly Asp His Ile Leu Ala Ser Asn
 20 25 30
 Trp Gly Ala Lys Ala Ala Leu Gln Leu Glu Gly Pro Gly Leu His Ser
 35 40 45
 Leu Thr Ser Cys Ser Thr Ala Lys Ser Leu Gly Lys Lys Pro Cys Val
 50 55 60
 Gly Met Arg Glu Ala Glu Leu Ser Arg Val Arg Val Gly Pro Lys Gln
 65 70 75 80
 Val Asn Ser Pro Leu Ala Pro Gln Thr Cys Ser Ala His Gly Gly Arg
 85 90 95
 Thr Gly Val Leu Leu Ser Pro Pro Pro Lys Ala Ala Cys Val Phe Leu
 100 105 110
 Ser Ser Asn Leu Gln Pro Gly Glu Glu Met Glu Ala Cys Glu Glu Leu
 115 120 125
 Ala Leu Ala Leu Ser Arg Gly Leu Gln Leu Asp Thr Gln Arg Ser Ser
 130 135 140
 Arg Asp Ser Leu Gln Cys Ser Ser Gly Tyr Ser Thr Gln Thr Thr Thr
 145 150 155 160
 Pro Cys Cys Ser Glu Asp Thr Ile Pro Ser Gln Val Ser Asp Tyr Asp
 165 170 175
 Tyr Phe Ser Val Ser Gly Asp Gln Glu Ala Asp Gln Gln Glu Phe Asp
 180 185 190
 Lys Ser Ser Thr Ile Pro Arg Asn Ser Asp Ile Ser Gln Ser Tyr Arg
 195 200 205

Arg Met Phe Gln Ala Lys Arg Pro Ala Ser Thr Ala Gly Leu Pro Thr
 210 215 220
 Thr Leu Gly Pro Ala Met Val Thr Pro Gly Val Ala Thr Ile Arg Arg
 225 230 235 240
 Thr Pro Ser Thr Lys Pro Ser Val Arg Arg Gly Thr Ile Gly Ala Gly
 245 250 255
 Pro Ile Pro Ile Lys Thr Pro Val Ile Pro Val Lys Thr Pro Thr Val
 260 265 270
 Pro Asp Leu Pro Gly Val Leu Pro Ala Pro Pro Asp Gly Pro Glu Glu
 275 280 285
 Arg Gly Glu His Ser Pro Glu Ser Pro Ser Val Gly Glu Gly Pro Gln
 290 295 300
 Gly Val Thr Ser Met Pro Ser Ser Met Trp Ser Gly Gln Ala Ser Val
 305 310 315 320
 Asn Pro Pro Leu Pro Gly Pro Lys Pro Ser Ile Pro Glu Glu His Arg
 325 330 335
 Gln Ala Ile Pro Glu Ser Glu Ala Glu Asp Gln Glu Arg Glu Pro Pro
 340 345 350
 Ser Ala Thr Val Ser Pro Gly Gln Ile Pro Glu Ser Asp Pro Ala Asp
 355 360 365
 Leu Ser Pro Arg Asp Ala Pro Gln Gly Glu Asp Met Leu Asn Ala Ile
 370 375 380
 Arg Arg Gly Val Lys Leu Lys Lys Thr Thr Thr Asn Asp Arg Ser Ala
 385 390 395 400
 Pro Arg Phe Ser

<210> 2047

<211> 382

<212> PRT

<213> Homo sapiens

<400> 2047

Met Val Pro Arg Thr His Met Ser Thr Asn Gly Thr Asn Pro Gln Ser

1 5 10 15

Leu Pro Cys Pro Gly Phe Arg Leu Ser Leu Leu Asp Met Thr Leu Leu

20 25 30

Asp Ser Pro Cys Thr Gln Phe Arg Cys Glu Glu Leu Gly Arg Val Pro

35 40 45

Phe Ile Ile Phe Leu Leu Ser Leu Phe Cys Gln Asn Thr Trp Glu Glu

50 55 60

Met Ala Leu Gln Val Thr Pro Thr Gln His Gln Ala Pro Gly Trp Gly

65 70 75 80

Ile His Ser Leu Ile Leu Ser Lys Ser Ser Ser Leu Leu Ile Pro Leu

85 90 95

His Phe Leu Cys Leu Leu Met Pro Val Ala Leu Ser Pro Leu Cys Phe

100 105 110

Gly Ser Gln Ala Gln Ile Phe Arg Pro Leu Lys Phe Asn Thr Thr Ser

115 120 125

Val Ile Lys Ile Ala Val Glu Pro Val Asn Pro Ser Glu Leu Pro Lys

130 135 140

Met Leu Asp Gly Leu Arg Lys Val Asn Lys Ser Tyr Pro Ser Leu Thr

145 150 155 160

Thr Lys Val Glu Glu Ser Gly Glu His Val Ile Leu Gly Thr Gly Glu

165 170 175

Leu Tyr Leu Asp Cys Val Met His Asp Leu Arg Lys Met Tyr Ser Glu

180 185 190

Ile Asp Ile Lys Val Ala Asp Pro Val Val Thr Phe Cys Glu Thr Val
195 200 205
Val Glu Thr Ser Ser Leu Lys Cys Phe Ala Glu Thr Pro Asn Lys Lys
210 215 220
Asn Lys Ile Thr Met Ile Ala Glu Pro Leu Glu Lys Gly Leu Ala Glu
225 230 235 240
Asp Ile Glu Asn Glu Val Val Gln Ile Thr Trp Asn Arg Lys Lys Leu
245 250 255
Gly Glu Phe Phe Gln Thr Lys Tyr Asp Trp Asp Leu Leu Ala Ala Arg
260 265 270
Ser Ile Trp Ala Phe Gly Pro Asp Ala Thr Gly Pro Asn Ile Leu Val
275 280 285
Asp Asp Thr Leu Pro Ser Glu Val Asp Lys Ala Leu Leu Gly Ser Val
290 295 300
Lys Asp Ser Ile Val Gln Gly Phe Gln Trp Gly Thr Arg Glu Gly Pro
305 310 315 320
Leu Cys Asp Glu Cys Lys Ser Thr Ser Thr Pro Pro Pro Gln Ser Ser
325 330 335
Arg Val Leu Ala Ala Arg His Met Ser Gly Met Gly Ser Pro Ser Leu
340 345 350
Gly Phe Gly Arg Arg Ser Ser Leu Gly Tyr Thr Gly Pro Ser Gln Val
355 360 365
Leu Gly Gln Leu Leu Pro Phe Ser Phe Leu Ile Leu Val Val
370 375 380

<210> 2048

<211> 109

<212> PRT

<213> Homo sapiens

<400> 2048

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Met Gly Glu Asp Phe Met Met Lys Met Pro Lys Ala Ile Ala Thr Lys
  1             5             10             15
Glu Lys Ile Asp Lys Arg Asn Leu Ile Lys Leu Asn Asn Phe Cys Thr
          20             25             30
Ala Lys Glu Thr Ser Asn Arg Val Lys Arg Gln Pro Arg Glu Trp Glu
          35             40             45
Gln Ile Phe Val Ser Tyr Pro Ser Asp Lys Gly Leu Ile Tyr Asn Ile
          50             55             60
Tyr Lys Glu Leu Lys Gln Ile Tyr Lys Asn Lys Thr Ser Asn Pro Ile
          65             70             75             80
Lys Lys Trp Ala Lys Asp Met Asn Arg His Ile Ser Lys Glu Gly Ile
          85             90             95
His Met Ala Asn Asn His Met Lys Leu Phe Ser Tyr His
          100             105

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<210> 2049

<211> 109

<212> PRT

<213> Homo sapiens

<400> 2049

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Met Ile Pro Arg Ala Ser Leu Ile Val Ala Thr Ala Tyr Pro Ala Arg
  1             5             10             15
Ser Ser Leu Trp Thr Asp Ser Leu Arg Gln Ala Gln Arg Ala His Ser
          20             25             30

```


Leu Gln Ser Ser Pro Val Ser Glu Ser Leu Pro Leu Pro Gln Arg Ser
 35 40 45
 Ser Glu Glu Val Ser Pro His Pro Leu Pro Arg Arg His Pro Pro Ala
 50 55 60
 Ser Val Cys Val Thr Val Gly Met Val Phe Val Val Ser Leu Ser Ser
 65 70 75 80
 Arg Ala Leu Leu Phe Leu Leu Phe Cys Thr His Trp Arg Gly Arg Thr
 85 90 95
 Asp Gly Pro Pro Ala Gly Gly Gln Pro Ser Trp Gln Arg
 100 105

<210> 2050

<211> 174

<212> PRT

<213> Homo sapiens

<400> 2050

Met Leu Glu Val His Ile Pro Ser Val Gly Pro Glu Ala Glu Gly Pro
 1 5 10 15
 Arg Gln Ser Pro Glu Lys Ser His Met Ile Lys Lys Leu Tyr Lys Val
 20 25 30
 Pro Asp Phe Pro Ser Lys Arg Leu Pro Asn Trp Arg Thr Arg Gly Leu
 35 40 45
 Glu Gln Arg Arg Gln Gly Leu Glu Ala Tyr Ile Gln Gly Ile Leu Tyr
 50 55 60
 Leu Asn Gln Glu Val Pro Lys Glu Leu Leu Glu Phe Leu Arg Leu Arg
 65 70 75 80
 His Phe Pro Thr Asp Pro Lys Ala Ser Asn Trp Gly Thr Leu Arg Glu

	85		90		95										
Phe	Leu	Pro	Gly	Asp	Ser	Ser	Ser	Gln	Gln	His	Gln	Arg	Pro	Val	Leu
	100		105		110										
Ser	Phe	His	Val	Asp	Pro	Tyr	Val	Cys	Asn	Pro	Ser	Pro	Gly	Glu	Glu
	115		120		125										
Val	Pro	Arg	Tyr	Gly	Ala	Thr	Gly	Leu	Gly	Cys	Gly	Leu	Cys	Ile	Ser
	130		135		140										
Arg	Leu	Leu	Gly	Pro	Ser	Asp	Ser	Ile	Ser	Phe	Leu	Leu	Pro	Thr	Ser
	145		150		155										
Gly	Ala	Thr	Thr	Ser	Cys	Ser	Cys	Pro	Leu	Glu	Pro	Ala	Leu		
	165		170												

<210> 2051

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2051

Met	Pro	Met	Ile	Ser	Val	Leu	Gly	Lys	Met	Phe	Leu	Trp	Gln	Arg	Glu
1			5					10					15		
Gly	Pro	Gly	Gly	Arg	Trp	Thr	Cys	Gln	Thr	Ser	Arg	Arg	Val	Ser	Ser
		20					25					30			
Asp	Pro	Ala	Trp	Ala	Val	Glu	Trp	Ile	Glu	Leu	Pro	Arg	Gly	Leu	Ser
		35					40					45			
Leu	Ser	Ser	Leu	Gly	Ser	Ala	Arg	Thr	Leu	Arg	Gly	Trp	Ser	Arg	Ser
	50					55					60				
Ser	Arg	Pro	Ser	Ser	Val	Asp	Ser	Gln	Asp	Leu	Pro	Glu	Val	Leu	Gly
	65				70					75				80	

Pro Trp Trp Trp Gly Glu Gly Gly Arg His Pro Tyr Lys Gly Asp Leu
 85 90 95
 Gln Pro Pro Pro Thr Pro Gly Gln Pro Ala Ser Gly Ser Leu Phe Arg
 100 105 110
 Arg Ala Glu Ala Leu Ser Gly Gly Gly Pro Gly Gly Arg Pro Arg Ala
 115 120 125
 Gly Leu Leu Cys Ser Ala Leu Cys Gln Gln Ala Glu Ser Ser Arg Leu
 130 135 140
 Pro Arg
 145

<210> 2052

<211> 117

<212> PRT

<213> Homo sapiens

<400> 2052

Met Tyr Leu Ile Arg Arg Ala His Cys Val Thr Gln Pro Ile Thr Thr
 1 5 10 15
 Ala Leu Ile Pro Ala His Arg Ala Ser Trp Pro Gly Pro Leu Ser Thr
 20 25 30
 Ala Val Val Ser Pro Asp Gly Pro His Leu Leu Leu Leu Gln Gly Cys
 35 40 45
 Ile Pro Leu Cys Cys Pro Pro Lys Ala Thr Ser Ala Ser Gly Glu Asp
 50 55 60
 Leu Ala Ile Thr His Trp Gly Arg Asp Lys Cys Gly Ser Arg Arg Gly
 65 70 75 80
 Asn Trp Gly Arg Arg Glu Ala Ala Cys Gly Thr Pro Ser Glu Ala Leu

	85	90	95
Val Phe Phe Val Val Pro Arg Glu Arg Asn Ala Cys Leu Leu Cys Arg			
100	105	110	
Gly Gln Ala Glu Leu			
115			

<210> 2053

<211> 248

<212> PRT

<213> Homo sapiens

<400> 2053

Met Cys Val Leu Tyr Thr Pro Ala Thr Tyr Asp Phe Glu Leu Glu Arg			
1	5	10	15
Gly Trp Gly Pro Thr Phe Glu Val Pro Ser His Val Gly Ile Gln Val			
20	25	30	
Met Ala Ser Ala Gln Thr Arg Lys Glu Thr Arg Gly Pro Pro Gly Arg			
35	40	45	
Arg Leu Gly Ser Gly Met Val Gly Pro Ile Arg Ala Ser Ser Ala Ala			
50	55	60	
Ser Ile Arg Ser Ser Ser Ala Asp Pro Ala Gly Pro Arg Pro Thr Cys			
65	70	75	80
Leu Gly Glu Gly Gln Arg Val Arg Ile Met Ala Arg Gln Gly Pro Arg			
85	90	95	
Lys Ser Gln Thr His Arg Arg Lys Thr Arg Gly Thr Ala Ser Pro Ala			
100	105	110	
Val Tyr Phe Ser Val Glu Trp Gly Asp Tyr Trp Gly Met Pro Asn Asp			
115	120	125	

Arg Lys Arg Cys Lys Ala Ala Thr Gly Trp Val Arg Gly Ser Pro Lys
 130 135 140
 Ser Arg Thr Glu Trp Gly Ala Arg Asp Arg Ala Gly Gln Arg Pro Gly
 145 150 155 160
 Leu Ser Gly Pro Arg Arg Arg Gln Arg Gln Ala Gly Ala Thr Pro Thr
 165 170 175
 Arg Ala Arg Ser Arg Gly Val Ser Gly Met Gly Gln Glu Ser Val His
 180 185 190
 Ser Pro Glu Ala Arg Pro Thr Gly Gly Gly Thr Gly Gly Cys Leu Ala
 195 200 205
 Gly Asp Gly Asp Thr Ser Arg Gly Leu Ser Gly Ala Leu Gly Thr Cys
 210 215 220
 Trp Lys Gln Ala Ala Gly Val Gly Val Ala Pro Gly Ala Gly Glu Trp
 225 230 235 240
 Tyr Ser Asp His Arg Arg Ala Arg
 245

<210> 2054

<211> 165

<212> PRT

<213> Homo sapiens

<400> 2054

Met Phe Tyr Asn Gln Ala Asp Arg Leu Ala Phe Val Asn Thr Val Leu
 1 5 10 15
 Thr Leu Leu Gly Gly Phe Val Cys Gln Lys His Pro His Ala Leu Leu
 20 25 30
 Phe Gln Pro Glu Val Lys Lys Ser Phe Thr Phe Val Ser Phe Leu Phe

35 40 45
 Val Cys Leu Arg Arg Ser Phe Thr Leu Val Ala Gln Ala Gly Val Gln
 50 55 60
 Trp Arg Asn Leu Gly Leu Pro Gln Pro Leu Pro Pro Arg Phe Lys Gln
 65 70 75 80
 Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp His Arg Cys Pro Pro
 85 90 95
 Pro Arg Leu Leu Ile Phe Val Leu Phe Val Glu Thr Gly Phe His Cys
 100 105 110
 Val Ser Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Leu Pro Ala
 115 120 125
 Ser Ala Pro Gln Asn Ala Gly Ile Thr Gly Val Ser His Arg Ala Gln
 130 135 140
 Pro Ser Cys Leu Leu Ser Cys Thr Arg Ser Thr Gly Lys Val Leu Pro
 145 150 155 160
 Gln Arg Glu Val Ala
 165

<210> 2055

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2055

Met Leu Asn Leu Val Phe Lys Tyr Trp Gln Gln Ile His Leu Leu Lys
 1 5 10 15
 Thr Ala Met Ile Lys His Val His Arg Ser Asn Leu Ala Ile Gly Gln
 20 25 30

Gln Ser Met Leu Ser Ser Trp Thr Cys Gln Gly Pro Asn Leu Leu Arg
 35 40 45
 Gln Leu Leu Ile Glu Pro Pro Ser Ser Leu Arg Asp Trp Gly Lys Ile
 50 55 60
 Gly Cys Leu Pro Ser Gly Pro Gln Ala Thr Gln Ala Ile Pro Glu Ser
 65 70 75 80
 Gly Pro Gln Gln Arg Leu Glu Lys Val Thr Ser Ile Pro Phe Thr Glu
 85 90 95
 Pro Phe Leu Phe
 100

<210> 2056

<211> 418

<212> PRT

<213> Homo sapiens

<400> 2056

Met Pro Met Leu Leu Pro His Pro His Gln His Phe Leu Lys Gly Leu
 1 5 10 15
 Leu Arg Ala Pro Phe Arg Cys Tyr His Phe Ile Phe His Ser Ser Thr
 20 25 30
 His Leu Gly Ser Gly Ile Pro Cys Ala Gln Pro Phe Asn Ser Leu Gly
 35 40 45
 Leu His Cys Thr Lys Trp Met Leu Leu Ser Asp Gly Leu Lys Arg Lys
 50 55 60
 Leu Cys Val Gln Thr Thr Leu Lys Asp His Thr Glu Gly Leu Ser Asp
 65 70 75 80
 Lys Glu Gln Arg Phe Val Asp Lys Leu Tyr Thr Gly Leu Ile Gln Gly

	85	90	95
Gln Arg Ala Cys Leu Ala Glu Ala Ile Thr Leu Val Glu Ser Thr His			
100	105	110	
Ser Arg Lys Lys Glu Leu Ala Gln Val Leu Leu Gln Lys Val Leu Leu			
115	120	125	
Tyr His Arg Glu Gln Glu Gln Ser Asn Lys Gly Lys Pro Leu Ala Phe			
130	135	140	
Arg Val Gly Leu Ser Gly Pro Pro Gly Ala Gly Lys Ser Thr Phe Ile			
145	150	155	160
Glu Tyr Phe Gly Lys Met Leu Thr Glu Arg Gly His Lys Leu Ser Val			
165	170	175	
Leu Ala Val Asp Pro Ser Ser Cys Thr Ser Gly Gly Ser Leu Leu Gly			
180	185	190	
Asp Lys Thr Arg Met Thr Glu Leu Ser Arg Asp Met Asn Ala Tyr Ile			
195	200	205	
Arg Pro Ser Pro Thr Arg Gly Thr Leu Gly Gly Val Thr Arg Thr Thr			
210	215	220	
Asn Glu Ala Ile Leu Leu Cys Glu Gly Ala Gly Tyr Asp Ile Ile Leu			
225	230	235	240
Ile Glu Thr Val Gly Val Gly Gln Ser Glu Phe Ala Val Ala Asp Met			
245	250	255	
Val Asp Met Phe Val Leu Leu Leu Pro Pro Ala Gly Gly Asp Glu Leu			
260	265	270	
Gln Gly Ile Lys Arg Gly Ile Ile Glu Met Ala Asp Leu Val Ala Val			
275	280	285	
Thr Lys Ser Asp Gly Asp Leu Ile Val Pro Ala Arg Arg Ile Gln Ala			
290	295	300	
Glu Tyr Val Ser Ala Leu Lys Leu Leu Arg Lys Arg Ser Gln Val Trp			
305	310	315	320

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Pro Ala Val Gln Lys Leu Ala Ser Leu Arg Leu Gly Gly Ala Glu Pro
 290 295 300
 Arg Leu Leu Arg Trp Asp Leu Thr Phe Ser Pro Pro Gln Lys Ser Leu
 305 310 315 320
 Pro Val Ala Leu Glu Ser Asp Glu Glu Asn Gly Asp Glu Leu Lys Ser
 325 330 335
 Ser Thr Gly Ser Ala Pro Ile Leu Val Val Met Val Ile Leu Leu Asn
 340 345 350
 Ile Gly Val Ala Ile Leu Phe Ile Asn Phe Phe Ile
 355 360

<210> 2058

<211> 1012

<212> PRT

<213> Homo sapiens

<400> 2058

Met Arg Gly Ala Trp Val His Leu His Ser Gly Ala Ala Ser Ser Leu
 1 5 10 15
 Arg Pro Cys Arg Cys Gly Ala Gly Ala Ala Pro Lys Ser Ser Pro Arg
 20 25 30
 Ser Pro Gly Gly Arg Arg Gly Asp Gly Ser Ser Asp Ser Glu Gly Gly
 35 40 45
 Val Ser Phe Ala Gly Val Leu Phe Leu Gln Phe Gly Glu Glu Thr Arg
 50 55 60
 Arg Val His Ile Thr His Glu Val Ser Ser Leu Asp Thr Leu His Ala
 65 70 75 80
 Leu Ile Ala His Met Phe Pro Gln Lys Leu Thr Met Gly Met Leu Lys

	85	90	95
Ser Pro Asn Thr Ala Ile Leu Ile Lys Asp Glu Ala Arg Asn Val Phe			
	100	105	110
Tyr Glu Leu Glu Asp Val Arg Asp Ile Gln Asp Arg Ser Ile Ile Lys			
	115	120	125
Ile Tyr Arg Lys Glu Pro Leu Tyr Ala Ala Phe Pro Gly Ser His Leu			
	130	135	140
Thr Asn Gly Asp Leu Arg Arg Glu Met Val Tyr Ala Ser Arg Glu Ser			
145	150	155	160
Ser Pro Thr Arg Arg Leu Asn Asn Leu Ser Pro Ala Pro His Leu Ala			
	165	170	175
Ser Gly Ser Pro Pro Pro Gly Leu Pro Ser Gly Leu Pro Ser Gly Leu			
	180	185	190
Gln Ser Gly Ser Pro Ser Arg Ser Arg Leu Ser Tyr Ala Gly Gly Arg			
	195	200	205
Pro Pro Ser Tyr Ala Gly Ser Pro Val His His Ala Ala Glu Arg Leu			
	210	215	220
Gly Gly Ala Pro Ala Ala Gln Gly Val Ser Pro Ser Pro Ser Ala Ile			
225	230	235	240
Leu Glu Arg Arg Asp Val Lys Pro Asp Glu Asp Leu Ala Ser Lys Ala			
	245	250	255
Gly Gly Met Val Leu Val Lys Gly Glu Gly Leu Tyr Ala Asp Pro Tyr			
	260	265	270
Gly Leu Leu His Glu Gly Arg Leu Ser Leu Ala Ala Ala Ala Gly Asp			
	275	280	285
Pro Phe Ala Tyr Pro Gly Ala Gly Gly Leu Tyr Lys Arg Gly Ser Val			
	290	295	300
Arg Ser Leu Ser Thr Tyr Ser Ala Ala Ala Leu Gln Ser Asp Leu Glu			
305	310	315	320

Asp Ser Leu Tyr Lys Ala Ala Gly Gly Gly Gly Pro Leu Tyr Gly Asp
325 330 335
Gly Tyr Gly Phe Arg Leu Pro Pro Ser Ser Pro Gln Lys Leu Ala Asp
340 345 350
Val Ala Ala Pro Pro Gly Gly Pro Pro Pro Pro His Ser Pro Tyr Ser
355 360 365
Gly Pro Pro Ser Arg Gly Ser Pro Val Arg Gln Ser Phe Arg Lys Asp
370 375 380
Ser Gly Ser Ser Ser Val Phe Ala Glu Ser Pro Gly Gly Lys Thr Arg
385 390 395 400
Ser Ala Gly Ser Ala Ser Thr Ala Gly Ala Pro Pro Ser Glu Leu Phe
405 410 415
Pro Gly Pro Gly Glu Arg Ser Leu Val Gly Phe Gly Pro Pro Val Pro
420 425 430
Ala Lys Asp Thr Glu Thr Arg Glu Arg Met Glu Ala Met Glu Lys Gln
435 440 445
Ile Ala Ser Leu Thr Gly Leu Val Gln Ser Ala Leu Leu Arg Gly Ser
450 455 460
Glu Pro Glu Thr Pro Ser Glu Lys Ile Glu Gly Ser Asn Gly Ala Ala
465 470 475 480
Ile Pro Ser Ala Pro Cys Gly Ser Gly Gly Arg Ser Ser Gly Ala Thr
485 490 495
Pro Val Ser Gly Pro Pro Pro Pro Ser Ala Ser Ser Thr Pro Ala Gly
500 505 510
Gln Pro Thr Ala Val Ser Arg Leu Gln Met Gln Leu His Leu Arg Gly
515 520 525
Leu Gln Asn Ser Ala Ser Asp Leu Arg Gly Gln Leu Gln Gln Leu Arg
530 535 540
Lys Leu Gln Leu Gln Asn Gln Glu Ser Val Arg Ala Leu Leu Lys Arg

545 550 555 560
Thr Glu Ala Glu Leu Ser Met Arg Val Ser Glu Ala Ala Arg Arg Gln
 565 570 575
Glu Asp Pro Leu Gln Arg Gln Arg Thr Leu Val Glu Glu Glu Arg Leu
 580 585 590
Arg Tyr Leu Asn Asp Glu Glu Leu Ile Thr Gln Gln Leu Asn Asp Leu
 595 600 605
Glu Lys Ser Val Glu Lys Ile Gln Arg Asp Val Ser His Asn His Arg
 610 615 620
Leu Val Pro Gly Pro Glu Leu Glu Glu Lys Ala Leu Val Leu Lys Gln
625 630 635 640
Leu Gly Glu Thr Leu Thr Glu Leu Lys Ala His Phe Pro Gly Leu Gln
 645 650 655
Ser Lys Met Arg Val Val Leu Arg Val Glu Val Glu Ala Val Lys Phe
 660 665 670
Leu Lys Glu Glu Pro Gln Arg Leu Asp Gly Leu Leu Lys Arg Cys Arg
 675 680 685
Gly Val Thr Asp Thr Leu Ala Gln Ile Arg Arg Gln Val Asp Glu Gly
 690 695 700
Val Trp Pro Pro Pro Asn Asn Leu Leu Ser Gln Ser Pro Lys Lys Val
705 710 715 720
Thr Ala Glu Thr Asp Phe Asn Lys Ser Val Asp Phe Glu Met Pro Pro
 725 730 735
Pro Ser Pro Pro Leu Asn Leu His Glu Leu Ser Gly Pro Ala Glu Gly
 740 745 750
Ala Ser Leu Thr Pro Lys Gly Gly Asn Pro Thr Lys Gly Leu Asp Thr
 755 760 765
Pro Gly Lys Arg Ser Val Asp Lys Ala Val Ser Val Glu Ala Ala Glu
 770 775 780

出証特 2 0 0 4 - 3 0 5 9 6 6 1

1010

<210> 2059

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2059

Met	Trp	Phe	Ser	Arg	Ser	Thr	Tyr	His	Arg	Leu	Arg	Gln	Pro	Arg	Thr
1					5					10					15
Ser	Ser	Glu	Pro	Phe	Phe	Cys	Met	Ser	Thr	Gln	Gly	Val	Val	Pro	Leu
			20						25					30	
Asn	Ser	Glu	Ser	Gly	Ser	Tyr	Leu	Ile	Leu	Ala	Trp	Gly	Thr	Ala	Glu
			35					40					45		
Glu	Phe	Gly	Leu	Pro	Glu	Leu	Gly	Arg	Lys	Thr	Phe	Phe	Phe	Phe	Phe
	50						55				60				
Trp	Arg	Trp	Cys	Leu	Cys	Cys	Gln	Ala	Glu	Val	Gln	Trp	Cys	Asp	Leu
65					70						75				80
Gly	Ser	Arg	Gln	Ser	Leu	Ser	Pro	Gly	Phe	Lys	Gln	Phe	Pro	Cys	Leu
					85					90				95	
Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Val	Pro	Pro	Gln	Ala	Ala
					100				105					110	
Asn	Phe	Leu	Tyr	Phe	Gly	Arg	Asp	Arg	Val	Ser	Pro	Cys	Cys	Pro	Gly
					115				120					125	
Trp	Ser	Leu	Ser	Pro	Asp	Tyr	Leu	Thr	Arg	Pro	Pro	Trp	Pro	Gly	Ile
					130				135					140	
Thr	Gly	Val	Ser	His	Cys	Ala	Arg	Leu	Glu	Gly	Lys	His	Ser	Glu	
145							150							155	

<210> 2060

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2060

Met Lys Val Asn Lys Lys Ile Lys Leu Glu Pro Gln Cys Leu Glu Phe

1 5 10 15

Phe Ser Asp Arg Val Ser Leu Phe Val Thr Gln Ala Gly Val Gln Trp

20 25 30

Cys Lys His Ser Ser Leu Gln Pro Gln His Pro Trp Leu Lys Gln Ser

35 40 45

Ser Asn Leu Asn Phe Gln Ser Ser Leu Asp Tyr Arg Cys Met Pro Gln

50 55 60

Trp Pro Ala Asn Phe Arg Ile Phe Cys Arg Asp Glu Ile Ser Pro Cys

65 70 75 80

Cys Pro Gly Arg Ser Arg Thr Pro Glu Leu Lys Gln Ser Thr Ser Leu

85 90 95

Asn Phe Pro Glu Cys Cys Asp Tyr Arg His Gly Pro Ser Cys Leu Ala

100 105 110

<210> 2061

<211> 795

<212> PRT

<213> Homo sapiens

<400> 2061

Met Lys Phe Thr Asn Thr Lys Val Gln Met Met Gln Asn Val His Leu
1 5 10 15
Ala Pro Glu Thr Asp Glu Asp Asp Leu Tyr Ser Gly Tyr Asn Asp Tyr
20 25 30
Asn Pro Ile Tyr Asp Ile Glu Glu Leu Glu Asn Asp Ala Ala Phe Gln
35 40 45
Gln Ala Val Arg Thr Ser His Gly Arg Arg Pro Pro Ile Thr Ala Lys
50 55 60
Ile Ser Ser Thr Ala Val Thr Arg Pro Ile Ala Thr Gly Tyr Gly Ser
65 70 75 80
Lys Thr Ser Leu Ala Ser Ser Ile Gly Arg Pro Met Thr Gly Ala Ile
85 90 95
Gln Asp Gly Val Thr Arg Pro Met Thr Ala Val Arg Ala Ala Gly Phe
100 105 110
Thr Lys Ala Ala Leu Arg Gly Ser Ala Phe Asp Pro Leu Ser Gln Ser
115 120 125
Arg Gly Pro Ala Ser Pro Leu Glu Ala Lys Lys Lys Asp Ser Pro Glu
130 135 140
Glu Lys Ile Lys Gln Leu Glu Lys Glu Val Asn Glu Leu Val Glu Glu
145 150 155 160
Ser Cys Ile Ala Asn Ser Cys Gly Asp Leu Lys Leu Ala Leu Glu Lys
165 170 175
Ala Lys Asp Ala Gly Arg Lys Glu Arg Val Leu Val Arg Gln Arg Glu
180 185 190
Gln Val Thr Thr Pro Glu Asn Ile Asn Leu Asp Leu Thr Tyr Ser Val
195 200 205
Leu Phe Asn Leu Ala Ser Gln Tyr Ser Val Asn Glu Met Tyr Ala Glu
210 215 220

Ala Leu Asn Thr Tyr Gln Val Ile Val Lys Asn Lys Met Phe Ser Asn
225 230 235 240
Ala Gly Ile Leu Lys Met Asn Met Gly Asn Ile Tyr Leu Lys Gln Arg
245 250 255
Asn Tyr Ser Lys Ala Ile Lys Phe Tyr Arg Met Ala Leu Asp Gln Val
260 265 270
Pro Ser Val Asn Lys Gln Met Arg Ile Lys Ile Met Gln Asn Ile Gly
275 280 285
Val Thr Phe Ile Gln Ala Gly Gln Tyr Ser Asp Ala Ile Asn Ser Tyr
290 295 300
Glu His Ile Met Ser Met Ala Pro Asn Leu Lys Ala Gly Tyr Asn Leu
305 310 315 320
Thr Ile Cys Tyr Phe Ala Ile Gly Asp Arg Glu Lys Met Lys Lys Ala
325 330 335
Phe Gln Lys Leu Ile Thr Val Pro Leu Glu Ile Asp Glu Asp Lys Tyr
340 345 350
Ile Ser Pro Ser Asp Asp Pro His Thr Asn Leu Val Thr Glu Ala Ile
355 360 365
Lys Asn Asp His Leu Arg Gln Met Glu Arg Glu Arg Lys Ala Met Ala
370 375 380
Glu Lys Tyr Ile Met Thr Ser Ala Lys Leu Ile Ala Pro Val Ile Glu
385 390 395 400
Thr Ser Phe Ala Ala Gly Tyr Asp Trp Cys Val Glu Val Val Lys Ala
405 410 415
Ser Gln Tyr Val Glu Leu Ala Asn Asp Leu Glu Ile Asn Lys Ala Val
420 425 430
Thr Tyr Leu Arg Gln Lys Asp Tyr Asn Gln Ala Val Glu Phe Leu Lys
435 440 445
Val Leu Glu Lys Lys Asp Asn Arg Val Lys Ser Ala Ala Ala Thr Asn

450 455 460
Leu Ser Ala Leu Tyr Tyr Met Gly Lys Asp Phe Ala Gln Ala Ser Ser
465 470 475 480
Tyr Ala Asp Ile Ala Val Asn Ser Asp Arg Tyr Asn Leu Ala Ala Leu
485 490 495
Thr Asn Lys Gly Asn Thr Val Phe Ala Asn Gly Asp Tyr Glu Lys Ala
500 505 510
Ala Glu Phe Tyr Lys Glu Ala Leu Arg Asn Asp Ser Ser Cys Thr Glu
515 520 525
Ala Leu Tyr Asn Ile Gly Leu Thr Tyr Glu Lys Leu Asn Arg Leu Asp
530 535 540
Glu Ala Leu Asp Cys Phe Leu Lys Leu His Ala Ile Leu Arg Asn Ser
545 550 555 560
Ala Glu Val Leu Tyr Gln Ile Ala Asn Ile Tyr Glu Leu Met Glu Asn
565 570 575
Pro Ser Gln Ala Ile Glu Trp Leu Met Gln Val Val Ser Val Ile Pro
580 585 590
Thr Asp Pro Gln Val Leu Ser Lys Leu Gly Glu Leu Tyr Asp Arg Glu
595 600 605
Gly Asp Lys Ser Gln Ala Phe Gln Tyr Tyr Tyr Glu Ser Tyr Arg Tyr
610 615 620
Phe Pro Cys Asn Ile Glu Val Ile Glu Trp Leu Gly Ala Tyr Tyr Ile
625 630 635 640
Asp Thr Gln Phe Trp Glu Lys Ala Ile Gln Tyr Phe Glu Arg Ala Ser
645 650 655
Leu Ile Gln Pro Thr Gln Val Lys Trp Gln Leu Met Val Ala Ser Cys
660 665 670
Phe Arg Arg Ser Gly Asn Tyr Gln Lys Ala Leu Asp Thr Tyr Lys Asp
675 680 685

Thr His Arg Lys Phe Pro Glu Asn Val Glu Cys Ser Gly Ser Val Arg
 690 695 700

Thr Gly His Met Glu Arg Asp Pro Leu Asn Leu Leu Pro Arg Lys Ser
 705 710 715 720

Val Leu Pro Gly Pro Glu Ile Ala Lys Arg Asn Tyr Phe Ser Gly Glu
 725 730 735

Lys Tyr Tyr Leu Ser Ala Phe Leu Ser Ser Ser Leu His Arg Ser Trp
 740 745 750

Ile Lys Arg Cys Ser Arg Ile Cys Gln Lys Thr Glu Glu Val Gly Lys
 755 760 765

Asn Glu Arg Asn Lys Gly Thr Ala His Lys Val Arg Gln Arg Trp Gln
 770 775 780

Trp Gly Leu Pro Trp Gln Lys Arg Arg Lys Cys
 785 790 795

<210> 2062

<211> 105

<212> PRT

<213> Homo sapiens

<400> 2062

Met Gly Asn Glu Asp Gly Arg Ala Gly Arg His Ser Pro Ala Thr Gly
 1 5 10 15

Gln Ala Ile Ala Pro Cys Ser Ala Val Leu Lys Leu Ala Ser Glu Gly
 20 25 30

Glu Gly Ile Val Gly Arg Arg Glu Gly Gly Gln Ala Arg Phe Gln Leu
 35 40 45

Asp Asn Ser Tyr Val Phe Ser Ser Ile Leu Leu His Ser Phe Ile Pro

50	55	60	
Leu Gln Val	Leu Ile Glu Ala Gly	Pro Gln Gly Lys His Lys Asp Gly	
65	70	75	80
Ser Gly Thr His	Leu Pro Phe Pro Arg Ala Tyr Thr	Leu Ala Gly Asp	
	85	90	95
Ile Lys His Asp	Arg Asn Asn His Arg		
100	105		

<210> 2063

<211> 152

<212> PRT

<213> Homo sapiens

<400> 2063

Met Pro Gln His	Leu Ser Gly Val	Gly Cys Gln Glu	Val Cys Val Ser
1	5	10	15
Met Lys Pro Asp	Gly Pro Val Cys	Leu Cys Ser Met	Asn Gly Ala Leu
	20	25	30
Ala Phe Val Asp	Thr Ser Asp Cys	Thr Val Met Asn	Ile Ala Glu His
	35	40	45
Tyr Met Ala Ser	Asp Val Glu Trp	Asp Pro Thr Gly	Arg Tyr Val Val
50	55	60	
Thr Ser Val Ser	Trp Trp Ser His	Lys Val Asp Asn	Ala Tyr Trp Leu
65	70	75	80
Trp Thr Phe Gln	Gly Arg Leu Leu	Gln Lys Asn Asn	Lys Asp Arg Phe
	85	90	95
Cys Gln Leu Leu	Trp Arg Pro Arg	Pro Pro Thr Leu	Leu Ser Gln Glu
100	105	110	

Gln Ile Lys Gln Ile Lys Lys Asp Leu Lys Lys Tyr Ser Lys Ile Phe
115 120 125
Glu Gln Lys Asp Arg Leu Ser Gln Ser Lys Ala Ser Lys Val Ser Leu
130 135 140
Ile Pro Lys Met Arg Ala Val Leu
145 150

<210> 2064

<211> 147

<212> PRT

<213> Homo sapiens

<400> 2064

Met Arg Ser Glu Ser Pro Gly Lys Trp Gly Asn Ser Pro Gly Leu His
1 5 10 15
His Ser Ser Thr Gly Lys Ser Pro Ala Ser Ser Leu Pro Gly Arg Gly
20 25 30
Val Pro Glu Leu Arg Val Thr Pro Thr Ala Pro Ser Ala Glu Gly Gly
35 40 45
Arg Lys Thr Ala Pro Ser His Gly Ser Ala His Ser Ala Ser Pro Pro
50 55 60
Ala Ser Leu Ser Ala Thr Asp Pro Trp Pro Leu Ala Ala Gln Thr Leu
65 70 75 80
Ser Thr Pro Arg Arg Thr Asn Thr Thr Leu Met Gly Pro Ala Ala Met
85 90 95
Ser Thr Pro Ala Ala Gly Ala Pro Ser Ala Ser Thr Asp Pro Ala Gln
100 105 110
Arg Ile Val Val Thr Gly Arg Gly Pro Thr Pro Arg Gly His Val Ala

115 120 125
His Ala Gln Leu Ala Gln Pro Thr Ala Arg Thr Lys Ser Lys Val Ser
130 135 140
Phe Arg Glu
145

<210> 2065

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2065

Met Trp Gln Ser Gly Arg Phe His Ala Leu Leu Trp Glu Glu Tyr Lys
1 5 10 15
Trp Val Gln Pro Leu Trp Arg Ile Val Leu His Phe Leu Leu Lys Leu
20 25 30
Lys Ile Thr Phe Pro Thr Lys Val Thr Thr Leu Tyr Thr Ser Arg Ser
35 40 45
Phe Ile His Val Val Ile Tyr Arg Asn Ala Thr Ala Ser Ser Cys Thr
50 55 60
Val Val His Gly Leu Cys Gly Tyr Thr His Phe Pro Phe Val Ser Pro
65 70 75 80
Met Thr Gln Leu Tyr Ile Ser Gln Phe Trp Ile Tyr Thr Leu Glu Asn
85 90 95
Leu Tyr Thr Ser Val
100

<210> 2066

<211> 323

<212> PRT

<213> Homo sapiens

<400> 2066

Met Leu Gln Glu Trp Leu Ala Ser Leu Pro Leu Asp Arg Ile Pro Tyr

1 5 10 15

Asn Ala Val Leu Asp Leu Val Asn Asn Lys Met Arg Ile Ser Gly Ile

20 25 30

Phe Leu Thr Asn His Ile Lys Trp Val Gly Cys Gln Gly Ser Arg Ser

35 40 45

Glu Leu Arg Gly Tyr Pro Cys Ser Leu Trp Lys Leu Phe His Thr Leu

50 55 60

Thr Val Glu Ala Ser Thr His Pro Asp Ala Leu Val Gly Thr Gly Phe

65 70 75 80

Glu Asp Asp Pro Gln Ala Val Leu Gln Thr Met Arg Arg Tyr Val His

85 90 95

Thr Phe Phe Gly Cys Lys Glu Cys Gly Glu His Phe Glu Glu Met Ala

100 105 110

Lys Glu Ser Met Asp Ser Val Lys Thr Pro Asp Gln Ala Ile Leu Trp

115 120 125

Leu Trp Lys Lys His Asn Met Val Asn Gly Arg Leu Ala Gly His Leu

130 135 140

Ser Glu Asp Pro Arg Phe Pro Lys Leu Gln Trp Pro Thr Pro Asp Leu

145 150 155 160

Cys Pro Ala Cys His Glu Glu Ile Lys Gly Leu Ala Ser Trp Asp Glu

165 170 175

Gly His Val Leu Thr Phe Leu Lys Gln His Tyr Gly Arg Asp Asn Leu

180	185	190
Leu Asp Thr Tyr Ser Ala Asp Gln Gly Gly Ser Ser Glu Gly Gly Thr		
195	200	205
Leu Ala Arg Gly Glu Glu Glu Glu Lys Arg Leu Thr Pro Pro Glu Val		
210	215	220
Ser His Gly Asp Arg Asp Thr Gln Ser Val Arg Pro Pro Gly Ala Leu		
225	230	235
Gly Pro Arg Pro Ala Leu Pro Glu Ser Leu His His Ser Leu Asp Gly		
245	250	255
Lys Leu Gln Ser Leu Asp Gly Pro Gly Ala His Lys Glu Val Gly Gly		
260	265	270
Ala Ala Pro Phe Leu Gly Val Asp Phe Ser Ser Leu Asp Met Ser Leu		
275	280	285
Cys Val Val Leu Tyr Val Ala Ser Ser Leu Phe Leu Met Val Met Tyr		
290	295	300
Phe Phe Phe Gln Val Arg Ser Arg Arg Trp Lys Val Lys His His His		
305	310	315
Pro Ala Val		320

<210> 2067

<211> 157

<212> PRT

<213> Homo sapiens

<400> 2067

Met	Leu	Val	Phe	Leu	Gln	Glu	Met	Asp	Lys	Pro	Cys	Gly	Cys	Pro	Pro
1				5					10				15		

Gly Val Cys Asp His Gly Thr Gly Asp Arg Arg Asp Pro Trp Tyr Ser
 20 25 30
 Thr Val Gly Leu Leu Pro Pro Val Arg Ala Met Ser Gln Arg Asn Leu
 35 40 45
 Asn Ala Lys Thr Glu Gln Gly Pro Thr Gly Val Thr Met Thr Ser Asn
 50 55 60
 Pro Ile Thr Trp Gly Gln Ile Lys Lys Thr Thr Gln Glu Ala Glu Lys
 65 70 75 80
 Leu Leu Glu Arg Gln Gly Gln Ala Lys Thr Pro Asp Ser Met Phe Leu
 85 90 95
 Ala Met Leu Ala Val Val Ser Cys Ala Val Cys Phe Pro Cys Val Glu
 100 105 110
 Ala Lys Thr Tyr Trp Ala Tyr Val Pro Asn Pro Leu Val Val Arg Leu
 115 120 125
 Val Leu Trp Ser Asp Thr Pro Pro Glu Ile Tyr Tyr Asp Gln Gly Ala
 130 135 140
 Trp Ala Pro Gly Pro Leu Thr Pro Ser Asp Thr Glu Gln
 145 150 155

<210> 2068

<211> 300

<212> PRT

<213> Homo sapiens

<400> 2068

Met Val Pro Pro His Arg Ala Leu His Phe Pro Val Ala Phe Pro Pro
 1 5 10 15
 Gly Gly Lys Pro Cys Ser Gln His Ile Ile Ser Val Thr Gly Phe Val

20	25	30
Asp Ser Asp Arg Asp Asp Leu Lys Leu Met Ala Tyr Leu Ala Gly Ala		
35	40	45
Lys Tyr Thr Gly Tyr Leu Cys Arg Ser Asn Thr Val Leu Ile Cys Lys		
50	55	60
Glu Pro Thr Gly Leu Lys Tyr Glu Lys Ala Lys Glu Trp Arg Ile Pro		
65	70	75
Cys Val Asn Ala Gln Trp Leu Gly Asp Ile Leu Leu Gly Asn Phe Glu		
85	90	95
Ala Leu Arg Gln Ile Gln Tyr Ser Arg Tyr Thr Ala Phe Ser Leu Gln		
100	105	110
Asp Pro Phe Ala Pro Thr Gln His Leu Val Leu Asn Leu Leu Asp Ala		
115	120	125
Trp Arg Val Pro Leu Lys Val Ser Ala Glu Leu Leu Met Ser Ile Arg		
130	135	140
Leu Pro Pro Lys Leu Lys Gln Asn Glu Val Ala Asn Val Gln Pro Ser		
145	150	155
Ser Lys Arg Ala Arg Ile Glu Asp Val Pro Pro Pro Thr Lys Lys Leu		
165	170	175
Thr Pro Glu Leu Thr Pro Phe Val Leu Phe Thr Gly Phe Glu Pro Val		
180	185	190
Gln Val Gln Gln Tyr Ile Lys Lys Leu Tyr Ile Leu Gly Gly Glu Val		
195	200	205
Ala Glu Ser Ala Gln Lys Cys Thr His Leu Ile Ala Ser Lys Val Thr		
210	215	220
Arg Thr Val Lys Phe Leu Thr Ala Ile Ser Val Val Lys His Ile Val		
225	230	235
Thr Pro Glu Trp Leu Glu Glu Cys Phe Arg Cys Gln Lys Phe Ile Asp		
245	250	255

Glu Gln Asn Tyr Ile Leu Arg Asp Ala Glu Ala Glu Val Leu Phe Ser
 260 265 270
 Phe Ser Leu Glu Glu Ser Leu Lys Arg Ala His Val Ser Pro Leu Phe
 275 280 285
 Lys Val His Phe Lys Gly Lys Val Asn Gln Ser Lys
 290 295 300

<210> 2069

<211> 301

<212> PRT

<213> Homo sapiens

<400> 2069

Met Leu Glu Phe Ser Lys Ile Leu Cys Thr Lys Asn Asn Lys Gln Asn
 1 5 10 15
 Asn Glu Phe Cys Lys Cys Ile Glu Thr Val Pro Gln Asp Ser Cys Lys
 20 25 30
 Thr Cys Phe Pro Gln Gln Asp Gln Arg Asp Thr Leu Ser Ile Leu Val
 35 40 45
 Pro His Gly Asp Lys Glu Ser Ser Asp Lys Lys Ile Ala Val Gly Thr
 50 55 60
 Glu Trp Asp Ile Pro Arg Asn Glu Ser Ser Asp Ser Ala Leu Gly Asp
 65 70 75 80
 Ser Glu Ser Glu Asp Thr Gly His Asp Met Thr Arg Gln Val Ser Ser
 85 90 95
 Tyr Tyr Gly Gly Glu Gln Glu Asp Trp Ala Glu Glu Asp Glu Ile Pro
 100 105 110
 Phe Pro Gly Ser Lys Leu Ile Glu Val Ser Ala Val Gln Pro Asn Ile

115 120 125
Ala Asn Phe Gly Arg Ser Leu Leu Gly Gly Tyr Cys Ser Ser Tyr Val
130 135 140
Pro Asp Phe Val Leu Gln Gly Ile Gly Ser Asp Glu Arg Phe Arg Gln
145 150 155 160
Cys Leu Met Ser Asp Leu Ser His Ala Val Gln His Pro Val Leu Asp
165 170 175
Glu Pro Ile Ala Glu Ala Val Cys Ile Ile Ala Asp Met Asp Lys Trp
180 185 190
Thr Val Gln Val Ala Ser Ser Gln Arg Arg Val Thr Asp Asn Lys Leu
195 200 205
Gly Lys Glu Val Leu Val Ser Ser Leu Val Ser Asn Leu Leu His Ser
210 215 220
Thr Leu Gln Leu Tyr Lys His Asn Leu Ser Pro Asn Phe Cys Val Met
225 230 235 240
His Leu Glu Asp Arg Leu Gln Glu Leu Tyr Phe Lys Ser Lys Met Leu
245 250 255
Ser Glu Tyr Leu Arg Gly Gln Met Arg Val His Val Lys Glu Leu Gly
260 265 270
Val Val Leu Gly Ile Glu Ser Ser Asp Leu Pro Leu Leu Ala Ala Val
275 280 285
Ala Ser Thr His Ser Pro Tyr Val Ala Gln Ile Leu Leu
290 295 300

<210> 2070

<211> 921

<212> PRT

<213> Homo sapiens

<400> 2070

Met Gly Met Leu Lys Ser Pro Asn Thr Ala Ile Leu Ile Lys Asp Glu
 1 5 10 15
 Ala Arg Asn Val Phe Tyr Glu Leu Glu Asp Val Arg Asp Ile Gln Asp
 20 25 30
 Arg Ser Ile Ile Lys Ile Tyr Arg Lys Glu Pro Leu Tyr Ala Ala Phe
 35 40 45
 Pro Gly Ser His Leu Thr Asn Gly Asp Leu Arg Arg Glu Met Val Tyr
 50 55 60
 Ala Ser Arg Glu Ser Ser Pro Thr Arg Arg Leu Asn Asn Leu Ser Pro
 65 70 75 80
 Ala Pro His Leu Ala Ser Gly Ser Pro Pro Pro Gly Leu Pro Ser Gly
 85 90 95
 Leu Pro Ser Gly Leu Gln Ser Gly Ser Pro Ser Arg Ser Arg Leu Ser
 100 105 110
 Tyr Ala Gly Gly Arg Pro Pro Ser Tyr Ala Gly Ser Pro Val His His
 115 120 125
 Ala Ala Glu Arg Leu Gly Gly Ala Pro Ala Ala Gln Gly Val Ser Pro
 130 135 140
 Ser Pro Ser Ala Ile Leu Glu Arg Arg Asp Val Lys Pro Asp Glu Asp
 145 150 155 160
 Leu Ala Ser Lys Ala Gly Gly Met Val Leu Val Lys Gly Glu Gly Leu
 165 170 175
 Tyr Ala Asp Pro Tyr Gly Leu Leu His Glu Gly Arg Leu Ser Leu Ala
 180 185 190
 Ala Ala Ala Gly Asp Pro Phe Ala Tyr Pro Gly Ala Gly Gly Leu Tyr
 195 200 205
 Lys Arg Gly Ser Val Arg Ser Leu Ser Thr Tyr Ser Ala Ala Ala Leu

210 215 220
Gln Ser Asp Leu Glu Asp Ser Leu Tyr Lys Ala Ala Gly Gly Gly Gly
225 230 235 240
Pro Leu Tyr Gly Asp Gly Tyr Gly Phe Arg Leu Pro Pro Ser Ser Pro
245 250 255
Gln Lys Leu Ala Asp Val Ala Ala Pro Pro Gly Gly Pro Pro Pro Pro
260 265 270
His Ser Pro Tyr Ser Gly Pro Pro Ser Arg Gly Ser Pro Val Arg Gln
275 280 285
Ser Phe Arg Lys Asp Ser Gly Ser Ser Ser Val Phe Ala Glu Ser Pro
290 295 300
Gly Gly Lys Thr Pro Ser Ala Gly Ser Ala Ser Thr Ala Gly Ala Pro
305 310 315 320
Pro Ser Glu Leu Phe Pro Gly Pro Gly Glu Arg Ser Leu Val Gly Phe
325 330 335
Gly Pro Pro Val Pro Ala Lys Asp Thr Glu Thr Arg Glu Arg Met Glu
340 345 350
Ala Met Glu Lys Gln Ile Ala Ser Leu Thr Gly Leu Val Gln Ser Ala
355 360 365
Leu Leu Arg Gly Ser Glu Pro Glu Thr Pro Ser Glu Lys Ile Glu Gly
370 375 380
Ser Asn Gly Ala Ala Thr Pro Ser Ala Pro Cys Gly Ser Gly Gly Arg
385 390 395 400
Ser Ser Gly Ala Thr Pro Val Ser Gly Pro Pro Pro Pro Ser Ala Ser
405 410 415
Ser Thr Pro Ala Gly Gln Pro Thr Ala Val Ser Arg Leu Gln Met Gln
420 425 430
Leu His Leu Arg Gly Leu Gln Asn Ser Ala Ser Asp Leu Arg Gly Gln
435 440 445

Leu Gln Gln Leu Arg Lys Leu Gln Leu Gln Asn Gln Glu Ser Val Arg
450 455 460

Ala Leu Leu Lys Arg Thr Glu Ala Glu Leu Ser Met Arg Val Ser Glu
465 470 475 480

Ala Ala Arg Arg Gln Glu Asp Pro Leu Gln Arg Gln Arg Thr Leu Val
485 490 495

Glu Glu Glu Arg Leu Arg Tyr Leu Asn Asp Glu Glu Leu Ile Thr Gln
500 505 510

Gln Leu Asn Asp Leu Glu Lys Ser Val Glu Lys Ile Gln Arg Asp Val
515 520 525

Ser His Asn His Arg Leu Val Pro Gly Pro Glu Leu Glu Glu Lys Ala
530 535 540

Leu Val Leu Lys Gln Leu Gly Glu Thr Leu Thr Glu Leu Lys Ala His
545 550 555 560

Phe Pro Gly Leu Gln Ser Lys Met Arg Val Val Leu Arg Val Glu Val
565 570 575

Glu Ala Val Lys Phe Leu Lys Glu Glu Pro Gln Arg Leu Asp Gly Leu
580 585 590

Leu Lys Arg Cys Arg Gly Val Thr Asp Thr Leu Ala Gln Ile Arg Arg
595 600 605

Gln Val Asp Glu Gly Val Trp Pro Pro Pro Asn Asn Leu Leu Ser Gln
610 615 620

Ser Pro Lys Lys Val Thr Ala Glu Thr Asp Phe Asn Lys Ser Val Asp
625 630 635 640

Phe Glu Met Pro Pro Pro Ser Pro Pro Leu Asn Leu His Glu Leu Ser
645 650 655

Gly Pro Ala Glu Gly Ala Ser Leu Thr Pro Lys Gly Gly Asn Pro Thr
660 665 670

Lys Gly Leu Asp Thr Pro Gly Lys Arg Ser Val Asp Lys Ala Val Ser

675 680 685
Val Glu Ala Ala Glu Arg Asp Trp Glu Glu Lys Arg Ala Ala Leu Thr
690 695 700
Gln Tyr Ser Ala Lys Asp Ile Asn Arg Leu Leu Glu Glu Thr Gln Ala
705 710 715 720
Glu Leu Leu Lys Ala Ile Pro Asp Leu Asp Cys Ala Ser Lys Ala His
725 730 735
Pro Gly Pro Ala Pro Thr Pro Asp His Lys Pro Pro Lys Ala Pro His
740 745 750
Gly Gln Lys Ala Ala Pro Arg Thr Glu Pro Ser Gly Arg Arg Gly Ser
755 760 765
Asp Glu Leu Thr Val Pro Arg Tyr Arg Thr Glu Lys Pro Ser Lys Ser
770 775 780
Pro Pro Pro Pro Pro Pro Arg Arg Ser Phe Pro Ser Ser His Gly Leu
785 790 795 800
Thr Thr Thr Arg Thr Gly Glu Val Val Val Thr Ser Lys Lys Asp Ser
805 810 815
Ala Phe Ile Lys Lys Ala Glu Ser Glu Glu Leu Glu Val Gln Lys Pro
820 825 830
Gln Val Lys Leu Arg Arg Ala Val Ser Glu Val Ala Arg Pro Ala Ser
835 840 845
Thr Pro Pro Ile Met Ala Ser Ala Ile Lys Asp Glu Asp Asp Glu Asp
850 855 860
Arg Ile Ile Ala Glu Leu Glu Ser Gly Gly Gly Ser Val Pro Pro Met
865 870 875 880
Lys Val Val Thr Pro Gly Ala Ser Arg Leu Lys Ala Ala Gln Gly Gln
885 890 895
Ala Gly Ser Pro Asp Lys Ser Lys His Gly Lys Gln Arg Ala Glu Tyr
900 905 910

Met Arg Ile Gln Ala Gln Gln Gln Val

915

920

<210> 2071

<211> 168

<212> PRT

<213> Homo sapiens

<400> 2071

Met Asn Phe Tyr Thr His Glu Val Cys Leu Gly Gly Pro Leu Leu Trp

1

5

10

15

Ala Pro Leu Pro Tyr Asp Gly Ser Ile Cys Ser Leu Leu Phe Gln Glu

20

25

30

Asp Leu Arg Pro Thr Ile Asn Gly Ser Gln Ile Gln Ile Pro Leu Gln

35

40

45

Ala Ala Asn Val His Pro His Tyr Arg Lys Pro Pro Asp Thr Ser His

50

55

60

Leu Leu Ala Ala Gln Asp Thr Gly Thr Gln Ile Leu Ala Cys Pro Glu

65

70

75

80

Gln Trp Leu Ser Arg Pro Gly Arg Gly Ala Arg Ala Gln Ser Gln Ala

85

90

95

Gly Leu Pro Ala His Phe Cys Leu Pro Gly His His His Leu Pro Pro

100

105

110

Arg Met Asn Leu Lys Leu Gln Gly Asn Glu Glu Lys Pro Arg Ser Glu

115

120

125

Gly Thr Cys Asn Gln Gly Cys Pro Lys Trp Pro Leu Ser Arg Pro Ile

130

135

140

Ser Lys Tyr Asn Pro His Arg Gly Cys Leu Val Gly Gln Lys Ser Leu

145 150 155 160
Gly Leu Val Pro Val Arg Gly Glu
165

<210> 2072

<211> 152

<212> PRT

<213> Homo sapiens

<400> 2072

Met Lys Thr Val Thr Asp Glu Ala Gly Glu Ser Ala Gly Lys Ala Trp
1 5 10 15
Ala Pro Arg Arg Gln Leu Gln Val Leu Arg Pro Gln Ala Thr Lys Ala
20 25 30
Glu Arg Leu Glu Ser Ala Glu Pro Arg Arg Arg Ala Glu Arg Ser Gly
35 40 45
Cys Gly Leu Thr Pro Pro Pro Gly Pro Ala Ala Ala Ala Ala Ala Ala
50 55 60
Ala Ser Ala Ser Arg Leu Ser Arg Ser Arg Leu Thr Ser Ala Ala Val
65 70 75 80
Pro Ala Gln Tyr Pro Pro Leu Arg Arg Arg Val Gly Val Gln His Pro
85 90 95
Gly Ala Leu His Pro Arg Pro His Arg Val His Ala Ala Ala Gln Arg
100 105 110
Leu Phe Leu His Ala Ala Ser Thr Pro Leu Asp Ala Phe Leu Asn Pro
115 120 125
Lys His Glu Asn Asn Leu Phe Leu Trp Lys Ile Ser Ser Pro Leu Lys
130 135 140

Lys Ile Lys Lys Lys Lys Lys Glu

145

150

<210> 2073

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2073

Met Glu Thr Val Leu Ala Ser Phe Cys Ile Phe Ser Arg Asp Gly Ser

1

5

10

15

Ser Pro Cys Trp Pro Gly Cys Ser Gln Thr Pro Asp Leu Lys Ser Ala

20

25

30

Cys Leu Arg Leu Pro Lys Cys Trp Asp Tyr Arg His Glu Pro Gly Leu

35

40

45

Asp Asp Leu Phe Asn Val Leu Leu Asn Leu Val Cys Trp Ser Cys Phe

50

55

60

Val Thr Gln Ala Gly Val Gln Trp His Asn Leu Gly Leu Leu Gln Ala

65

70

75

80

Leu Asn Ser Trp Ala Gln Val Ile Leu Leu Ser Gln Ser Phe Lys Val

85

90

95

Leu Val Leu Gln Val

100

<210> 2074

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2074

Met Pro Ser Thr Pro Gln Ser Gln Ser His Arg Gly Thr His Ser Asp
1 5 10 15
Ser Tyr His His Ser Ser Leu Pro Pro Ala Cys His Gly Phe His Val
20 25 30
His Gly Ser Gly Gln Ser Val Ser Leu Arg Ala Ser Val Tyr Val Cys
35 40 45
Val Tyr Leu Leu Thr Phe Ala Gln His Leu Arg Phe Thr Gln Ala Phe
50 55 60
Ala Trp Ile Ser Gly Arg Leu Leu Ile Ala Ala Trp Arg Pro Val Val
65 70 75 80
Trp Val Cys Ala Ala Cys Val Ser Ser Pro Tyr Ser Gly Val Tyr Val
85 90 95
Ser Ser Val Gly Cys Ser Gln Asp Pro Phe Leu Pro
100 105

<210> 2075

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2075

Met Ala His Ser Ile Pro Phe Thr Gly Leu His Phe Pro Ser Ala Leu
1 5 10 15
Cys Met Leu Ser Lys Ser Ser Phe Leu Arg Pro Gln Pro Tyr Leu Leu
20 25 30

Lys Pro Phe Ser Asn Asn Asn Tyr Lys Met Val Phe Leu Ser Leu Asn
 35 40 45
 Leu Met Leu Ile Ser Pro Ser Ala Ile Leu Pro Phe Glu Val Leu Phe
 50 55 60
 Leu Phe Val Asp Cys Leu Pro His Trp Thr Glu Ser Tyr Leu Lys Pro
 65 70 75 80
 Gly Ala Met Leu Val Phe Phe Thr Val Val Thr Ser Ala Pro Gly Met
 85 90 95
 Met Pro Gly Asn Gly Arg His Ser Ile Asn Ile His
 100 105

<210> 2076

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2076

Met Gly Asn Tyr Leu Leu Arg Lys Leu Arg Gln Glu Met Thr Thr Phe
 1 5 10 15
 Glu Arg Lys Leu Gln Asp Gln Asp Lys Lys Ser Gln Glu Val Ser Ser
 20 25 30
 Thr Ser Asn Gln Glu Asn Glu Asn Gly Ser Gly Ser Glu Glu Val Cys
 35 40 45
 Tyr Thr Val Ile Asn His Ile Pro His Gln Arg Ser Ser Leu Ser Ser
 50 55 60
 Asn Asp Asp Gly Tyr Glu Asn Ile Asp Ser Leu Thr Arg Lys Val Arg
 65 70 75 80
 Gln Phe Arg Glu Arg Ser Glu Thr Glu Tyr Ala Leu Leu Arg Thr Ser

	85	90	95
Val Ser Arg Pro Cys Ser Cys Thr His Glu His Asp Tyr Glu Val Val			
	100	105	110
Phe Pro His			
	115		

<210> 2077

<211> 214

<212> PRT

<213> Homo sapiens

<400> 2077

Met Ala Asp Val Trp Phe Ile Val Ala Ser Phe Leu Ser Gly Pro Ile			
1	5	10	15
Thr His His Lys Gly Cys Val Ala Ala Thr Phe Phe Val His Phe Phe			
	20	25	30
Tyr Leu Ser Val Phe Phe Trp Met Leu Ala Lys Ala Leu Leu Ile Leu			
	35	40	45
Tyr Gly Ile Met Ile Val Phe His Thr Leu Pro Lys Ser Val Leu Val			
	50	55	60
Ala Ser Leu Phe Ser Val Gly Tyr Gly Cys Pro Leu Ala Ile Ala Ala			
65	70	75	80
Ile Thr Val Ala Ala Thr Glu Pro Gly Lys Gly Tyr Leu Arg Pro Glu			
	85	90	95
Ile Cys Trp Leu Asn Trp Asp Met Thr Lys Ala Leu Leu Ala Phe Val			
	100	105	110
Ile Pro Ala Leu Ala Ile Val Val Val Asn Leu Ile Thr Val Thr Leu			
	115	120	125

Val Ile Val Lys Thr Gln Arg Ala Ala Ile Gly Asn Ser Met Phe Gln
 130 135 140
 Glu Val Arg Ala Ile Val Arg Ile Ser Lys Asn Ile Ala Ile Leu Thr
 145 150 155 160
 Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Val Ala Thr Val Ile Asp
 165 170 175
 Asp Arg Ser Leu Ala Phe His Ile Ile Phe Ser Leu Leu Asn Ala Phe
 180 185 190
 Gln Gly Phe Phe Ile Leu Val Phe Gly Thr Ile Leu Asp Pro Lys Ile
 195 200 205
 Arg Glu Ala Leu Lys Gly
 210

<210> 2078

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2078

Met Ser Phe Phe Phe Phe Phe Phe Phe Glu Thr Glu Cys Ser Gly Thr
 1 5 10 15
 Ile Leu Ala His Cys Asn Leu Cys Phe Leu Gly Ser Ser Asp Ser His
 20 25 30
 Ala Ser Asp Ser Gln Val Ala Gly Thr Thr Gly Ala Arg His His Thr
 35 40 45
 Trp Leu Ile Phe Val Phe Leu Val Glu Ala Gly Phe His His Val Gly
 50 55 60
 Gln Thr Gly Leu Lys Leu Leu Thr Ser Ser Asp Leu Pro Ala Leu Ala

65 70 75 80
 Ser Gln Ser Ala Gly Ile Thr Gly Val Arg His Tyr Thr Arg Pro Ser
 85 90 95
 Thr Ala Ile Leu Thr Ile Phe Leu Leu His Glu His Glu Met Cys Ser
 100 105 110
 Ile Tyr Leu Ser Tyr Phe Phe Ser Asn Val Leu
 115 120

<210> 2079

<211> 566

<212> PRT

<213> Homo sapiens

<400> 2079

Met Ala Lys Arg Glu Asp Ser Pro Gly Pro Glu Val Gln Pro Met Asp
 1 5 10 15
 Lys Gln Phe Leu Val Cys Ser Ile Cys Leu Asp Arg Tyr Gln Cys Pro
 20 25 30
 Lys Val Leu Pro Cys Leu His Thr Phe Cys Glu Arg Cys Leu Gln Asn
 35 40 45
 Tyr Ile Pro Ala Gln Ile Ser Ala Ala Phe Glu Asp Leu Glu Thr Ile
 50 55 60
 Cys Gly Ala Lys Gln Lys Val Leu Gln Ser Gln Leu Asp Thr Leu Arg
 65 70 75 80
 Gln Gly Gln Glu His Ile Gly Ser Ser Cys Ser Phe Ala Glu Gln Ala
 85 90 95
 Leu Arg Leu Gly Ser Ala Pro Glu Val Leu Leu Val Arg Lys His Met
 100 105 110

Arg Glu Arg Leu Ala Ala Leu Ala Ala Gln Ala Phe Pro Glu Arg Pro
115 120 125
His Glu Asn Ala Gln Leu Glu Leu Val Leu Glu Val Asp Gly Leu Arg
130 135 140
Arg Ser Val Leu Asn Leu Gly Ala Leu Leu Thr Thr Ser Ala Thr Ala
145 150 155 160
His Glu Thr Val Ala Thr Gly Glu Gly Leu Arg Gln Ala Leu Val Gly
165 170 175
Gln Pro Ala Ser Leu Thr Val Thr Thr Lys Asp Lys Asp Gly Arg Leu
180 185 190
Val Arg Thr Gly Ser Ala Glu Leu Arg Ala Glu Ile Thr Gly Pro Asp
195 200 205
Gly Thr Arg Leu Pro Val Pro Val Val Asp His Lys Asn Gly Thr Tyr
210 215 220
Glu Leu Val Tyr Thr Ala Arg Thr Glu Gly Glu Leu Leu Leu Ser Val
225 230 235 240
Leu Leu Tyr Gly Gln Pro Val Arg Gly Ser Pro Phe Arg Val Arg Ala
245 250 255
Leu Arg Pro Gly Asp Leu Pro Pro Ser Pro Asp Asp Val Lys Arg Arg
260 265 270
Val Lys Ser Pro Gly Gly Pro Gly Ser His Val Arg Gln Lys Ala Val
275 280 285
Arg Arg Pro Ser Ser Met Tyr Ser Thr Gly Gly Lys Arg Lys Asp Asn
290 295 300
Pro Ile Glu Asp Glu Leu Val Phe Arg Val Gly Ser Arg Gly Arg Glu
305 310 315 320
Lys Gly Glu Phe Thr Asn Leu Gln Gly Val Ser Ala Ala Ser Ser Gly
325 330 335
Arg Ile Val Val Ala Asp Ser Asn Asn Gln Cys Ile Gln Val Phe Ser

340	345	350
Asn Glu Gly Gln Phe Lys Phe Arg Phe Gly Val Arg Gly Arg Ser Pro		
355	360	365
Gly Gln Leu Gln Arg Pro Thr Gly Val Ala Val Asp Thr Asn Gly Asp		
370	375	380
Ile Ile Val Ala Asp Tyr Asp Asn Arg Trp Val Ser Ile Phe Ser Pro		
385	390	395
Glu Gly Lys Phe Lys Thr Lys Ile Gly Ala Gly Arg Leu Met Gly Pro		
405	410	415
Lys Gly Val Ala Val Asp Arg Asn Gly His Ile Ile Val Val Asp Asn		
420	425	430
Lys Ser Cys Cys Val Phe Thr Phe Gln Pro Asn Gly Lys Leu Val Gly		
435	440	445
Arg Phe Gly Gly Arg Gly Ala Thr Asp Arg His Phe Ala Gly Pro His		
450	455	460
Phe Val Ala Val Ser Asn Lys Asn Glu Ile Val Val Thr Asp Phe His		
465	470	475
Asn His Ser Val Lys Val Ser Val Phe Pro Pro Ser Val Thr Thr Val		
485	490	495
Pro Thr Ser Phe Pro Leu Pro Gln Ala Ser Ser Leu Phe Tyr Leu Leu		
500	505	510
Leu Phe Pro Phe Glu Ile Ile His Ser Asn Asn Thr His Leu His Ile		
515	520	525
Tyr Ala Trp Leu Leu Cys Pro Arg Gln Tyr Ala Arg Ser Trp Arg Tyr		
530	535	540
Ser Asp Ala Gln Ser Lys Cys Ile Leu Cys Leu Leu Asp Tyr Ser Leu		
545	550	555
Val Gly Lys Arg Lys Arg		560
565		

<210> 2080

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2080

Met His Asn Lys Arg Lys Tyr Ile Cys Thr Ser Phe Phe Phe Thr Glu

1 5 10 15

Lys Ser Pro Ser Ser Tyr Ser Gly Val Glu Asn Leu Ser Leu Ala Gly

20 25 30

Tyr Asn Leu Ser Ser Gln Ser Phe Leu Ile Ala Leu Gln Gln Cys Pro

35 40 45

Asp Gln Ile Glu Phe Phe Leu Ile Gly Asn Ser Ser Phe Leu Tyr Pro

50 55 60

Phe Ala His Ser Val Pro Phe Phe Leu Glu Lys Leu Phe Ala His Val

65 70 75 80

Phe Tyr Pro Pro Ile Leu Ser Phe Ser Met Pro Thr Ser Cys Pro Thr

85 90 95

Pro Leu Tyr Phe Pro Ser Lys Leu Thr Gln Thr Leu Gly Glu Leu Phe

100 105 110

Leu Asn Val Phe Ser Glu Cys Leu Leu Leu Lys Glu Leu Pro Ser His

115 120 125

Lys Val

130

<210> 2081

<211> 1004

<212> PRT

<213> Homo sapiens

<400> 2081

Met His Gly Ser Cys Cys Leu Gly Gly Gly Gln Pro Leu Ser Val Phe

1 5 10 15

Ala Ser Leu His Met Gly Pro Glu Ala Leu Ala Leu Lys Ala Gly Arg

20 25 30

Gly Trp Cys Pro Thr Phe Gln Ser Phe Pro Glu Pro Thr Pro Ser Tyr

35 40 45

Gly Ala Pro Gly Val Glu Phe Met Gly Leu His Gln Glu Asn Asn Ala

50 55 60

Val Thr Gln Ile His Leu Leu Pro Gly Gln Cys Gln Leu Val Thr Leu

65 70 75 80

Leu Asp Asp Asn Ser Leu His Leu Trp Ser Leu Lys Val Lys Gly Gly

85 90 95

Ala Ser Glu Leu Gln Glu Asp Glu Ser Phe Thr Leu Arg Gly Pro Pro

100 105 110

Gly Ala Ala Pro Ser Ala Thr Gln Ile Thr Val Val Leu Pro His Ser

115 120 125

Ser Cys Glu Leu Leu Tyr Leu Gly Thr Glu Ser Gly Asn Val Phe Val

130 135 140

Val Gln Leu Pro Ala Phe Arg Ala Leu Glu Asp Arg Thr Ile Ser Ser

145 150 155 160

Asp Ala Val Leu Gln Arg Leu Pro Glu Glu Ala Arg His Arg Arg Val

165 170 175

Phe Glu Met Val Glu Ala Leu Gln Glu His Pro Arg Asp Pro Asn Gln

180 185 190

Ile Leu Ile Gly Tyr Ser Arg Gly Leu Val Val Ile Trp Asp Leu Gln
195 200 205
Gly Ser Arg Val Leu Tyr His Phe Leu Ser Ser Gln Gln Leu Glu Asn
210 215 220
Ile Trp Trp Gln Arg Asp Gly Arg Leu Leu Val Ser Cys His Ser Asp
225 230 235 240
Gly Ser Tyr Cys Gln Trp Pro Val Ser Ser Glu Ala Gln Gln Pro Glu
245 250 255
Pro Leu Arg Ser Leu Val Pro Tyr Gly Pro Phe Pro Cys Lys Ala Ile
260 265 270
Thr Arg Ile Leu Trp Leu Thr Thr Arg Gln Gly Leu Pro Phe Thr Ile
275 280 285
Phe Gln Gly Gly Met Pro Arg Ala Ser Tyr Gly Asp Arg His Cys Ile
290 295 300
Ser Val Ile His Asp Gly Gln Gln Thr Ala Phe Asp Phe Thr Ser Arg
305 310 315 320
Val Ile Gly Phe Thr Val Leu Thr Glu Ala Asp Pro Ala Ala Thr Phe
325 330 335
Asp Asp Pro Tyr Ala Leu Val Val Leu Ala Glu Glu Glu Leu Val Val
340 345 350
Ile Asp Leu Gln Thr Ala Gly Trp Pro Pro Val Gln Leu Pro Tyr Leu
355 360 365
Ala Ser Leu His Cys Ser Ala Ile Thr Cys Ser His His Val Ser Asn
370 375 380
Ile Pro Leu Lys Leu Trp Glu Arg Ile Ile Ala Ala Gly Ser Arg Gln
385 390 395 400
Asn Ala His Phe Ser Thr Met Glu Trp Pro Ile Asp Gly Gly Thr Ser
405 410 415
Leu Thr Pro Ala Pro Pro Gln Arg Asp Leu Leu Leu Thr Gly His Glu

420 425 430
Asp Gly Thr Val Arg Phe Trp Asp Ala Ser Gly Val Cys Leu Arg Leu
435 440 445
Leu Tyr Lys Leu Ser Thr Val Arg Val Phe Leu Thr Asp Thr Asp Pro
450 455 460
Asn Glu Asn Phe Ser Ala Gln Gly Glu Asp Glu Trp Pro Pro Leu Arg
465 470 475 480
Lys Val Gly Ser Phe Asp Pro Tyr Ser Asp Asp Pro Arg Leu Gly Ile
485 490 495
Gln Lys Ile Phe Leu Cys Lys Tyr Ser Gly Tyr Leu Ala Val Ala Gly
500 505 510
Thr Ala Gly Gln Val Leu Val Leu Glu Leu Asn Asp Glu Ala Ala Glu
515 520 525
Gln Ala Val Glu Gln Val Glu Ala Asp Leu Leu Gln Asp Gln Glu Gly
530 535 540
Tyr Arg Trp Lys Gly His Glu Arg Leu Ala Ala Arg Ser Gly Pro Val
545 550 555 560
Arg Phe Glu Pro Gly Phe Gln Pro Phe Val Leu Val Gln Cys Gln Pro
565 570 575
Pro Ala Val Val Thr Ser Leu Ala Leu His Ser Glu Trp Arg Leu Val
580 585 590
Ala Phe Gly Thr Ser His Gly Phe Gly Leu Phe Asp His Gln Gln Arg
595 600 605
Arg Gln Val Phe Val Lys Cys Thr Leu His Pro Ser Asp Gln Leu Ala
610 615 620
Leu Glu Gly Pro Leu Ser Arg Val Lys Ser Leu Lys Lys Ser Leu Arg
625 630 635 640
Gln Ser Phe Arg Arg Met Arg Arg Ser Arg Val Ser Ser Arg Lys Arg
645 650 655

His Pro Ala Gly Pro Pro Gly Glu Ala Gln Glu Gly Ser Ala Lys Ala
660 665 670
Glu Arg Pro Gly Leu Gln Asn Met Glu Leu Ala Pro Val Gln Arg Lys
675 680 685
Ile Glu Ala Arg Ser Ala Glu Asp Ser Phe Thr Gly Phe Val Arg Thr
690 695 700
Leu Tyr Phe Ala Asp Thr Tyr Leu Lys Asp Ser Ser Arg His Cys Pro
705 710 715 720
Ser Leu Trp Ala Gly Thr Asn Gly Gly Thr Ile Tyr Ala Phe Ser Leu
725 730 735
Arg Val Pro Pro Ala Glu Arg Arg Met Asp Glu Pro Val Arg Ala Glu
740 745 750
Gln Ala Lys Glu Ile Gln Leu Met His Arg Ala Pro Val Val Gly Ile
755 760 765
Leu Val Leu Asp Gly His Ser Val Pro Leu Pro Glu Pro Leu Glu Val
770 775 780
Ala His Asp Leu Ser Lys Ser Pro Asp Met Gln Gly Ser His Gln Leu
785 790 795 800
Leu Val Val Ser Glu Glu Gln Phe Lys Val Phe Thr Leu Pro Lys Val
805 810 815
Ser Ala Lys Leu Lys Leu Lys Leu Thr Ala Leu Glu Gly Ser Arg Val
820 825 830
Arg Arg Val Ser Val Ala His Phe Gly Ser Arg Arg Ala Glu Asp Tyr
835 840 845
Gly Glu His His Leu Ala Val Leu Thr Asn Leu Gly Asp Ile Gln Val
850 855 860
Val Ser Leu Pro Leu Leu Lys Pro Gln Val Arg Tyr Ser Cys Ile Arg
865 870 875 880
Arg Glu Asp Val Ser Gly Ile Ala Ser Cys Val Phe Thr Lys Tyr Gly

885 890 895
 Gln Gly Phe Tyr Leu Ile Ser Pro Ser Glu Phe Glu Arg Phe Ser Leu
 900 905 910
 Ser Thr Lys Trp Leu Val Glu Pro Arg Cys Leu Val Asp Ser Ala Glu
 915 920 925
 Thr Lys Asn His Arg Pro Gly Asn Gly Ala Gly Pro Lys Lys Ala Pro
 930 935 940
 Ser Arg Ala Arg Asn Ser Gly Thr Gln Ser Asp Gly Glu Glu Lys Gln
 945 950 955 960
 Pro Gly Leu Val Met Glu Arg Ala Leu Leu Ser Asp Glu Arg Ala Ala
 965 970 975
 Thr Gly Val His Ile Glu Pro Pro Trp Gly Ala Ala Ser Ala Met Ala
 980 985 990
 Glu Gln Ser Glu Trp Leu Ser Val Gln Ala Ala Arg
 995 1000

<210> 2082

<211> 180

<212> PRT

<213> Homo sapiens

<400> 2082

Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu Thr Phe Leu
 1 5 10 15
 Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser Glu Thr Leu
 20 25 30
 Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg
 35 40 45

Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
 50 55 60
 Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
 65 70 75 80
 Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
 85 90 95
 Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
 100 105 110
 Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
 115 120 125
 Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
 130 135 140
 Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
 145 150 155 160
 Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
 165 170 175
 Ser Asn Arg Lys
 180

<210> 2083

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2083

Met Gln Lys Val Ile Lys Phe Thr Ser Glu Leu Leu Ala Phe Glu Pro
 1 5 10 15
 Ala Ala Thr Ser Leu Ser Arg Pro Gly Leu Asn Ile Val Leu Ser Glu

20	25	30
Val Leu Lys Met Leu Gln Ser Trp Ile Ser Gly Asn Val Ala Ala Pro		
35	40	45
Leu Leu Thr Thr Ser Ser Leu Ile Val Leu Lys Leu Ala Leu Gly Met		
50	55	60
Ala Ala Phe Ser Asn His Phe Gln Leu Glu Trp Val Leu Leu Lys Lys		
65	70	75
Ser Asn Ile Ile Pro Ala Val Glu Lys Gly Ser Leu Arg Glu Lys Val		
85	90	95
Leu Val Lys Ile Leu Phe Phe Val Leu Val Tyr Glu		
100	105	

<210> 2084

<211> 320

<212> PRT

<213> Homo sapiens

<400> 2084

Met Glu Lys Val Arg Leu Trp Arg Gly Ser Glu Ser Arg Ala Ala Ile		
1	5	10
Cys Thr Gly Ile Gly Ile Gly Phe Tyr Gly Asn Ser Glu Thr Ser Asp		
20	25	30
Gly Val Ser Gln Leu Ser Ser Ala Leu Leu His Ala Asn His Thr Leu		
35	40	45
Ser Thr Ile Asp His Leu Thr Val Glu Arg Leu Gly Glu Ala Val Arg		
50	55	60
Thr Glu Leu Thr Thr Leu Glu Glu Val Leu Glu Pro Arg Thr Glu Leu		
65	70	75
		80

Val Ala Ala Ala Arg Gly Ala Arg Arg Gln Ala Glu Ala Ala Ala Gln
 85 90 95
 Gln Leu Gln Gly Leu Ala Phe Trp Gln Gly Val Pro Leu Ser Pro Leu
 100 105 110
 Gln Val Ala Glu Asn Val Ser Phe Val Glu Glu Tyr Arg Trp Leu Ala
 115 120 125
 Tyr Val Leu Leu Leu Leu Leu Glu Leu Leu Val Cys Leu Phe Thr Leu
 130 135 140
 Leu Gly Leu Ala Lys Gln Ser Lys Trp Leu Val Ile Val Met Thr Val
 145 150 155 160
 Met Ser Leu Leu Val Leu Val Leu Ser Trp Gly Ser Met Gly Leu Glu
 165 170 175
 Ala Ala Thr Ala Val Gly Leu Ser Asp Phe Cys Ser Asn Pro Asp Pro
 180 185 190
 Tyr Val Leu Asn Leu Thr Gln Glu Glu Thr Gly Leu Ser Ser Asp Ile
 195 200 205
 Leu Ser Tyr Tyr Leu Leu Cys Asn Arg Ala Val Ser Asn Pro Phe Gln
 210 215 220
 Gln Arg Leu Thr Leu Ser Gln Arg Ala Leu Ala Asn Ile His Ser Gln
 225 230 235 240
 Leu Leu Gly Leu Glu Arg Glu Ala Val Pro Gln Phe Pro Ser Ala Gln
 245 250 255
 Lys Pro Leu Leu Ser Leu Glu Glu Thr Leu Asn Val Thr Glu Gly Asn
 260 265 270
 Phe His Gln Leu Val Ala Leu Leu His Cys Arg Ser Leu His Lys Val
 275 280 285
 Lys Pro Leu Pro Ser Gln Phe Leu Leu Pro Arg Gly Ala Ser Val Ser
 290 295 300
 Thr His Arg Thr Thr Ser Ser Phe Ser Leu Asp Pro Cys His Cys Ala

305

310

315

320

<210> 2085

<211> 616

<212> PRT

<213> Homo sapiens

<400> 2085

Met Asp Val Met Leu Glu Asn Tyr Cys His Leu Ile Ser Val Gly Cys

1

5

10

15

His Met Thr Lys Pro Asp Val Ile Leu Lys Leu Glu Arg Gly Glu Glu

20

25

30

Pro Trp Thr Ser Phe Ala Gly His Thr Cys Leu Glu Glu Asn Trp Lys

35

40

45

Ala Glu Asp Phe Leu Val Lys Phe Lys Glu His Gln Glu Lys Tyr Ser

50

55

60

Arg Ser Val Val Ser Ile Asn His Lys Lys Leu Val Lys Glu Lys Ser

65

70

75

80

Lys Ile Tyr Glu Lys Thr Phe Thr Leu Gly Lys Asn Pro Val Asn Ser

85

90

95

Lys Asn Leu Pro Pro Glu Tyr Asp Thr His Gly Arg Ile Leu Lys Asn

100

105

110

Val Ser Glu Leu Ile Ile Ser Asn Leu Asn Pro Ala Arg Lys Arg Leu

115

120

125

Ser Glu Tyr Asn Gly Tyr Gly Lys Ser Leu Leu Ser Thr Lys Gln Glu

130

135

140

Thr Thr His Pro Glu Val Lys Ser His Asn Gln Ser Ala Arg Ala Phe

145

150

155

160

Ser His Asn Glu Val Leu Met Gln Tyr Gln Lys Thr Glu Thr Pro Ala
 165 170 175
 Gln Ser Phe Gly Tyr Asn Asp Cys Glu Lys Ser Phe Leu Gln Arg Gly
 180 185 190
 Gly Leu Ile Thr His Ser Arg Pro Tyr Lys Gly Glu Asn Pro Ser Val
 195 200 205
 Tyr Asn Lys Lys Arg Arg Ala Thr Asn Ile Glu Lys Lys His Thr Cys
 210 215 220
 Asn Glu Cys Gly Lys Ser Phe Cys Arg Lys Ser Val Leu Ile Leu His
 225 230 235 240
 Gln Gly Ile His Ser Glu Glu Lys Pro Tyr Gln Cys His Gln Cys Gly
 245 250 255
 Asn Ala Phe Arg Arg Lys Ser Tyr Leu Ile Asp His Gln Arg Thr His
 260 265 270
 Thr Gly Glu Lys Pro Phe Val Cys Asn Glu Cys Gly Lys Ser Phe Arg
 275 280 285
 Leu Lys Thr Ala Leu Thr Asp His Gln Arg Thr His Thr Gly Glu Lys
 290 295 300
 Ser Tyr Glu Cys Leu Gln Cys Arg Asn Ala Phe Arg Leu Lys Ser His
 305 310 315 320
 Leu Ile Arg His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys
 325 330 335
 Asn Asp Cys Gly Lys Ser Phe Arg Gln Lys Thr Thr Leu Ser Leu His
 340 345 350
 Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Ile Cys Lys Glu Cys Gly
 355 360 365
 Lys Ser Phe His Gln Lys Ala Asn Leu Thr Val His Gln Arg Thr His
 370 375 380
 Thr Gly Glu Lys Pro Tyr Ile Cys Asn Glu Cys Gly Lys Ser Phe Ser

385	390	395	400
Gln Lys Thr Thr Leu Ala Leu His Glu Lys Thr His Asn Glu Glu Lys			
	405	410	415
Pro Tyr Ile Cys Ser Glu Cys Gly Lys Ser Phe Arg Gln Lys Thr Thr			
	420	425	430
Leu Val Ala His Gln Arg Thr His Thr Gly Glu Lys Ser Tyr Glu Cys			
	435	440	445
Pro His Cys Gly Lys Ala Phe Arg Met Lys Ser Tyr Leu Ile Asp His			
	450	455	460
His Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly			
465	470	475	480
Lys Ser Phe Ser Gln Lys Thr Asn Leu Asn Leu His Gln Arg Ile His			
	485	490	495
Thr Gly Glu Lys Pro Tyr Val Cys Asn Glu Cys Gly Lys Ser Phe Arg			
	500	505	510
Gln Lys Ala Thr Leu Thr Val His Gln Lys Ile His Thr Gly Gln Lys			
	515	520	525
Ser Tyr Glu Cys Pro Gln Cys Gly Lys Ala Phe Ser Arg Lys Ser Tyr			
	530	535	540
Leu Ile His His Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys			
545	550	555	560
Ser Glu Cys Gly Lys Cys Phe Arg Gln Lys Thr Asn Leu Ile Val His			
	565	570	575
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Val Cys Asn Glu Cys Gly			
	580	585	590
Lys Ser Phe Ser Tyr Lys Arg Asn Leu Ile Val His Gln Arg Thr His			
	595	600	605
Lys Gly Glu Asn Ile Glu Met Gln			
	610	615	

<210> 2086

<211> 773

<212> PRT

<213> Homo sapiens

<400> 2086

Met Asn Arg Glu Leu Glu Ser Met Ala Met Arg Pro Leu Ala Lys Glu
1 5 10 15
Leu Thr Arg Ser Leu Glu Asp Val Arg Gly Ala Leu Arg Asp Gln Ala
20 25 30
Leu Arg Asp Leu Asn Thr Tyr Thr Glu Lys Ile Arg Glu Ala Leu Arg
35 40 45
His Phe Asp Val Leu Phe Ala Glu Phe Glu Leu Ser Tyr Val Ser Ala
50 55 60
Met Val Pro Val Lys Ser Pro Arg Glu Tyr Tyr Val Gln Gln Glu Val
65 70 75 80
Ile Val Leu Phe Cys Glu Thr Val Glu Arg Ala Leu Asp Phe Gly Tyr
85 90 95
Leu Thr Gln Asp Met Ile Asp Asp Tyr Glu Pro Ala Leu Met Phe Ser
100 105 110
Ile Pro Arg Leu Ala Ile Val Cys Gly Leu Val Val Tyr Ala Asp Gly
115 120 125
Pro Leu Asn Leu Asp Arg Lys Val Glu Asp Met Ser Glu Leu Phe Arg
130 135 140
Pro Phe His Thr Leu Leu Arg Lys Ile Arg Asp Leu Leu Gln Thr Leu
145 150 155 160
Thr Glu Glu Glu Leu His Thr Leu Glu Arg Asn Leu Cys Ile Ser Gln

165	170	175
Asp Val Glu Phe Pro Ile Arg Ala Asp Val Gln Gly Pro Ala Ala Leu		
180	185	190
Ala Pro Ala Leu Ser Ala Pro Leu Pro Pro Glu Gly Pro Leu Ser Ala		
195	200	205
Lys Ala Lys Asp Pro Asp Ala Glu Leu Ala Cys Ser Met Gln Tyr Asp		
210	215	220
Asp Gln Gly Leu Glu Gln Leu Ser Arg Met Val His Arg Ala Gly Asp		
225	230	235
Glu Met Ser Ser Leu Leu Ser Pro Pro Ile Ala Cys Gln Ser Pro Ala		
245	250	255
His Arg Pro Gly Ala Glu Gly Ser Pro Gly Gly Glu Ala Ser Pro Gly		
260	265	270
Arg Pro Arg Leu Arg Ser Gly Ser Asp Glu Glu Glu Arg Val Phe Phe		
275	280	285
Met Asp Asp Val Glu Gly Thr Ala Glu Ala Leu Ala Arg Pro Glu Ser		
290	295	300
Pro Ala Gly Pro Phe Gly Trp Ala Gly Ser Thr Trp Ala Asp Pro Gln		
305	310	315
Glu Lys Gly Gln Gly Gly Pro Gly Gly Ala Ala Gly Ile Ser Leu Pro		
325	330	335
Ala Ser Glu Lys Glu Glu Asp Leu Ser Asn Asn Asn Leu Glu Ala Glu		
340	345	350
Gly Thr Asp Gly Ala Ser Leu Ala Gly Thr Ser Ser Cys Ser Cys Leu		
355	360	365
Asp Ser Arg Leu His Leu Asp Gly Trp Glu Val Gly Ala Asp Asp Ala		
370	375	380
Glu Thr Ala Glu Met Ile Ala His Arg Thr Gly Gly Met Lys Leu Ser		
385	390	395
		400

Ala Thr Val Ile Phe Asn Pro Lys Ser Pro Thr Ser Leu Asp Ser Ala
 405 410 415
 Val Ala Thr Gln Glu Ala Ala Ser Glu Pro Val Ala Glu Gly Met Asp
 420 425 430
 Gly Gly Pro His Lys Leu Ser Thr Gly Ala Thr Asn Cys Leu Leu His
 435 440 445
 Ser Cys Val Cys Cys Gly Ser Cys Gly Asp Ser Arg Glu Asp Val Val
 450 455 460
 Glu Arg Leu Arg Glu Lys Cys Ser Pro Gly Gly Val Ile Gly Ala Ser
 465 470 475 480
 Tyr Ala Ala Gly Leu Ala Lys Ala Ser Asp Arg Ala Pro Glu Arg Gln
 485 490 495
 Glu Glu Ala Pro Pro Pro Ser Glu Asp Ala Ser Asn Gly Arg Glu Pro
 500 505 510
 Lys Ala Pro Thr Ser Asp Lys Cys Leu Pro His Thr Ser Gly Ser Gln
 515 520 525
 Val Asp Thr Ala Ser Gly Leu Gln Gly Glu Ala Gly Val Ala Gly Gln
 530 535 540
 Gln Glu Pro Glu Ala Arg Glu Leu His Ala Gly Ser Pro Pro Ala His
 545 550 555 560
 Glu Ala Pro Gln Gly Leu Ser Gly Ser Ser Ser Ser Thr Ala Gly Ser
 565 570 575
 Cys Ser Ser Asp Lys Met Gly Pro Glu Ala Ala Pro Ala Ala Thr His
 580 585 590
 Ala Ala Pro Gln Ala Thr Arg Glu Lys Ile Arg Ser Arg Phe His Gly
 595 600 605
 Ser His Asp Leu Ile His Arg Leu Phe Val Cys Ile Ser Gly Val Ala
 610 615 620
 Asp Gln Leu Gln Thr Asn Tyr Ala Ser Asp Leu Arg Ser Ile Leu Lys

625 630 635 640
Thr Leu Phe Glu Val Met Ala Thr Lys Pro Glu Thr Asp Asp Lys Glu
 645 650 655
Lys Leu Arg Lys Val Thr Gln Thr Leu Arg Ser Ala Ala Leu Glu Asp
 660 665 670
Cys Ala Leu Cys Gln Glu Thr Leu Ser Ser Ser Glu Leu Ala Ala Lys
 675 680 685
Thr Arg Asp Gly Asp Phe Glu Asp Pro Pro Glu Trp Val Pro Asp Glu
 690 695 700
Ala Cys Gly Phe Cys Thr Ala Cys Lys Ala Pro Phe Thr Val Ile Arg
705 710 715 720
Arg Lys His His Cys Arg Ser Cys Gly Lys Ile Phe Cys Ser Arg Cys
 725 730 735
Ser Ser His Ser Ala Pro Leu Pro Arg Tyr Gly Gln Val Lys Pro Val
 740 745 750
Arg Val Cys Thr His Cys Tyr Met Phe His Val Thr Pro Phe Tyr Ser
 755 760 765
Asp Lys Ala Gly Leu
770

<210> 2087

<211> 116

<212> PRT

<213> Homo sapiens

<400> 2087

Met Gly Val Arg Pro Ser Thr Leu Gly Thr Leu Gly His Asp Val His
1 5 10 15

Pro Arg Val Phe Ala Glu Gln Arg Glu Arg Thr Leu Leu Ala Gly Thr

20

25

30

Val Pro Val Ser Ala Pro Gly Ser Ala Pro Thr Ala Pro Ser Pro Arg

35

40

45

Ala Ala Arg Arg Arg Gly Ser Val Ile Pro Pro Arg Pro Arg Leu Leu

50

55

60

Ser Pro Thr His His Thr Gly Arg Arg Gln Pro Glu Gly Arg Phe Ile

65

70

75

80

Asp Asn Leu Thr Gly His Lys Gln Ala Gly Asp Arg Thr Ala Thr Gly

85

90

95

Ser Gly Gly Gly Gly Gly Gly Ala Thr Cys Gly Thr Arg Ser Ala Ala

100

105

110

Ser Ala Pro Ala

115

<210> 2088

<211> 398

<212> PRT

<213> Homo sapiens

<400> 2088

Met Gln Leu Asn Ser His Cys Val Cys Asn Ser Thr Arg Thr Ala Tyr

1

5

10

15

Ala Asn Pro Leu Thr Ala Tyr Ala Thr Gln Leu Ala Leu Arg Met Gln

20

25

30

Leu Ser Ser Leu Cys Val Cys Asn Pro Ala Arg Ser Ala Tyr Ala Thr

35

40

45

Gln Val Ala Leu Arg Met Gln Leu Ser Ser Leu Cys Val Cys Asn Ser

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Met Gln Leu Asn Ser His Cys Val Cys Asn Ser Ala Arg Thr Ala Tyr
 290 295 300

Ala Thr Gln Leu Leu Gln Val Leu Ile Ser Gly His Phe Leu Phe Leu
 305 310 315 320

Thr Thr Thr Pro Ser Gln Tyr Phe Ser Ser Leu Lys Ser Ala Gln Asp
 325 330 335

Glu Ala Leu Asp Ser Arg Thr Cys Cys Met Pro Leu Gly Leu Leu Glu
 340 345 350

Val Cys Arg Leu Ala Ser Pro Arg Leu His Pro Ala Leu Ser Cys Leu
 355 360 365

Ser Cys Glu Asn Pro Val Ala Ser Ala Ser Pro Gly Ser Asp Phe Cys
 370 375 380

Leu Leu Pro Ser Ser Ala Ala Pro Leu Gly Pro Cys Leu Glu
 385 390 395

<210> 2089

<211> 144

<212> PRT

<213> Homo sapiens

<400> 2089

Met Ser Pro Val Ala Val Cys Gly His Pro Arg Phe Ser Phe Leu Pro
 1 5 10 15

Phe Leu Ser Phe Phe Pro Ser Phe Leu Pro Pro Ser Leu Phe Pro Ser
 20 25 30

Phe Leu Pro Ser Phe Phe Phe Leu Ser Phe Ser Phe Leu Ser Phe Phe
 35 40 45

Pro Pro Leu Ser Leu Pro Ser Phe Phe Val Phe Leu Ser Ile Leu Pro

50	55	60
Ser Phe Ser Pro Pro Leu Pro Ser Ser Pro Leu Pro Asp Gly Val Ser		
65	70	75
Leu Leu Leu Pro Gly Leu Glu Cys Ser Glu Pro Arg Met His His Cys		
85	90	95
Thr Pro Ala Trp Val Thr Glu Arg Asp Cys Val Ser Lys Ile Lys Ile		
100	105	110
Lys Val Ser Lys Ala Trp Trp Cys Ala Pro Val Val Pro Ala Thr Gln		
115	120	125
Glu Ala Glu Leu Gly Gly Ser Leu Glu Leu Thr Ser Ser Arg Leu Gln		
130	135	140

<210> 2090

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2090

Met Leu Arg Phe Cys Ala Gly Leu Ser Asp Phe Ala Pro Val Ala Val
1 5 10 15
Arg Ser Leu Gln Asp Leu Ala Arg Ile Ala Ile Arg Gly Thr Ile Lys
20 25 30
Lys Ile Ile His Gln Glu Thr Val Ser Lys Asn Gly Asn Gly Leu Lys
35 40 45
Asn Thr Pro Arg Phe Lys Arg Arg Arg Val Arg Arg Arg Arg Met Glu
50 55 60
Thr Ile Val Phe Leu Asp Lys Glu Val Phe Ala Ser Arg Ile Ser Asn
65 70 75 80

Pro Ser Asp Asp Asn Ser Cys Glu Asp Leu Glu Glu Glu Arg Arg Glu
 85 90 95
 Glu Glu Glu Lys Thr Pro Pro Glu Thr Lys Pro Asp Pro Pro Val Asn
 100 105 110
 Phe Leu Arg Gln Lys Val Leu Ser Leu Pro Leu Pro Asp Pro Leu Lys
 115 120 125
 Tyr Tyr Leu Leu Tyr Tyr Arg Glu Lys
 130 135

<210> 2091

<211> 173

<212> PRT

<213> Homo sapiens

<400> 2091

Met Ser Ser Trp Lys Ala Glu Asn Gly Thr Leu Leu Glu Trp Asp Thr
 1 5 10 15
 Gly Trp Pro Gly Phe Ser Arg Ala Cys Pro Thr Lys Val Ala Ser Glu
 20 25 30
 Leu Ala Leu Phe Ser Gly Arg Leu Phe Leu Asp Ser Gly Lys His Ser
 35 40 45
 His Ser Lys Tyr Trp Leu Thr Phe Tyr Gln Pro Ala Thr Leu Val Glu
 50 55 60
 Arg Gly Pro Leu Thr Gln Leu Tyr Gln Gln Ala Val Ser Arg Ser Arg
 65 70 75 80
 Gly Trp Arg Asp Thr Gln Cys Cys Ser Arg Pro Val Trp Leu Arg Val
 85 90 95
 Cys Leu Val Cys Pro Cys Thr His Gly Phe Leu Phe Ser Cys Arg Arg

100	105	110	
Pro Leu Leu Leu Gly Ser Thr Ser Phe Ile Pro Ile Gly Arg Arg Thr			
115	120	125	
Tyr Ala Ser Ala Ala Glu Pro Val Gly Ser Lys Ala Val Leu Val Thr			
130	135	140	
Gly Cys Asp Ser Gly Phe Gly Phe Ser Leu Ala Lys His Leu His Ser			
145	150	155	160
Lys Gly Phe Leu Val Phe Ala Gly Cys Leu Met Lys Leu			
165	170		

<210> 2092

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2092

Met Trp Asp Pro Phe Phe Phe Leu Asp Gly Val Ser Leu Leu Leu Pro			
1	5	10	15
Arg Leu Glu Cys Asn Gly Val Ile Ser Ala His Cys Asn Leu Cys Leu			
20	25	30	
Leu Asp Ser Ser Asp Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Ile			
35	40	45	
Thr Gly Ala Tyr His Arg Ala Trp Leu Ile Phe Ser Phe Leu Val Glu			
50	55	60	
Met Gly Phe His His Val Gly Gln Ala Gly Leu Lys Leu Pro Thr Ser			
65	70	75	80
Gly Asp Pro Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val			
85	90	95	

Ser His His Thr Trp Leu Gly Ser Ser Glu Leu Tyr Phe Phe Phe Leu
100 105 110
Ser Lys Asp Gly Val Ser Pro Cys Trp Pro Gly Trp Ser
115 120 125

<210> 2093

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2093

Met Trp Lys His Ala Ser Asp Gln Asn Tyr Asn Tyr Glu Gln Val Asn
1 5 10 15
Lys Ala Ile Asn Asp Ala Ile Ser Gln Ser Gly Arg Val Leu Gly Lys
20 25 30
Ser Pro Gly Lys Thr Gln Leu Lys Ser Ser Glu Glu Ser Ala Asp Pro
35 40 45
Val Thr Gly Ser Ser Glu Asn Ala Val Ser Ser Ser Glu Leu Met Ser
50 55 60
Gln Thr Pro Ser Glu Val Leu Gly Thr Asn Glu Asn Glu Lys Leu Ser
65 70 75 80
Pro Thr Ser Asn Thr Ser Tyr Ser Leu Glu Lys Ile Ser Ser Leu Ala
85 90 95
Pro Pro Ser Met Glu Tyr Cys Val Leu Leu Phe Cys Cys Cys Ile Cys
100 105 110
Gly Phe Glu Ser Thr Ser Lys Glu Asn Leu Leu Asp His Met Lys Glu
115 120 125
His Glu Gly Glu Ile Val Asn Ile Ile Leu Asn Lys Asp His Asn Thr

130
Ala Leu Asn Thr Asn
145

135

140

<210> 2094

<211> 243

<212> PRT

<213> Homo sapiens

<400> 2094

Met Glu Ile Arg Leu Val Val Asn Gly Asn Leu Val His Thr Ala Val

1

5

10

15

Val Pro Gln Leu Gln Leu Val Ala Ser Arg Ser Asp Ile Tyr Phe Thr

20

25

30

Ala Thr Ala Ala Val Asn Glu Val Ser Ser Gly Gly Ser Ser Lys Gly

35

40

45

Ala Ser Ala Arg Asn Ser Pro Gln Thr Pro Pro Gly Arg Asp Thr Pro

50

55

60

Val Phe Pro Ser Ser Leu Gly Glu Gly Glu Ile Gln Ser Lys Asn Leu

65

70

75

80

Tyr Lys Ile Pro Leu Arg Asn Leu Val Gly Arg Ser Ile Glu Arg Pro

85

90

95

Leu Lys Ser Pro Leu Val Ser Lys Val Ile Thr Pro Pro Thr Pro Ile

100

105

110

Ser Val Gly Leu Ala Ala Ile Pro Val Thr His Ser Leu Ser Leu Ser

115

120

125

Arg Met Glu Ile Lys Glu Ile Ala Ser Arg Thr Arg Arg Glu Leu Leu

130

135

140

Gly Leu Ser Asp Glu Gly Gly Pro Lys Ser Glu Gly Ala Pro Lys Ala
 145 150 155 160
 Lys Ser Lys Pro Arg Lys Arg Leu Glu Glu Ser Gln Gly Gly Pro Lys
 165 170 175
 Pro Gly Ala Val Arg Ser Ser Ser Ser Asp Arg Ile Pro Ser Gly Ser
 180 185 190
 Leu Glu Ser Ala Ser Thr Ser Glu Ala Asn Pro Glu Gly His Ser Ala
 195 200 205
 Ser Ser Asp Gln Asp Pro Val Ala Asp Arg Glu Gly Ser Pro Val Ser
 210 215 220
 Gly Ser Ser Pro Phe Gln Leu Thr Ala Phe Ser Asp Glu Asp Ile Ile
 225 230 235 240
 Asp Leu Lys

<210> 2095

<211> 183

<212> PRT

<213> Homo sapiens

<400> 2095

Met Cys Pro Lys His Trp Ser Leu Ser Pro His Val Ser Val Gln Thr
 1 5 10 15
 Pro Val Trp Lys Phe Gly Arg Gly Ser Lys Ser Cys Pro Pro Arg Phe
 20 25 30
 Pro Leu Gln Thr Gln Leu His Gly Pro Gly Trp Pro Gly Leu Arg Thr
 35 40 45
 Cys Leu Pro Asp Ser Ala Pro Cys Cys Arg Ala Val Thr Pro Ser Ser

50 55 60
 Gln Ser Leu Gly Pro Leu Arg Pro Leu Cys Ala Ser Cys Ser Gln Pro
 65 70 75 80
 Gly Cys Ser Ile Ser Cys Gly Thr Ala Ala Leu Pro Thr Gln Ser Val
 85 90 95
 Val Pro Pro Pro Ser Pro Leu Leu Ser Leu Pro Pro Thr Leu Ser Phe
 100 105 110
 Pro His Ser Ser Ala Arg Pro Ala Pro Ala Ser Val Phe Cys His Ser
 115 120 125
 Leu Ser Trp Val Ser Arg Gly Pro Cys Gly Gly Leu Gln Gly Ser Pro
 130 135 140
 Cys Cys Pro Gly Gly Thr Ser Gln Ser Ile Ile Pro Ala Gln Pro Ala
 145 150 155 160
 Gly Pro Thr Ser Ser Val Gln Thr Leu Arg Gly Cys Pro Gln Arg Gln
 165 170 175
 Gln Val Pro Arg Val Arg Ser
 180

<210> 2096

<211> 191

<212> PRT

<213> Homo sapiens

<400> 2096

Met Arg Ala Pro Pro Phe Ser Gln Ala Ser Lys Pro Asp Met Arg Leu
 1 5 10 15
 Thr Gly Ser Leu Leu Cys Ser Gln Phe Cys Leu Cys Met Ala Glu Ala
 20 25 30

Ile Leu Leu Phe Ser Pro Glu His Ser Leu Phe Phe Phe Cys Ser Arg
 35 40 45
 Lys Ala Arg Ile Arg Leu His Trp Ala Gly Gln Thr Leu Ala Ile Leu
 50 55 60
 Cys Ala Ala Leu Gly Leu Gly Phe Ile Ile Ser Ser Arg Thr Arg Ser
 65 70 75 80
 Glu Leu Pro His Leu Val Ser Trp His Ser Trp Val Gly Ala Leu Thr
 85 90 95
 Leu Leu Ala Thr Ala Val Gln Ala Leu Cys Gly Leu Cys Leu Leu Cys
 100 105 110
 Pro Arg Ala Ala Arg Val Ser Arg Val Ala Arg Leu Lys Leu Tyr His
 115 120 125
 Leu Thr Cys Gly Leu Val Val Tyr Leu Met Ala Thr Val Thr Val Leu
 130 135 140
 Leu Gly Met Tyr Ser Val Trp Phe Gln Ala Gln Ile Lys Gly Ala Ala
 145 150 155 160
 Trp Tyr Leu Cys Leu Ala Leu Pro Val Tyr Pro Ala Leu Val Ile Met
 165 170 175
 His Gln Ile Ser Arg Ser Tyr Leu Pro Arg Lys Lys Met Glu Met
 180 185 190

<210> 2097

<211> 118

<212> PRT

<213> Homo sapiens

<400> 2097

Met Arg Ala Leu His Leu Pro Cys Leu Leu Pro Ser Leu Pro Leu Leu

1	5	10	15
Ser Val Pro Lys Ala Phe Leu Ser Asp Thr Pro Ser Tyr Leu Ser Tyr			
20	25	30	
Pro Ala Leu Cys Leu Lys Ile Thr Pro Tyr Leu Asn Phe Leu Leu Tyr			
35	40	45	
Cys Thr Met Val Ser Ser Asp Asp Gln Gln Lys Gly Asn His Met Val			
50	55	60	
Leu Val Lys Val Ile Gln Thr Lys Met Leu Val Thr Glu Lys Leu Gly			
65	70	75	80
Ser Val Ala Trp Gln Leu Ala Ser Glu Lys Leu His Thr Ser Ala Leu			
85	90	95	
Tyr Arg Val Thr Asn Leu Ser Val Ile Ala Lys Asn Ser Arg Leu Gly			
100	105	110	
Ala Thr Pro Ile Gln Leu			
115			

<210> 2098

<211> 121

<212> PRT

<213> Homo sapiens

<400> 2098

Met Glu Arg Arg Trp Ala Leu Cys Ser Lys Thr Glu Lys Ser Gly Arg			
1	5	10	15
Ala Glu Leu Asp Gly Ser Gly Gly Lys Glu Pro Ala Cys Arg Glu Ala			
20	25	30	
Glu Arg Val Leu Trp Gln Arg Glu Trp Gln Gly Lys Gly Pro Gly Gln			
35	40	45	

Glu Gln Gly Gln Gly His Ser Cys Val Ala Gly Val Gln Trp Ala Arg
 50 55 60
 Gly Arg Val Met Glu Gly Lys Val Lys Val Gly Trp Gly Gln Thr Leu
 65 70 75 80
 Gln Cys Phe Val Ser His Gly Lys Asp Leu Gly Phe Tyr Ser Lys Cys
 85 90 95
 Ile Ser Glu Cys Arg His Leu Tyr Leu Gly Val Met Leu Ala Tyr Ser
 100 105 110
 His Gln Asp Lys Leu Thr Phe Ser Pro
 115 120

<210> 2099

<211> 119

<212> PRT

<213> Homo sapiens

<400> 2099

Met Asn Leu Leu Lys Gly Pro Trp Ile Ala His Gly Asn Ser Arg Gly
 1 5 10 15
 Ala Thr Glu Pro Leu Trp Lys Leu Pro Ser Arg Asp Asn Gly Gln Asn
 20 25 30
 Leu Ala Ala Ala Ala Thr Ser Leu Thr Met Ala Trp Met Leu Arg
 35 40 45
 Leu Ala Met Leu Thr His Trp Gly Trp Met Leu Gly Ala Ala Glu Asn
 50 55 60
 Ser Thr Ser Ser Val Ile Leu Leu Trp Pro Pro Leu Ser Leu Gln Ala
 65 70 75 80
 Leu Gly Ser Leu Leu Pro Gly Ile Thr Gly Ser Gly Leu Lys Ala Trp

	85	90	95
Ala Ser Asp Glu Trp Asn Val Cys Ala Cys Glu Thr Ala Phe Ala Lys			
100	105	110	
Met Met Thr Val Arg Glu Val			
115			

<210> 2100

<211> 447

<212> PRT

<213> Homo sapiens

<400> 2100

Met Asp Ala Cys Ser Leu Leu Asp Glu Thr Pro Pro Gln Ser Pro Thr			
1	5	10	15
Arg Ala Leu Pro Arg Pro Leu His Pro Thr Pro Val Val Asp Trp Asp			
20	25	30	
Ala Arg Pro Leu Pro Pro Pro Pro Ala Tyr Asp Asp Val Ala Gln Asp			
35	40	45	
Glu Asp Asp Phe Glu Ile Cys Ser Ile Asn Ser Thr Leu Val Gly Ala			
50	55	60	
Gly Val Pro Ala Gly Pro Ser Gln Gly Gln Thr Asn Tyr Ala Phe Val			
65	70	75	80
Pro Glu Gln Ala Arg Pro Pro Pro Pro Leu Glu Asp Asn Leu Phe Leu			
85	90	95	
Pro Pro Gln Gly Gly Gly Lys Pro Pro Ser Ser Ala Gln Thr Ala Glu			
100	105	110	
Ile Phe Gln Ala Leu Gln Gln Glu Cys Met Arg Gln Leu Gln Ala Pro			
115	120	125	

Ala Gly Ser Pro Ala Pro Ser Pro Ser Pro Gly Gly Asp Asp Lys Pro
 130 135 140
 Gln Val Pro Pro Arg Val Pro Ile Pro Pro Arg Pro Thr Arg Pro His
 145 150 155 160
 Val Gln Leu Ser Pro Ala Pro Pro Gly Glu Glu Glu Thr Ser Gln Trp
 165 170 175
 Pro Gly Pro Ala Ser Pro Pro Arg Val Pro Pro Arg Glu Pro Leu Ser
 180 185 190
 Pro Gln Gly Ser Arg Thr Pro Ser Pro Leu Val Pro Pro Gly Ser Ser
 195 200 205
 Pro Leu Pro Pro Arg Leu Ser Ser Ser Pro Gly Lys Thr Met Pro Thr
 210 215 220
 Thr Gln Ser Phe Ala Ser Asp Pro Lys Tyr Ala Thr Pro Gln Val Ile
 225 230 235 240
 Gln Ala Pro Gly Pro Arg Ala Gly Pro Cys Ile Leu Pro Ile Val Arg
 245 250 255
 Asp Gly Lys Lys Val Ser Ser Thr His Tyr Tyr Leu Leu Pro Glu Arg
 260 265 270
 Pro Ser Tyr Leu Glu Arg Tyr Gln Arg Phe Leu Arg Glu Ala Gln Ser
 275 280 285
 Pro Glu Glu Pro Thr Pro Leu Pro Val Pro Leu Leu Leu Pro Pro Pro
 290 295 300
 Ser Thr Pro Ala Pro Ala Ala Pro Thr Ala Thr Val Arg Pro Met Pro
 305 310 315 320
 Gln Ala Ala Leu Asp Pro Lys Ala Asn Phe Ser Thr Asn Asn Ser Asn
 325 330 335
 Pro Gly Ala Arg Pro Pro Pro Pro Arg Ala Thr Ala Arg Leu Pro Gln
 340 345 350
 Arg Gly Cys Pro Gly Asp Gly Pro Glu Ala Gly Arg Pro Ala Asp Lys

355	360	365
Ile Gln Met Leu Gln Ala Met Val His Gly Val Thr Thr Glu Glu Cys		
370	375	380
Arg Ala Ala Leu Gln Cys His Gly Trp Ser Val Gln Arg Ala Ala Gln		
385	390	395
Tyr Leu Lys Val Glu Gln Leu Phe Gly Leu Gly Leu Arg Pro Arg Gly		
405	410	415
Glu Cys His Lys Val Leu Glu Met Phe Asp Trp Asn Leu Glu Gln Ala		
420	425	430
Gly Cys His Leu Leu Gly Ser Trp Gly Pro Ala His His Lys Arg		
435	440	445

<210> 2101

<211> 280

<212> PRT

<213> Homo sapiens

<400> 2101

Met Cys His Leu Gly Val Gly Arg Phe Ser Cys Ser Leu His Leu Ile
1 5 10 15
Leu Phe Ala Glu Asn Lys Gln Leu Thr Thr Val Met Thr Leu Ala Lys
20 25 30
Ala Ala Ala Val Val Thr Phe Pro Glu Pro Leu Pro Phe Ser Val Leu
35 40 45
Trp Ser Pro Leu Val Thr Cys Pro Gly Ile Cys Leu Gly Ala Met Phe
50 55 60
Tyr Gln Gly Arg Gly Leu Ser Leu Glu Ser Arg His Pro Gln Trp Thr
65 70 75 80

Leu Ala Ile Leu Gly Cys Ser Ala Gln Leu Lys Pro Ala Asp Ala Pro
 85 90 95
 Pro Ala Leu Pro Thr Arg Arg Ser Ser Met Arg Glu Arg Val Trp Leu
 100 105 110
 Gly Pro Trp Ser His Pro Val Leu Leu Arg Val Cys Ser Ser Pro Pro
 115 120 125
 Pro Pro Ser Trp Leu Lys Thr Ser Pro Phe Ser Glu Pro Gly Pro Gly
 130 135 140
 Pro Pro Leu Pro Ala Ala Pro Phe Arg Thr Phe Trp Val Val Ser Val
 145 150 155 160
 Val Leu Gly Ser Leu Leu Gly Leu Leu Leu Pro Gly Leu Met Ala Phe
 165 170 175
 Leu Ile Leu Pro Arg Val Thr Gln Ala Met Gln Arg Gly Leu Gly Arg
 180 185 190
 Ser Glu Val Ser Pro Gly Glu Ala Ile Tyr Asp Val Ile Gly Glu Met
 195 200 205
 Pro Pro Ala Gly Leu Tyr Glu Glu Ile Met Glu Ala Glu Ala Val Leu
 210 215 220
 Gln Asp Glu Glu Asp Gly Ser Val Val Lys Val Asp Thr Glu Ala Ala
 225 230 235 240
 Val Ser Gly Glu Val Ser Asn Leu Leu Glu Gly Gln Ser Ile Arg Ala
 245 250 255
 Glu Gly Gly His Ser Arg Pro Val Ser Gln Gly Tyr Asp Glu Ala Ala
 260 265 270
 Phe Pro Leu Glu Glu Met Thr Leu
 275 280

<210> 2102

<211> 147

<212> PRT

<213> Homo sapiens

<400> 2102

Met Leu Pro Leu Gly Glu Tyr Gln Glu Gln Pro His Ser Ser Phe Phe

1 5 10 15

Leu Ser Phe Pro Pro Leu Ser Ala Pro Ser Pro Val Gly His Cys Ile

20 25 30

Ser Leu Pro Thr Ile Ile Gly Ser Val Leu Leu Pro Thr Gly Met Thr

35 40 45

Pro Asn Leu Gly Val Ser Ser Gln Pro Leu Cys Tyr Thr Pro Pro Phe

50 55 60

Thr Leu Pro Leu Arg Pro Ser Cys Ala Lys Asp Pro Ser Pro Ser His

65 70 75 80

Ser Arg Leu Cys Ser Asp Ser Leu Leu Ala Ser Leu Asn Leu Leu Tyr

85 90 95

Pro Leu Ser Gln Met Trp His Ser Cys His Ser Ala Gly Phe Pro Ser

100 105 110

Gly Gly Leu Val Ser Ile Leu Leu Leu Ser Pro Ser Met Arg Glu Cys

115 120 125

Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys

130 135 140

Val Cys Val

145

<210> 2103

<211> 724

<212> PRT

<213> Homo sapiens

<400> 2103

Met	Asn	Phe	Glu	Ile	Ala	Ser	Phe	Ser	Ser	Leu	Ser	Gly	Thr	Gln	Pro
1				5						10				15	
Ile	Thr	Trp	Gln	Val	Glu	Tyr	Pro	Arg	Lys	Gly	Thr	Thr	Asp	Ile	Ala
			20						25				30		
Leu	Ser	Glu	Ile	Phe	Val	Ser	Gln	Lys	Asp	Leu	Val	Gly	Ile	Val	Pro
			35					40					45		
Leu	Ala	Met	Asp	Thr	Glu	Ile	Leu	Asn	Thr	Ala	Val	Leu	Thr	Gly	Lys
	50					55				60					
Thr	Val	Ala	Met	Pro	Ile	Lys	Val	Val	Ser	Val	Glu	Glu	Asn	Ser	Ala
65				70					75					80	
Val	Met	Asp	Ile	Ser	Glu	Ser	Val	Glu	Cys	Lys	Ser	Thr	Asp	Glu	Asp
			85						90				95		
Val	Ile	Lys	Val	Ser	Glu	Arg	Cys	Asp	Tyr	Ile	Phe	Val	Asn	Gly	Lys
		100						105					110		
Glu	Ile	Lys	Gly	Lys	Met	Asp	Ala	Val	Val	Asn	Phe	Thr	Tyr	Gln	Tyr
		115						120					125		
Leu	Ser	Ala	Pro	Leu	Cys	Val	Thr	Val	Trp	Val	Pro	Arg	Leu	Pro	Leu
	130					135					140				
Gln	Ile	Glu	Val	Ser	Asp	Thr	Glu	Leu	Ser	Gln	Ile	Lys	Gly	Trp	Arg
145				150						155				160	
Val	Pro	Ile	Val	Thr	Asn	Lys	Arg	Pro	Thr	Arg	Glu	Ser	Glu	Asp	Glu
			165						170				175		
Asp	Glu	Glu	Glu	Arg	Arg	Gly	Arg	Gly	Cys	Ala	Leu	Gln	Tyr	Gln	His
		180						185					190		
Ala	Thr	Val	Arg	Val	Leu	Thr	Gln	Phe	Val	Ser	Glu	Gly	Ala	Gly	Pro

195	200	205
Trp Gly Gln Pro Asn Tyr Leu Leu Ser Pro Asn Trp Gln Phe Asp Ile		
210	215	220
Thr His Leu Val Ala Asp Phe Met Lys Leu Glu Glu Pro His Val Ala		
225	230	235
Thr Leu Gln Asp Ser Arg Val Leu Val Gly Arg Glu Val Gly Met Thr		
245	250	255
Thr Ile Gln Val Leu Ser Pro Leu Ser Asp Ser Ile Leu Ala Glu Lys		
260	265	270
Thr Ile Thr Val Leu Asp Asp Lys Val Ser Val Thr Asp Leu Ala Ile		
275	280	285
Gln Leu Val Ala Gly Leu Ser Val Ala Leu Tyr Pro Asn Ala Glu Asn		
290	295	300
Ser Lys Ala Val Thr Ala Val Val Thr Ala Glu Glu Val Leu Arg Thr		
305	310	315
Pro Lys Gln Glu Ala Val Phe Ser Thr Trp Leu Gln Phe Ser Asp Gly		
325	330	335
Ser Val Thr Pro Leu Asp Ile Tyr Asp Thr Lys Asp Phe Ser Leu Ala		
340	345	350
Ala Ile Ser Gln Asp Gly Ala Val Val Ser Val Pro Gln Pro Arg Ser		
355	360	365
Pro Arg Trp Pro Val Val Val Ala Glu Gly Glu Gly Gln Gly Pro Leu		
370	375	380
Ile Arg Val Asp Met Thr Ile Ala Glu Ala Cys Gln Lys Ser Lys Arg		
385	390	395
Lys Ser Ile Leu Ala Val Gly Val Gly Asn Val Arg Val Lys Phe Gly		
405	410	415
Gln Asn Asp Ala Asp Ser Ser Pro Gly Arg Asp Tyr Glu Glu Asp Glu		
420	425	430

Ile Lys Asn His Ala Ser Asp Arg Arg Gln Lys Gly Gln His His Glu
435 440 445
Arg Thr Gly Gln Asp Gly His Leu Tyr Gly Ser Ser Pro Val Glu Arg
450 455 460
Glu Glu Gly Ala Leu Arg Arg Ala Thr Thr Thr Ala Arg Ser Leu Leu
465 470 475 480
Asp Asn Lys Val Val Lys Asn Ser Arg Ala Asp Gly Gly Arg Leu Ala
485 490 495
Gly Glu Gly Gln Leu Gln Asn Ile Pro Ile Asp Phe Thr Asn Phe Pro
500 505 510
Ala His Val Asp Leu Pro Lys Ala Gly Ser Gly Leu Glu Glu Asn Asp
515 520 525
Leu Val Gln Thr Pro Arg Gly Leu Ser Asp Leu Glu Ile Gly Met Tyr
530 535 540
Ala Leu Leu Gly Val Phe Cys Leu Ala Ile Leu Val Phe Leu Ile Asn
545 550 555 560
Cys Ala Thr Phe Ala Leu Lys Tyr Arg His Lys Gln Val Pro Leu Glu
565 570 575
Gly Gln Ala Ser Met Thr His Ser His Asp Trp Val Trp Leu Gly Asn
580 585 590
Glu Ala Glu Leu Leu Glu Ser Met Gly Asp Ala Pro Pro Pro Gln Asp
595 600 605
Glu His Thr Thr Ile Ile Asp Arg Gly Pro Gly Ala Cys Glu Glu Ser
610 615 620
Asn His Leu Leu Leu Asn Gly Gly Ser His Lys His Val Gln Ser Gln
625 630 635 640
Ile His Arg Ser Ala Asp Ser Gly Gly Arg Gln Gly Arg Glu Gln Lys
645 650 655
Gln Asp Pro Leu His Ser Pro Thr Ser Lys Arg Lys Lys Val Lys Phe

660 665 670
Thr Thr Phe Thr Thr Ile Pro Pro Asp Asp Ser Cys Pro Thr Val Asn
675 680 685
Ser Ile Val Ser Ser Asn Asp Glu Asp Ile Lys Trp Val Cys Gln Asp
690 695 700
Val Ala Val Gly Ala Pro Lys Glu Leu Arg Asn Tyr Leu Glu Lys Leu
705 710 715 720
Lys Asp Lys Ala

<210> 2104

<211> 250

<212> PRT

<213> Homo sapiens

<400> 2104

Met Asn Arg Pro Ile Gln Val Lys Pro Ala Asp Ser Glu Ser Arg Gly
1 5 10 15
Asp Arg Lys Leu Phe Val Gly Met Leu Asn Lys Gln Gln Ser Glu Asp
20 25 30
Asp Val Arg Arg Leu Phe Glu Ala Phe Gly Asn Ile Glu Glu Cys Thr
35 40 45
Ile Leu Arg Gly Pro Asp Gly Asn Ser Lys Gly Cys Ala Phe Val Lys
50 55 60
Tyr Ser Ser His Ala Glu Ala Gln Ala Ala Ile Asn Ala Leu His Gly
65 70 75 80
Ser Gln Thr Met Pro Val Ser Ala Gly Pro Leu Gly Arg Gly Arg Gly
85 90 95

Gln Arg Arg Ala Glu Thr Pro Ala Pro Ala Thr Pro Arg Arg Leu Ser
100 105 110
Ser Leu Pro Lys Arg Gln Glu Ser Met Thr Leu Ile Pro Gly Leu Arg
115 120 125
Gln Gly Arg Gly Ser Pro Gly Met Leu Arg Asn Trp Pro Glu Val Thr
130 135 140
Gln Val Glu Asn Ala Arg Gly Gly Val His Thr Ser Phe Pro Trp Ala
145 150 155 160
Ser Ala Asp Ala Ala Ser Ser Lys Ala Pro Arg Gly Ala Gly Gly Val
165 170 175
Gly Ala Gly Gln Arg His Arg Gln Leu Arg Ala Glu Ala Leu Glu Gln
180 185 190
Val Gly Leu Thr Arg Arg Pro Gly Arg Arg Glu Pro Arg Pro Val Trp
195 200 205
Trp Ser Ser Ser Pro Thr Pro Thr Arg Ser Ala Arg Cys Gly Glu Cys
210 215 220
Ser Arg Trp Leu Ala Arg Trp Ala Cys Ser Thr Pro Trp Pro Ser Leu
225 230 235 240
Ser Gly Pro Thr Ala Pro Thr Leu Arg Gln
245 250

<210> 2105

<211> 104

<212> PRT

<213> Homo sapiens

<400> 2105

Met Lys Gly Ser Val Ile Asn Ser Thr Glu Thr Ser Lys Asn Leu Gly

1	5	10	15
Ser Gln Lys Tyr Cys Ser Cys Pro Gly Lys Ile Tyr Asn Lys Leu Trp			
20	25	30	
Gln Gln Gln Ser Gly Leu Lys Glu Lys Ile Asp Phe Ile Gly Phe Val			
35	40	45	
Ser Lys Ala Leu Gly Asp Cys Leu Asn Val Glu Asp Arg Gln Glu Cys			
50	55	60	
Lys Arg Gly Leu Ser Gln Thr Gln Leu Ser Asn Ser Arg His Ile Cys			
65	70	75	80
Lys Arg Glu Lys Val Leu Thr Thr Pro Gly Ile Gln Ala Glu Ser Gln			
85	90	95	
His Pro Ser Tyr Met Cys Leu Pro			
100			

<210> 2106

<211> 634

<212> PRT

<213> Homo sapiens

<400> 2106

Met Leu Ala Leu Phe Glu Val Leu Ser Leu Lys Gly Trp Val Glu Val			
1	5	10	15
Arg Asp Val Ile Ile His Arg Val Gly Pro Ile His Gly Ile Tyr Ile			
20	25	30	
His Val Phe Val Phe Leu Gly Cys Met Ile Gly Leu Thr Leu Phe Val			
35	40	45	
Gly Val Val Ile Ala Asn Phe Asn Glu Asn Lys Gly Thr Ala Leu Leu			
50	55	60	

Thr Val Asp Gln Arg Arg Trp Glu Asp Leu Lys Ser Arg Leu Lys Ile
65 70 75 80
Ala Gln Pro Leu His Leu Pro Pro Arg Pro Asp Asn Asp Gly Phe Arg
85 90 95
Ala Lys Met Tyr Asp Ile Thr Gln His Pro Phe Phe Lys Arg Thr Ile
100 105 110
Ala Leu Leu Val Leu Ala Gln Ser Val Leu Leu Ser Val Lys Trp Asp
115 120 125
Val Glu Asp Pro Val Thr Val Pro Leu Ala Thr Met Ser Val Val Phe
130 135 140
Thr Phe Ile Phe Val Leu Glu Val Thr Met Lys Ile Ile Ala Met Ser
145 150 155 160
Pro Ala Gly Phe Trp Gln Ser Arg Arg Asn Arg Tyr Asp Leu Leu Val
165 170 175
Thr Ser Leu Gly Val Val Trp Val Val Leu His Phe Ala Leu Leu Asn
180 185 190
Ala Tyr Thr Tyr Met Met Gly Ala Cys Val Ile Val Phe Arg Phe Phe
195 200 205
Ser Ile Cys Gly Lys His Val Thr Leu Lys Met Leu Leu Leu Thr Val
210 215 220
Val Val Ser Met Tyr Lys Ser Phe Phe Ile Ile Val Gly Met Phe Leu
225 230 235 240
Leu Leu Leu Cys Tyr Ala Phe Ala Gly Val Val Leu Phe Gly Thr Val
245 250 255
Lys Tyr Gly Glu Asn Ile Asn Arg His Ala Asn Phe Ser Ser Ala Gly
260 265 270
Lys Ala Ile Thr Val Leu Phe Arg Ile Val Thr Gly Glu Asp Trp Asn
275 280 285
Lys Ile Met His Asp Cys Met Val Gln Pro Pro Phe Cys Thr Pro Asp

290 295 300
Glu Phe Thr Tyr Trp Ala Thr Asp Cys Gly Asn Tyr Ala Gly Ala Leu
305 310 315 320
Met Tyr Phe Cys Ser Phe Tyr Val Ile Ile Ala Tyr Ile Met Leu Asn
325 330 335
Leu Leu Val Ala Ile Ile Val Glu Asn Phe Ser Leu Phe Tyr Ser Thr
340 345 350
Glu Glu Asp Gln Leu Leu Ser Tyr Asn Asp Leu Arg His Phe Gln Ile
355 360 365
Ile Trp Asn Met Val Asp Asp Lys Arg Glu Gly Val Ile Pro Thr Phe
370 375 380
Arg Val Lys Phe Leu Leu Arg Leu Leu Arg Gly Arg Leu Glu Val Asp
385 390 395 400
Leu Asp Lys Asp Lys Leu Leu Phe Lys His Met Cys Tyr Glu Met Glu
405 410 415
Arg Leu His Asn Gly Gly Asp Val Thr Phe His Asp Val Leu Ser Met
420 425 430
Leu Ser Tyr Arg Ser Val Asp Ile Arg Lys Ser Leu Gln Leu Glu Glu
435 440 445
Leu Leu Ala Arg Glu Gln Leu Glu Tyr Thr Ile Glu Glu Glu Val Ala
450 455 460
Lys Gln Thr Ile Arg Met Trp Leu Lys Lys Cys Leu Lys Arg Ile Arg
465 470 475 480
Ala Lys Gln Gln Gln Ser Cys Ser Ile Ile His Ser Leu Arg Glu Ser
485 490 495
Gln Gln Gln Glu Leu Ser Arg Phe Leu Asn Pro Pro Ser Ile Glu Thr
500 505 510
Thr Gln Pro Ser Glu Asp Thr Asn Ala Asn Ser Gln Asp Asn Ser Met
515 520 525

Gln Pro Glu Thr Ser Ser Gln Gln Gln Leu Leu Ser Pro Thr Leu Ser
 530 535 540
 Asp Arg Gly Gly Ser Arg Gln Asp Ala Ala Asp Ala Gly Lys Pro Gln
 545 550 555 560
 Arg Lys Phe Gly Gln Trp Arg Leu Pro Ser Ala Pro Lys Pro Ile Ser
 565 570 575
 His Ser Val Ser Ser Val Asn Leu Arg Phe Gly Gly Arg Thr Thr Met
 580 585 590
 Lys Ser Val Val Cys Lys Met Asn Pro Met Thr Asp Ala Ala Ser Cys
 595 600 605
 Gly Ser Glu Val Lys Lys Trp Trp Thr Arg Gln Leu Thr Val Glu Ser
 610 615 620
 Asp Glu Ser Gly Asp Asp Leu Leu Asp Ile
 625 630

<210> 2107

<211> 186

<212> PRT

<213> Homo sapiens

<400> 2107

Met Cys Ala Arg Cys Ala Ala Ala Ser Ser Cys Pro Pro Pro Ala Trp
 1 5 10 15
 Ala Ser Gly Met Ala Pro Gly Ala Thr Val Cys Ala Pro Thr Val Leu
 20 25 30
 Ala Ala Ala Trp Pro Gly Pro Trp Thr Met Ala Ala Glu Ala Ala Arg
 35 40 45
 Ala Leu Gln Arg Arg Cys Ser Gln Ala Thr Gly Pro Ile Trp Arg Thr

50	55	60	
Leu Arg Thr His Glu Gly Arg Arg Arg Ser Trp Ala Arg Thr Thr Arg			
65	70	75	80
Ala Trp Pro Leu Arg Met Arg Cys Trp Gln Thr Thr Arg Met Lys Lys			
85	90	95	
Thr Arg Arg Gly Arg Ala Ala Pro Gln Glu Ala Leu Thr Arg Thr Ser			
100	105	110	
Pro Gly Ser Pro Arg Pro Ala Arg Arg Gln Gly Arg Trp Leu Pro Arg			
115	120	125	
Ser Val His Pro Cys Val Cys Pro Val Gly Leu His Cys Gly Ala Arg			
130	135	140	
Ala Thr Leu Thr Pro Leu Ala Ala Pro Pro Leu Leu Pro Pro Glu Pro			
145	150	155	160
Thr Pro His Gly Asn Gln Pro Cys Gly Leu Ser Arg Cys Asp Pro Ser			
165	170	175	
Lys Arg Gly Ala Leu Gly Pro Asp Met Lys			
180	185		

<210> 2108

<211> 293

<212> PRT

<213> Homo sapiens

<400> 2108

Met Glu Leu Ser Asp Phe Glu Asp Cys Leu Thr Leu Phe Ala Gly Asp	
1	5
Pro Gly Leu Gly Pro Glu Glu Leu Arg Ala Ala Met Gly Lys Ala Lys	
20	30

Gln Leu Trp Gly Pro Pro Arg Gly Phe Arg Pro Glu Gln Ile Leu Gln
 35 40 45
 Leu Gly Arg Leu Leu Ile Gly Leu Gly Asp Arg Glu Leu Gln Glu Leu
 50 55 60
 Ile Leu Val Asp Trp Gly Val Leu Ser Thr Leu Gly Gln Ile Asp Gly
 65 70 75 80
 Trp Ser Thr Thr Gln Leu Arg Ile Val Val Ser Ser Phe Leu Arg Gln
 85 90 95
 Ser Gly Arg His Val Ser His Leu Asp Phe Val His Leu Thr Ala Leu
 100 105 110
 Gly Tyr Thr Leu Cys Gly Leu Arg Pro Glu Glu Leu Gln His Ile Ser
 115 120 125
 Ser Trp Glu Phe Ser Gln Ala Ala Leu Phe Leu Gly Thr Leu His Leu
 130 135 140
 Gln Cys Ser Glu Glu Gln Leu Glu Val Leu Ala His Leu Leu Val Leu
 145 150 155 160
 Pro Gly Gly Phe Gly Pro Ile Ser Asn Trp Gly Pro Glu Ile Phe Thr
 165 170 175
 Glu Ile Gly Thr Ile Ala Ala Gly Ile Pro Asp Leu Ala Leu Ser Ala
 180 185 190
 Leu Leu Arg Gly Gln Ile Gln Gly Val Thr Pro Leu Ala Ile Ser Val
 195 200 205
 Ile Pro Pro Pro Lys Phe Ala Val Val Phe Ser Pro Ile Gln Leu Ser
 210 215 220
 Ser Leu Thr Ser Ala Gln Ala Val Ala Val Thr Pro Glu Gln Met Ala
 225 230 235 240
 Phe Leu Ser Pro Glu Gln Arg Arg Ala Val Ala Trp Ala Gln His Glu
 245 250 255
 Gly Lys Glu Ser Pro Glu Gln Gln Gly Arg Ser Thr Ala Trp Gly Leu

260 265 270
 Gln Asp Trp Ser Arg Pro Ser Trp Ser Leu Val Leu Thr Ile Ser Phe
 275 280 285
 Leu Gly His Leu Leu
 290

<210> 2109

<211> 303

<212> PRT

<213> Homo sapiens

<400> 2109

Met Ser Asp Asn Gly Val Cys Val Leu Ala Phe Lys Cys Pro Gly Leu
 1 5 10 15
 Leu Arg Tyr Thr Ala Tyr Arg Cys Lys Gln Leu Ser Asp Thr Ser Ile
 20 25 30
 Ile Ala Val Ala Ser His Cys Pro Leu Leu Gln Lys Val His Val Gly
 35 40 45
 Asn Gln Asp Lys Leu Thr Asp Glu Gly Leu Lys Gln Leu Gly Ser Lys
 50 55 60
 Cys Arg Glu Leu Lys Asp Ile His Phe Gly Gln Cys Tyr Lys Ile Ser
 65 70 75 80
 Asp Glu Gly Met Ile Val Ile Ala Lys Gly Cys Leu Lys Leu Gln Arg
 85 90 95
 Ile Tyr Met Gln Glu Asn Lys Leu Val Thr Asp Gln Ser Val Lys Ala
 100 105 110
 Phe Ala Glu His Cys Pro Glu Leu Gln Tyr Val Gly Phe Met Gly Cys
 115 120 125

Ser Val Thr Ser Lys Gly Val Ile His Leu Thr Lys Leu Arg Asn Leu
130 135 140
Ser Ser Leu Asp Leu Arg His Ile Thr Glu Leu Asp Asn Glu Thr Val
145 150 155 160
Met Glu Ile Val Lys Arg Cys Lys Asn Leu Ser Ser Leu Asn Leu Cys
165 170 175
Leu Asn Trp Ile Ile Asn Asp Arg Cys Val Glu Val Ile Ala Lys Glu
180 185 190
Gly Gln Asn Leu Lys Glu Leu Tyr Leu Val Ser Cys Lys Ile Thr Asp
195 200 205
Tyr Ala Leu Ile Ala Ile Gly Arg Tyr Ser Met Thr Ile Glu Thr Val
210 215 220
Asp Val Gly Trp Cys Lys Glu Ile Thr Asp Gln Gly Ala Thr Leu Ile
225 230 235 240
Ala Gln Ser Ser Lys Ser Leu Arg Tyr Leu Gly Leu Met Arg Cys Asp
245 250 255
Lys Val Asn Glu Val Thr Val Glu Gln Leu Val Gln Gln Tyr Pro His
260 265 270
Ile Thr Phe Ser Thr Val Leu Gln Asp Cys Lys Arg Thr Leu Glu Arg
275 280 285
Ala Tyr Gln Met Gly Trp Thr Pro Asn Met Ser Ala Ala Ser Ser
290 295 300

<210> 2110

<211> 131

<212> PRT

<213> Homo sapiens

<400> 2110

Met Pro Ser Thr Phe Val His Asn Leu Tyr Phe Tyr Phe Phe Cys Pro

1 5 10 15

Pro Leu Leu Val Ile Met Val Leu Lys Asn Tyr Ile Tyr Arg His Lys

20 25 30

Met His Tyr Phe Phe Ser Phe Leu Phe Phe Phe Phe Glu Thr Glu

35 40 45

Ser Cys Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asp Leu Gly Ser

50 55 60

Leu Gln Pro Leu Pro Pro Gly Phe Thr Gln Phe Ser Cys Leu Ser Leu

65 70 75 80

Pro Ser Ser Trp Asp Tyr Arg His Met Pro Pro Cys Pro Ala Asn Phe

85 90 95

Leu Tyr Phe Phe Ser Arg Asp Arg Val Ser Pro Cys Trp Pro Gly Trp

100 105 110

Ser Arg Thr Pro Asp Leu Val Ile His Pro Pro Gln Pro Ser Lys Val

115 120 125

Leu Gly Leu

130

<210> 2111

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2111

Met Glu Ser Ser Cys Thr Ile Glu Gly Gly Ser Ala Ser Gly Leu Leu

1 5 10 15

Leu Ala Asp Leu Gly Ser Cys Ser Ile Gly Cys Arg Gly Gly Thr Gly
 20 25 30
 Gly Ala Ser Cys Cys Val Phe Val Cys Val Cys Gly Cys Gly Leu Arg
 35 40 45
 Gln Ala Gly Pro Pro Pro Phe Gln Leu Ser Pro Cys Ser Ser Pro Ala
 50 55 60
 Ala Leu Pro Ser Pro Met Ser Cys Gly Leu Val Ser Trp Cys Leu His
 65 70 75 80
 Pro Glu Cys Leu Leu Pro Ser Leu Pro Ala Arg Ala Ile Thr Gln Leu
 85 90 95
 Leu Pro Leu Pro Arg Gln Trp Val Gly Ala His Met
 100 105

<210> 2112

<211> 498

<212> PRT

<213> Homo sapiens

<400> 2112

Met Glu Ser Pro Arg Gly Trp Thr Leu Gln Val Ala Pro Glu Glu Gly
 1 5 10 15
 Gln Val Leu Cys Asn Val Lys Thr Ala Thr Arg Gly Leu Ser Glu Gly
 20 25 30
 Ala Val Ser Gly Gly Trp Gly Ala Trp Glu Asn Ser Thr Glu Val Pro
 35 40 45
 Arg Glu Ala Gly Asp Gly Gln Arg Gln Gln Ala Thr Leu Gly Ala Ala
 50 55 60
 Asp Glu Gln Gly Gly Pro Gly Arg Glu Leu Gly Pro Ala Asp Gly Gly

65	70	75	80
Arg Asp Gly Ala Gly Pro Arg Ser Glu Pro Ala Asp Arg Ala Leu Arg			
	85	90	95
Pro Ser Pro Leu Pro Glu Glu Pro Gly Cys Arg Cys Gly Glu Cys Gly			
	100	105	110
Lys Ala Phe Ser Gln Gly Ser Tyr Leu Leu Gln His Arg Arg Val His			
	115	120	125
Thr Gly Glu Lys Pro Tyr Thr Cys Pro Glu Cys Gly Lys Ala Phe Ala			
	130	135	140
Trp Ser Ser Asn Leu Ser Gln His Gln Arg Ile His Ser Gly Glu Lys			
	145	150	155
Pro Tyr Ala Cys Arg Glu Cys Gly Lys Ala Phe Arg Ala Gln Ser Gln			
	165	170	175
Leu Ile His His Gln Glu Thr His Ser Gly Leu Lys Pro Phe Arg Cys			
	180	185	190
Pro Asp Cys Gly Lys Ser Phe Gly Arg Ser Thr Thr Leu Val Gln His			
	195	200	205
Arg Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Pro Glu Cys Gly			
	210	215	220
Lys Ala Phe Ser Trp Asn Ser Asn Phe Leu Glu His Arg Arg Val His			
	225	230	235
Thr Gly Ala Arg Pro His Ala Cys Arg Asp Cys Gly Lys Ala Phe Ser			
	245	250	255
Gln Ser Ser Asn Leu Ala Glu His Leu Lys Ile His Ala Gly Ala Arg			
	260	265	270
Pro His Ala Cys Pro Asp Cys Gly Lys Ala Phe Val Arg Val Ala Gly			
	275	280	285
Leu Arg Gln His Arg Arg Thr His Ser Ser Glu Lys Pro Phe Pro Cys			
	290	295	300

<210> 2113

<211> 372

<212> PRT

<213> Homo sapiens

<400> 2113

Met Leu Leu Ala Glu Leu Ser Arg Glu Arg Gly Glu Leu Gln Gly Glu

1 5 10 15

Arg Gly Glu Leu Arg Gly Arg Leu Ala Arg Leu Glu Leu Glu Arg Ala

20 25 30

Gln Leu Glu Met Gln Ser Gln Gln Leu Arg Glu Ser Asn Gln Gln Leu

35 40 45

Asp Leu Ser Ala Cys Arg Leu Thr Thr Gln Cys Glu Leu Leu Thr Gln

50 55 60

Leu Arg Ser Ala Gln Glu Glu Glu Asn Arg Gln Leu Leu Ala Glu Val

65 70 75 80

Gln Ala Leu Ser Arg Glu Asn Arg Glu Leu Leu Glu Arg Ser Leu Glu

85 90 95

Ser Arg Asp His Leu His Arg Glu Gln Arg Glu Tyr Leu Asp Gln Leu

100 105 110

Asn Ala Leu Arg Arg Glu Lys Gln Lys Leu Val Glu Lys Ile Met Asp

115 120 125

Gln Tyr Arg Val Leu Glu Pro Val Pro Leu Pro Arg Thr Lys Lys Gly

130 135 140

Ser Trp Leu Ala Asp Lys Val Lys Arg Leu Met Arg Pro Arg Arg Glu

145 150 155 160

Gly Gly Pro Pro Gly Gly Leu Arg Leu Gly Ala Asp Gly Ala Gly Ser

165 170 175

Thr Glu Ser Leu Gly Gly Pro Pro Glu Thr Glu Leu Pro Glu Gly Arg

180 185 190

Glu Ala Asp Gly Thr Gly Ser Pro Ser Pro Ala Pro Met Arg Arg Ala
 195 200 205
 Gln Ser Ser Leu Cys Leu Arg Asp Glu Thr Leu Ala Gly Gly Gln Arg
 210 215 220
 Arg Lys Leu Ser Ser Arg Phe Pro Val Gly Arg Ser Ser Glu Ser Phe
 225 230 235 240
 Ser Pro Trp Asp Thr Pro Arg Gln Arg Phe Arg Gln Arg His Pro Gly
 245 250 255
 Pro Leu Gly Ala Pro Val Ser His Ser Lys Gly Glu Gly Gln Gly Ser
 260 265 270
 Leu Tyr Gln Pro Ala Pro Gln Leu Phe Val Asp Pro Pro Ala Pro Trp
 275 280 285
 Gly Arg Arg Leu Pro Ser Cys Pro Leu Cys Leu Leu Gln Ala Leu Ser
 290 295 300
 Thr Ser Ala Leu Ala Leu Gly Pro Val Val Ala Leu Cys Leu Pro Gly
 305 310 315 320
 Pro Gly Val Gly Trp Glu Asn Ser Ala Glu Thr Leu Gln Glu His Glu
 325 330 335
 Thr Asp Ala Asn Arg Glu Gly Glu Trp Gly Thr Val Glu Gly Val Val
 340 345 350
 Phe Phe Val Leu Pro Gly Ala Pro Gly Arg Thr Ser Phe Ile His Ser
 355 360 365
 Phe Ile Arg Gln
 370

<210> 2114

<211> 297

<212> PRT

<213> Homo sapiens

<400> 2114

Met	Gln	Glu	Ile	Thr	Lys	His	Phe	Val	Val	Cys	His	Val	Asp	Ala	Pro
1				5					10					15	
Gly	Gln	Gln	Val	Gly	Ala	Ser	Gln	Phe	Pro	Gln	Gly	Tyr	Gln	Phe	Pro
			20					25						30	
Ser	Met	Glu	Gln	Leu	Ala	Ala	Met	Leu	Pro	Ser	Val	Val	Gln	His	Phe
			35				40						45		
Gly	Phe	Lys	Tyr	Val	Ile	Gly	Ile	Gly	Val	Gly	Ala	Gly	Ala	Tyr	Val
		50				55					60				
Leu	Ala	Lys	Phe	Ala	Leu	Ile	Phe	Pro	Asp	Leu	Val	Glu	Gly	Leu	Val
		65			70				75					80	
Leu	Val	Asn	Ile	Asp	Pro	Asn	Gly	Lys	Gly	Trp	Ile	Asp	Trp	Ala	Ala
			85					90						95	
Thr	Lys	Leu	Ser	Gly	Leu	Thr	Ser	Thr	Leu	Pro	Asp	Thr	Val	Leu	Ser
			100					105					110		
His	Leu	Phe	Ser	Gln	Glu	Glu	Leu	Val	Asn	Asn	Thr	Glu	Leu	Val	Gln
			115				120					125			
Ser	Tyr	Arg	Gln	Gln	Ile	Gly	Asn	Val	Val	Asn	Gln	Ala	Asn	Leu	Gln
			130				135					140			
Leu	Phe	Trp	Asn	Met	Tyr	Asn	Ser	Arg	Arg	Asp	Leu	Asp	Ile	Asn	Arg
			145				150				155			160	
Pro	Gly	Thr	Val	Pro	Asn	Ala	Lys	Thr	Leu	Arg	Cys	Pro	Val	Met	Leu
				165					170				175		
Val	Val	Gly	Asp	Asn	Ala	Pro	Ala	Glu	Asp	Gly	Val	Val	Glu	Cys	Asn
			180					185					190		
Ser	Lys	Leu	Asp	Pro	Thr	Thr	Thr	Thr	Phe	Leu	Lys	Met	Ala	Asp	Ser
			195					200					205		

Gly Gly Leu Pro Gln Val Thr Gln Pro Gly Lys Leu Thr Glu Ala Phe

210

215

220

Lys Tyr Phe Leu Gln Gly Met Gly Tyr Ile Ala Tyr Leu Lys Asp Arg

225

230

235

240

Arg Leu Ser Gly Gly Ala Val Pro Ser Ala Ser Met Thr Arg Leu Ala

245

250

255

Arg Ser Arg Thr Ala Ser Leu Thr Ser Ala Ser Ser Val Asp Gly Ser

260

265

270

Arg Pro Gln Ala Cys Thr His Ser Glu Ser Ser Glu Gly Leu Gly Gln

275

280

285

Val Asn His Thr Met Glu Val Ser Cys

290

295

<210> 2115

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2115

Met Ile Ile His Phe Gln Gln His Phe Leu Val Cys Ser Leu Val Ser

1

5

10

15

Arg Lys Lys Met Ser Leu Arg Ser Glu Arg Arg Gly Ile His Val Asp

20

25

30

Pro Val Gln Glu Arg Met Trp Leu Leu Trp Gln Pro Tyr Leu Ala Gly

35

40

45

Phe Leu Leu Gln Val Leu Glu Gly Arg Val Ala Gln Ser Gln Ala Glu

50

55

60

Ala Asp Ser Gly Val Leu Gly Ala Gly Gly Thr Thr Pro Ala Gly Gly

65 70 75 80
 Arg Arg Gly Leu Cys Gln Gln Ser Glu Gln Pro Arg Gly Pro Ile Pro
 85 90 95
 His Ile Leu Gln Val
 100

<210> 2116

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2116

Met Val Phe Leu Leu Gln Pro Leu Asp Ile Pro Asp Gly Arg Arg Ala
 1 5 10 15
 Pro Leu Pro Ala His Tyr Arg Ser Ser Ser Thr Arg Ser Ile Asp Thr
 20 25 30
 Gln Thr Pro Ser Val Gln Glu Arg Ser Ser Ser Cys Ser Ser His Ser
 35 40 45
 Pro Cys Val Ser Pro Phe Cys Pro Pro Glu Ser Gln Asp Gly Ser Pro
 50 55 60
 Cys Ser Thr Glu Asp Leu Leu Tyr Asp Arg Asp Lys Gly Leu Val Ser
 65 70 75 80
 Leu Ser Arg Pro Leu Ser Phe His Val Leu Thr Lys Thr Arg Leu Ile
 85 90 95
 Ser Ser Gln Pro Asp Gln Leu Ser Val Leu
 100 105

<210> 2117

<211> 111

<212> PRT

<213> Homo sapiens

<400> 2117

Met Arg Leu Thr Gly Arg Thr Thr Ala Pro Pro Ala Pro Thr Pro Thr

1 5 10 15

Pro Ala Gln Ser Pro Ala Gln Ser Pro Thr Pro Leu Gln Cys Ser Arg

20 25 30

Ser Gln Ala Arg Gly Asp Gly Pro Thr Glu Arg Ser Arg His Ser Pro

35 40 45

Leu Pro Cys Cys Arg Ser Ala Ser Arg Leu Arg Leu Pro Gly Gly Gly

50 55 60

Ala Gly Ser Asp Val Thr Gln Ser Gln Trp Glu Cys Ser Ala Leu Arg

65 70 75 80

Val Gly Gly Leu Arg Val His Arg Ala Val Ala Leu Val Gly Leu Pro

85 90 95

Leu Arg Ser Ala Pro Arg Asp Gly Asp Val Trp Leu Arg Ser Gly

100 105 110

<210> 2118

<211> 368

<212> PRT

<213> Homo sapiens

<400> 2118

Met Leu Ala Ser Tyr Gln Ser Tyr Ser Ser Thr Phe His Ser Leu Glu

1	5	10	15
Glu Gln Gln Val Cys Met Ala Val Asp Ile Gly Arg His Arg Trp Asp			
20	25	30	
Gln Val Lys Lys Glu Asp Gln Glu Ala Thr Gly Pro Arg Leu Ser Arg			
35	40	45	
Glu Leu Leu Asp Glu Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp			
50	55	60	
Arg Cys Tyr Ser Thr Pro Ser Gly Cys Leu Glu Leu Thr Asp Ser Cys			
65	70	75	80
Gln Pro Tyr Arg Ser Ala Phe Tyr Val Leu Glu Gln Gln Arg Val Gly			
85	90	95	
Leu Ala Ile Asp Met Asp Glu Ile Glu Lys Tyr Gln Glu Val Glu Glu			
100	105	110	
Asp Gln Asp Pro Ser Cys Pro Arg Leu Ser Arg Glu Leu Leu Asp Glu			
115	120	125	
Lys Glu Pro Glu Val Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr			
130	135	140	
Pro Ser Asp Tyr Leu Glu Leu Pro Asp Leu Gly Gln Pro Tyr Ser Ser			
145	150	155	160
Ala Val Tyr Ser Leu Glu Glu Gln Tyr Leu Gly Leu Ala Leu Asp Val			
165	170	175	
Asp Arg Ile Lys Lys Asp Gln Glu Glu Glu Glu Asp Gln Gly Pro Pro			
180	185	190	
Cys Pro Arg Leu Ser Arg Glu Leu Leu Glu Val Val Glu Pro Glu Val			
195	200	205	
Leu Gln Asp Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Ser Cys Leu			
210	215	220	
Glu Gln Pro Asp Ser Cys Gln Pro Tyr Gly Ser Ser Phe Tyr Ala Leu			
225	230	235	240

Glu Glu Lys His Val Gly Phe Ser Leu Asp Val Gly Glu Ile Glu Lys

245

250

255

Lys Gly Lys Gly Lys Lys Arg Arg Gly Arg Arg Ser Lys Lys Lys Arg

260

265

270

Arg Arg Gly Arg Lys Glu Gly Glu Asp Asp Asn Pro Pro Cys Pro Arg

275

280

285

Leu Tyr Gly Val Leu Leu Glu Val Glu Glu Pro Glu Val Leu Gln Asp

290

295

300

Ser Leu Asp Arg Cys Tyr Ser Thr Pro Ser Met Tyr Phe Glu Gln Pro

305

310

315

320

Asp Ser Phe Gln His Tyr Arg Ser Val Phe Tyr Ser Phe Glu Glu Glu

325

330

335

His Ile Ser Phe Ala Leu Tyr Val Asp Asn Arg Phe Phe Thr Leu Thr

340

345

350

Val Thr Ser Leu His Leu Val Phe Gln Met Gly Val Ile Phe Pro Gln

355

360

365

<210> 2119

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2119

Met Pro Val Val Pro Ala Thr Trp Glu Ala Glu Ala Arg Gly Ser Leu

1

5

10

15

Glu Ala Gly Arg Gln Arg Leu Gln Arg Ala Glu Ile Thr Pro Leu His

20

25

30

Ser Gly Leu Gly Asp Arg Val Glu Thr Leu Ser Gln Thr Lys Lys Ser

35 40 45
Phe Cys Ser Phe Leu Ala Gln Lys Pro Lys Val Ser Glu Asn Asp Phe
50 55 60
Glu Asp Leu Leu Ser Asn Gln Gly Phe Ser Ser Arg Ser Asp Lys Lys
65 70 75 80
Gly Pro Lys Thr Ile Ala Glu Met Arg Lys Gln Asp Leu Ala Lys Asp
85 90 95
Thr Asp Pro Leu Lys Leu Lys Leu Leu Asp Trp Ile Glu Gly Lys Glu
100 105 110
Arg Asn Ile Arg Ala Leu Leu Ser Thr Leu His Thr Val Leu Trp Asp
115 120 125
Gly Glu Ser Arg Trp Thr Pro Val Gly Met Ala Asp Leu Val Ala Pro
130 135 140
Glu Gln Val Lys Lys His Tyr Arg Arg Ala Val Leu Ala Val His Pro
145 150 155 160
Asp Lys Ala Ala Gly Gln Pro Tyr Glu Gln His Ala Lys Met Ile Phe
165 170 175
Met Glu Leu Asn Asp Ala Trp Ser Glu Phe Glu Asn Gln Gly Ser Arg
180 185 190
Pro Leu Phe
195

<210> 2120

<211> 163

<212> PRT

<213> Homo sapiens

<400> 2120

Met Glu Arg Asn His Lys Arg Lys Glu Gly Glu Gly Arg Ile Ser Ile
 1 5 10 15
 Lys Gly His Ile Cys Gly Ser Arg His Ile Val Ser Asn Val Phe Cys
 20 25 30
 Ser Phe Phe Pro Arg Tyr Leu Phe Asn Phe Arg Gly Val Ala Ala Ser
 35 40 45
 Phe Arg Phe Lys His Leu Phe Leu Cys Gly Ser Leu Val Phe His Val
 50 55 60
 Gly Asp Glu Trp Leu Glu Phe Phe Tyr Pro Gln Leu Lys Pro Trp Val
 65 70 75 80
 His Tyr Ile Pro Val Lys Thr Asp Leu Ser Asn Val Gln Glu Leu Leu
 85 90 95
 Gln Phe Val Lys Ala Asn Asp Asp Val Ala Gln Glu Ile Ala Glu Arg
 100 105 110
 Gly Ser Gln Phe Ile Arg Asn His Leu Gln Met Asp Asp Ile Thr Cys
 115 120 125
 Tyr Trp Glu Asn Leu Leu Ser Glu Tyr Ser Lys Phe Leu Ser Tyr Asn
 130 135 140
 Val Thr Arg Arg Lys Gly Tyr Asp Gln Ile Ile Pro Lys Met Leu Lys
 145 150 155 160
 Thr Glu Leu

<210> 2121

<211> 123

<212> PRT

<213> Homo sapiens

<400> 2121

Met Gly Gly Ser Gly Gln Gln Lys Val Ile Leu Ser Ser Ser Arg Ser
 1 5 10 15
 Leu Met Ser Glu Thr Arg Arg Ala Met Leu Pro Leu Lys Ala Leu Gly
 20 25 30
 Val Asn Pro Ser Leu Pro Leu Leu Ala Ser Gly Gly Cys Trp His Ser
 35 40 45
 Leu Ala Cys Val His Ile Ile Pro Phe Ser Ser Phe Ile Leu Met Trp
 50 55 60
 Pro Ser Pro Leu Cys Val Ser Val Ser Ser Ser Leu Pro Met Arg Met
 65 70 75 80
 Pro Leu Leu Leu Asp Leu Arg Phe Thr Leu Phe Gln Tyr Asp Leu Phe
 85 90 95
 Val Met Arg Ser Ala Val Thr Leu Phe Ser Phe Leu Phe Phe Val Met
 100 105 110
 Glu Ser Cys Ser Val Ala Gln Ala Gly Val Gln
 115 120

<210> 2122

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2122

Met Leu Phe Cys Phe Ile Leu Phe Thr His His Lys Arg Cys Phe Phe
 1 5 10 15
 Val Cys Leu Phe Leu Phe Cys Phe Val Leu Phe Phe Glu Ile Glu Ser
 20 25 30

Phe Ala Leu Ile Thr Gln Ala Gly Val Gln Trp His Asp Leu Ser Ser
 35 40 45
 Leu Gln Pro Pro Pro Pro Gly Phe Lys Lys Leu Ser Cys Leu Ser Leu
 50 55 60
 Leu Ser Trp Asp Tyr Arg His Gly Thr Leu Arg His Tyr Ala Trp Leu
 65 70 75 80
 Ile Phe Val Phe Leu Val Glu Met Val Phe His His Val Gly Gln Ala
 85 90 95
 Gly Leu Lys Leu Leu Thr Ser Ser Asp Leu Pro Ala Ser Ala Phe Gln
 100 105 110
 Ser Ala Gly Ile Thr Gly Val Ser His Cys Thr Arg Ile
 115 120 125

<210> 2123

<211> 166

<212> PRT

<213> Homo sapiens

<400> 2123

Met Ser Leu His Ser Ser Pro Thr Leu Pro Thr Ser Leu Tyr Gln Ser
 1 5 10 15
 Cys Asp Leu Ser Val Gly Gly Pro Ser Leu Leu Thr Trp Val Trp Arg
 20 25 30
 Arg Glu Arg Arg Cys Cys Lys Val Phe Ser Val Ser His Cys Leu Glu
 35 40 45
 Ala Gly Pro Ala Lys Ala Trp Ala His Ser Cys Thr Gly Ser Pro Arg
 50 55 60
 Gly Arg Thr Gly Trp Gly Ser Arg Ala Cys Glu Ala Leu Gly Lys Gly

65 70 75 80
 Met Gly Leu Trp Gly Arg Gly Gly Met Gly Phe Arg Ser Ile Cys Thr
 85 90 95
 Ile Arg Lys Val Leu Arg Ser Phe Phe Leu Glu Gly Thr Leu Ser Ser
 100 105 110
 Leu Ser Leu Phe Leu Asp Leu Gly Leu Glu Leu Arg Met Gly Arg Cys
 115 120 125
 Ala Gln Gly Gly Thr His Gln Ser Thr Arg Glu Gly Gly Tyr Leu Gly
 130 135 140
 Val Ser Gln Gly Leu Cys Gln Cys Leu Gln Pro Thr Ser Arg Ser Leu
 145 150 155 160
 Glu Phe Gly Glu Trp Gly
 165

<210> 2124

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2124

Met Val His Ser Val Ser Asp Ser Ile Thr Gly Gly Arg Pro Gln Pro
 1 5 10 15
 Tyr Glu His Ile Phe Ile Thr Pro Tyr Ser Leu Thr Arg Lys Gly Arg
 20 25 30
 Ser Phe Val His Cys Ser Pro Pro Leu Asn Cys Ser Leu Thr Gly Ser
 35 40 45
 Val Ser Leu Ser Glu Ile Phe Leu Asn Ser Gly Lys Cys Phe Gly Asp
 50 55 60

115 120 125
Thr Ser Tyr Ile
130

<210> 2126

<211> 253

<212> PRT

<213> Homo sapiens

<400> 2126

Met Glu Arg Cys Arg Pro Asp Thr Ala Gly Ser Ser Leu Leu Ser Ala
1 5 10 15
Pro Glu Gly Gly Arg Lys Glu Ser Gln Gly Pro Pro Gln Cys Leu Phe
20 25 30
Pro Pro Asp Ser Arg Ala Pro Glu Val Glu Pro Thr Gln Leu Gly Leu
35 40 45
Gln Ala Trp Gly Thr Gly His Phe Gly Gln Arg Pro Pro Glu Gly Gln
50 55 60
His Trp Glu Gly Arg Gly Pro Ala Ser Gly Ala Leu Gly Trp Leu Pro
65 70 75 80
Pro Ser Gly Asp Ala Pro Gln Asp Pro Ser Cys Pro Gly Pro Pro Ser
85 90 95
Gln Pro Gly Pro Thr Ser Ser Pro Ala Gly Arg Ala Ala Ser Gly His
100 105 110
Ala Ser Ala Ala Pro Val Cys Ser Ser Cys Pro Pro Trp Ala Ser Leu
115 120 125
Pro Ala Ala Pro Gly Ala Arg Pro Trp Arg Arg Leu Leu Ala His Arg
130 135 140

Ala Ala Arg Gly Thr Arg Val Gly Ser Leu Gly Ala Arg Leu Gly Leu
 145 150 155 160
 Arg Gly Gly Ala Ala Ser Trp Thr Gly Thr Leu Gly Gly Ile Pro Phe
 165 170 175
 Pro Glu Leu Arg Ala Leu Gly Trp Val Arg Arg Pro His Thr Ile Thr
 180 185 190
 Arg Pro Arg Gln Pro Trp Gly Ala Trp Ala Gly Ala Gly Arg Ala Val
 195 200 205
 Trp Glu Gly Thr Pro Asn Leu Leu Pro Arg Pro Ala Ser Ser Cys Arg
 210 215 220
 Gln Ala Ala Pro Arg Leu Pro Leu Gly Val Arg Val His Asn Leu Trp
 225 230 235 240
 Glu Ala Ala Pro Arg Pro Gly Arg Pro Gln Cys Arg Val
 245 250

<210> 2127

<211> 211

<212> PRT

<213> Homo sapiens

<400> 2127

Met Gln Leu Gly Glu His Thr His Pro Gln Lys Asn Pro Lys Ser Leu
 1 5 10 15
 Ala Gly Cys Leu Leu Pro Asn Pro His Pro Gln Leu Gln Leu Arg Gly
 20 25 30
 Lys Arg Ala Ala Gly Leu Leu Leu Arg Arg Asn Pro Trp Cys His Pro
 35 40 45
 Gln Ala Pro Gly Gly Ser Ser Thr Trp Ala Pro Ser Leu Pro Pro Ile

<210> 2128

<211> 759

<212> PRT

<213> Homo sapiens

<400> 2128

Met Ser Ser Leu Ala Gln Ser Gln Arg Pro Ala Gly Leu Gly Arg Arg
 1 5 10 15
 Trp Ala Pro Gly Ser Arg Pro Thr Gly Trp Asp Leu Asp His Asn Glu
 20 25 30
 Ile Ser Gly Thr Ile Glu Asp Thr Ser Gly Ala Phe Ser Gly Leu Asp
 35 40 45
 Ser Leu Ser Lys Leu Thr Leu Phe Gly Asn Lys Ile Lys Ser Val Ala
 50 55 60
 Lys Arg Ala Phe Ser Gly Leu Glu Gly Leu Glu His Leu Asn Leu Gly
 65 70 75 80
 Gly Asn Ala Ile Arg Ser Val Gln Phe Asp Ala Phe Val Lys Met Lys
 85 90 95
 Asn Leu Lys Glu Leu His Ile Ser Ser Asp Ser Phe Leu Cys Asp Cys
 100 105 110
 Gln Leu Lys Trp Leu Pro Pro Trp Leu Ile Gly Arg Met Leu Gln Ala
 115 120 125
 Phe Val Thr Ala Ala Cys Ala His Pro Glu Ser Leu Lys Gly Gln Ser
 130 135 140
 Ile Phe Ser Val Pro Pro Glu Ser Phe Val Cys Asp Asp Phe Leu Lys
 145 150 155 160
 Pro Gln Ile Ile Thr Gln Pro Glu Thr Thr Met Ala Met Val Gly Lys
 165 170 175
 Asp Ile Arg Phe Thr Cys Ser Ala Ala Ser Ser Ser Ser Ser Pro Met
 180 185 190
 Thr Phe Ala Trp Lys Lys Asp Asn Glu Val Leu Thr Asn Ala Asp Met
 195 200 205
 Glu Asn Phe Val His Val His Ala Gln Asp Gly Glu Val Met Glu Tyr
 210 215 220
 Thr Thr Ile Leu His Leu Arg Gln Val Thr Phe Gly His Glu Gly Arg

225 230 235 240
Tyr Gln Cys Val Ile Thr Asn His Phe Gly Ser Thr Tyr Ser His Lys
 245 250 255
Ala Arg Leu Thr Val Asn Val Leu Pro Ser Phe Thr Lys Thr Pro His
 260 265 270
Asp Ile Thr Ile Arg Thr Thr Thr Val Ala Arg Leu Glu Cys Ala Ala
 275 280 285
Thr Gly His Pro Asn Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr
 290 295 300
Asp Phe Pro Ala Ala Arg Glu Arg Arg Met His Val Met Pro Asp Asp
305 310 315 320
Asp Val Phe Phe Ile Thr Asp Val Lys Ile Asp Asp Ala Gly Val Tyr
 325 330 335
Ser Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
 340 345 350
Leu Thr Val Leu Glu Thr Pro Ser Leu Val Val Pro Leu Glu Asp Arg
 355 360 365
Val Val Ser Val Gly Glu Thr Val Ala Leu Gln Cys Lys Ala Thr Gly
 370 375 380
Asn Pro Pro Pro Arg Ile Thr Trp Phe Lys Gly Asp Arg Pro Leu Ser
385 390 395 400
Leu Thr Glu Arg His His Leu Thr Pro Asp Asn Gln Leu Leu Val Val
 405 410 415
Gln Asn Val Val Ala Glu Asp Ala Gly Arg Tyr Thr Cys Glu Met Ser
 420 425 430
Asn Thr Leu Gly Thr Glu Arg Ala His Ser Gln Leu Ser Val Leu Pro
 435 440 445
Ala Ala Gly Cys Arg Lys Asp Gly Thr Thr Val Gly Ile Phe Thr Ile
 450 455 460

Ala Val Val Ser Ser Ile Val Leu Thr Ser Leu Val Trp Val Cys Ile
465 470 475 480
Ile Tyr Gln Thr Arg Lys Lys Ser Glu Glu Tyr Ser Val Thr Asn Thr
485 490 495
Asp Glu Thr Val Val Pro Pro Asp Val Pro Ser Tyr Leu Ser Ser Gln
500 505 510
Gly Thr Leu Ser Asp Arg Gln Glu Thr Val Val Arg Thr Glu Gly Gly
515 520 525
Pro Gln Ala Asn Gly His Ile Glu Ser Asn Gly Val Cys Pro Arg Asp
530 535 540
Ala Ser His Phe Pro Glu Pro Asp Thr His Ser Val Ala Cys Arg Gln
545 550 555 560
Pro Lys Leu Cys Ala Gly Ser Ala Tyr His Lys Glu Pro Trp Lys Ala
565 570 575
Met Glu Lys Ala Glu Gly Thr Pro Gly Pro His Lys Met Glu His Gly
580 585 590
Gly Arg Val Val Cys Ser Asp Cys Asn Thr Glu Val Asp Cys Tyr Ser
595 600 605
Arg Gly Gln Ala Phe His Pro Gln Pro Val Ser Arg Asp Ser Ala Gln
610 615 620
Pro Ser Ala Pro Asn Gly Pro Glu Pro Gly Gly Ser Asp Gln Glu His
625 630 635 640
Ser Pro His His Gln Cys Ser Arg Thr Ala Ala Gly Ser Cys Pro Glu
645 650 655
Cys Gln Gly Ser Leu Tyr Pro Ser Asn His Asp Arg Met Leu Thr Ala
660 665 670
Val Lys Lys Lys Pro Met Ala Ser Leu Asp Gly Lys Gly Asp Ser Ser
675 680 685
Trp Thr Leu Ala Arg Leu Tyr His Pro Asp Ser Thr Glu Leu Gln Pro

690 695 700
 Ala Ser Ser Leu Thr Ser Gly Ser Pro Glu Arg Ala Glu Ala Gln Tyr
 705 710 715 720
 Leu Leu Val Ser Asn Gly His Leu Pro Lys Ala Cys Asp Ala Ser Pro
 725 730 735
 Glu Ser Thr Pro Leu Thr Gly Gln Leu Pro Gly Lys Gln Arg Val Pro
 740 745 750
 Leu Leu Leu Ala Pro Lys Ser
 755

<210> 2129

<211> 591

<212> PRT

<213> Homo sapiens

<400> 2129

Met Gly Ser Asp Ser Trp Gly Ser Lys Ile Ala Pro Val Leu His Leu
 1 5 10 15
 Glu Glu Val Ala Glu Gly Ala Val Thr Ile Leu Pro Lys Arg Met Ser
 20 25 30
 Val Arg Gly Phe Asp Arg Tyr Phe Ser Ser Arg Thr Leu Asp Asn Asn
 35 40 45
 Arg Arg Asn Ile Trp Phe Ala Glu Phe Trp Glu Asp Asn Phe His Cys
 50 55 60
 Lys Leu Ser Arg His Ala Leu Lys Lys Gly Ser His Val Lys Lys Cys
 65 70 75 80
 Thr Asn Arg Glu Arg Ile Gly Gln Asp Ser Ala Tyr Glu Gln Glu Gly
 85 90 95

Lys Val Gln Phe Val Ile Asp Ala Val Tyr Ala Met Gly His Ala Leu
100 105 110
His Ala Met His Arg Asp Leu Cys Pro Gly Arg Val Gly Leu Cys Pro
115 120 125
Arg Met Asp Pro Val Asp Gly Thr Gln Leu Leu Lys Tyr Ile Arg Asn
130 135 140
Val Asn Phe Ser Gly Ile Ala Gly Asn Pro Val Thr Phe Asn Glu Asn
145 150 155 160
Gly Asp Ala Pro Gly Arg Tyr Asp Ile Tyr Gln Tyr Gln Leu Arg Asn
165 170 175
Asp Ser Ala Glu Tyr Lys Val Ile Gly Ser Trp Thr Asp His Leu His
180 185 190
Leu Arg Ile Glu Arg Met His Trp Pro Gly Ser Gly Gln Gln Leu Pro
195 200 205
Arg Ser Ile Cys Ser Leu Pro Cys Gln Pro Gly Glu Arg Lys Lys Thr
210 215 220
Val Lys Gly Met Pro Cys Cys Trp His Cys Glu Pro Cys Thr Gly Tyr
225 230 235 240
Gln Tyr Gln Val Asp Arg Tyr Thr Cys Lys Thr Cys Pro Tyr Asp Met
245 250 255
Arg Pro Thr Glu Asn Arg Thr Gly Cys Arg Pro Ile Pro Ile Ile Lys
260 265 270
Leu Glu Trp Gly Ser Pro Trp Ala Val Leu Pro Leu Phe Leu Ala Val
275 280 285
Val Gly Ile Ala Ala Thr Leu Phe Val Val Ile Thr Phe Val Arg Tyr
290 295 300
Asn Asp Thr Pro Ile Val Arg Ala Ser Gly Arg Glu Leu Ser Tyr Val
305 310 315 320
Leu Leu Ala Gly Ile Phe Leu Cys Tyr Ala Thr Thr Phe Leu Met Ile

325 330 335
Ala Glu Pro Asp Leu Gly Thr Cys Ser Leu Arg Arg Ile Phe Leu Gly
340 345 350
Leu Gly Met Ser Ile Ser Tyr Ala Ala Leu Leu Thr Lys Thr Asn Arg
355 360 365
Ile Tyr Arg Ile Phe Glu Gln Gly Lys Arg Ser Val Ser Ala Pro Arg
370 375 380
Phe Ile Ser Pro Val Ser Gln Leu Ala Ile Thr Phe Ser Leu Ile Ser
385 390 395 400
Leu Gln Leu Leu Gly Ile Cys Val Trp Phe Val Val Asp Pro Ser His
405 410 415
Ser Val Leu Asp Phe Gln Asp Gln Arg Thr Leu Asp Pro Arg Phe Ala
420 425 430
Arg Gly Val Leu Lys Cys Asp Ile Ser Asp Leu Ser Leu Ile Cys Leu
435 440 445
Leu Gly Tyr Ser Met Leu Leu Met Val Thr Cys Thr Val Tyr Ala Ile
450 455 460
Lys Thr Arg Gly Val Pro Glu Thr Phe Asn Glu Ala Lys Pro Ile Gly
465 470 475 480
Phe Thr Met Tyr Thr Thr Cys Ile Val Trp Leu Ala Phe Ile Pro Ile
485 490 495
Phe Phe Gly Thr Ser Gln Ser Ala Asp Lys Leu Tyr Ile Gln Thr Thr
500 505 510
Thr Leu Thr Val Ser Val Ser Leu Ser Ala Ser Val Ser Leu Gly Met
515 520 525
Leu Tyr Met Pro Lys Val Tyr Ile Ile Leu Phe His Pro Glu Gln Asn
530 535 540
Val Pro Lys Arg Lys Arg Ser Leu Lys Ala Val Val Thr Ala Ala Thr
545 550 555 560

Met Ser Asn Lys Phe Thr Gln Lys Gly Asn Phe Arg Pro Asn Gly Glu

565

570

575

Ala Lys Ser Glu Leu Cys Glu Asn Leu Glu Ala Pro Gly Ser Ser

580

585

590

<210> 2130

<211> 240

<212> PRT

<213> Homo sapiens

<400> 2130

Met Val Thr Pro Ser Pro Ala Gln Leu Pro Leu Ile Cys Cys Ala Asn

1

5

10

15

Ile Phe Leu Asp Glu Met Leu Gly Arg Lys Ile Ile Arg Val Leu Pro

20

25

30

Pro Leu Ser Asn Phe Gly Leu Ile Lys Leu Ser Leu Ser Ser Ala Lys

35

40

45

Ile Tyr Ser Phe Pro Leu Asn Thr Gly Pro Val Pro Gly Ile Asp Phe

50

55

60

Leu Tyr Asp Asn Thr Thr His Ala Ser Thr Ala Met Pro Ser Leu Ala

65

70

75

80

Pro Pro Arg Gly Trp Asp Thr Glu Ala Leu Val Gly Leu Pro Leu Ser

85

90

95

Pro Gln His Cys Pro Pro Pro Pro Arg Ser Leu Leu Ala Thr Leu Thr

100

105

110

Pro Pro Ser Leu Ser Trp Leu Leu Glu Cys Leu Ala Ser Val Ser Ser

115

120

125

Val Phe Val Leu Pro Arg Trp Leu Phe Trp Gly Ser Pro Ser Ser Gln

130 135 140
Asp Gly Val Glu Trp Ile Glu Glu Val Trp Arg Val Trp Pro Leu Arg
145 150 155 160
Ser Pro Gly Thr Thr Gly Asn Gly Leu Gln Pro Gln Ala Leu Gly Gly
165 170 175
Pro Gly Phe Gly Gly Leu Ser Pro Ser Leu Ala Gln Glu Glu Gly Gln
180 185 190
Gly Gly Gly Pro Gly Leu Leu Arg Gly Leu Arg Gly His Ala Met Tyr
195 200 205
Val Gly Trp Glu His Thr Cys Arg Gly Ser Asn Arg Ser Pro Ala Pro
210 215 220
Lys Gly Leu Gln Asp Glu Gly Thr Ser Trp Leu Pro Gly Leu Arg Ala
225 230 235 240

<210> 2131

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2131

Met Leu Glu Arg Leu Trp Lys Gly Pro Thr Glu Leu Asp Arg Ala Ala
1 5 10 15
Lys Glu Pro Arg Pro Arg Gly Val Leu Pro Asp Arg Trp Val Arg Ser
20 25 30
Cys Ser Leu Cys Lys Ser Gln Leu Arg Pro Arg Thr Leu Gly Gln Arg
35 40 45
Pro Ala Phe Pro Thr Val Leu Ser Glu Phe Pro Ala Glu Thr Ile Arg
50 55 60

<210> 2132

<211> 347

<212> PRT

<213> Homo sapiens

<400> 2132

出証特 2 0 0 4 - 3 0 5 9 6 6 1

115	120	125	
Pro Leu Leu Pro Pro Gly Ala Arg Gly Leu Pro Pro Pro Pro Pro Pro			
130	135	140	
Leu Pro Pro Pro Leu Pro Pro Arg Leu Arg Glu Glu Ala Glu Glu Gln			
145	150	155	160
Glu Ser Thr Cys Pro Ile Cys Leu Gly Glu Ile Gln Asn Ala Lys Thr			
165	170	175	
Leu Glu Lys Cys Arg His Ser Phe Cys Glu Gly Cys Ile Thr Arg Ala			
180	185	190	
Leu Gln Val Lys Lys Ala Cys Pro Met Cys Gly Arg Phe Tyr Gly Gln			
195	200	205	
Leu Val Gly Asn Gln Pro Gln Asn Gly Arg Met Leu Val Ser Lys Asp			
210	215	220	
Ala Thr Leu Leu Leu Pro Ser Tyr Glu Lys Tyr Gly Thr Ile Val Ile			
225	230	235	240
Gln Tyr Val Phe Pro Pro Gly Val Gln Gly Ala Glu His Pro Asn Pro			
245	250	255	
Gly Val Arg Tyr Pro Gly Thr Thr Arg Val Ala Tyr Leu Pro Asp Cys			
260	265	270	
Pro Glu Gly Asn Lys Val Leu Thr Leu Phe Arg Lys Ala Phe Asp Gln			
275	280	285	
Arg Leu Thr Phe Thr Ile Gly Thr Ser Met Thr Thr Gly Arg Pro Asn			
290	295	300	
Val Ile Thr Trp Asn Asp Ile His His Lys Thr Ser Cys Thr Gly Gly			
305	310	315	320
Pro Gln Leu Phe Gly Tyr Pro Asp Pro Thr Tyr Leu Thr Arg Val Gln			
325	330	335	
Glu Glu Leu Arg Ala Lys Gly Ile Thr Asp Asp			
340	345		

<210> 2133

<211> 143

<212> PRT

<213> Homo sapiens

<400> 2133

Met Gly Leu Cys Glu Arg Pro Asn Leu Arg Leu Ile Gly Val Pro Glu

1 5 10 15

Asn Asp Arg Glu Asn Gly Thr Lys Leu Glu Asn Thr Pro Gln Asp Ile

20 25 30

Ile Lys Glu Asn Phe Pro Asn Leu Ala Lys Gln Ala Asn Ile Gln Ile

35 40 45

Gln Asp Ile Gln Arg Met Pro Gln Arg Tyr Ser Ser Arg Arg Ala Asn

50 55 60

Pro Arg His Ile Ile Gly Arg Phe Thr Lys Val Glu Met Lys Glu Lys

65 70 75 80

Met Leu Ser Ala Ala Arg Glu Lys Gly Arg Val Thr His Lys Gly Lys

85 90 95

Pro Ile Arg Leu Thr Ala Asp Leu Ser Ala Glu Thr Leu Gln Ala Arg

100 105 110

Arg Glu Trp Gly Pro Ile Phe Asn Ile Leu Lys Glu Lys Asn Phe Gln

115 120 125

Pro Arg Ile Ser Tyr Pro Ala Lys Leu Ser Phe Ile Ser Glu Glu

130 135 140

<210> 2134

<211> 644

<212> PRT

<213> Homo sapiens

<400> 2134

Met Gly Asn Tyr Leu Pro Ala Phe Gly Pro Arg Pro Pro Gly Arg Arg

1 5 10 15

Glu Ala Leu Leu Ser Pro Asp Cys Pro Leu Leu Arg Leu His Pro Thr

20 25 30

Gly Lys Leu Gly Gln Ala Ser Cys Gln Ala Asp Glu Phe Arg Cys Asp

35 40 45

Asn Gly Lys Cys Leu Pro Gly Pro Trp Gln Cys Asn Thr Val Asp Glu

50 55 60

Cys Gly Asp Gly Ser Asp Glu Gly Asn Cys Ser Ala Pro Ala Ser Glu

65 70 75 80

Pro Pro Gly Ser Leu Cys Pro Gly Gly Thr Phe Pro Cys Ser Gly Ala

85 90 95

Arg Ser Thr Arg Cys Leu Pro Val Glu Arg Arg Cys Asp Gly Leu Gln

100 105 110

Asp Cys Gly Asp Gly Ser Asp Glu Ala Gly Cys Pro Asp Leu Ala Cys

115 120 125

Gly Arg Arg Leu Gly Ser Phe Tyr Gly Ser Phe Ala Ser Pro Asp Leu

130 135 140

Phe Gly Ala Ala Arg Gly Pro Ser Asp Leu His Cys Thr Trp Leu Val

145 150 155 160

Asp Thr Gln Asp Ser Arg Arg Val Leu Leu Gln Leu Glu Leu Arg Leu

165 170 175

Gly Tyr Asp Asp Tyr Val Gln Val Tyr Glu Gly Leu Gly Glu Arg Gly

180 185 190

Asp Arg Leu Leu Gln Thr Leu Ser Tyr Arg Ser Asn His Arg Pro Val
195 200 205

Ser Leu Glu Ala Ala Gln Gly Arg Leu Thr Val Ala Tyr His Ala Arg
210 215 220

Ala Arg Ser Ala Gly His Gly Phe Asn Ala Thr Tyr Gln Val Lys Gly
225 230 235 240

Tyr Cys Leu Pro Trp Glu Gln Pro Cys Gly Ser Ser Ser Asp Ser Asp
245 250 255

Gly Gly Ser Leu Gly Asp Gln Gly Cys Phe Ser Glu Pro Gln Arg Cys
260 265 270

Asp Gly Trp Trp His Cys Ala Ser Gly Arg Asp Glu Gln Gly Cys Pro
275 280 285

Ala Cys Pro Pro Asp Gln Tyr Pro Cys Glu Gly Gly Gly Gly Leu Cys
290 295 300

Tyr Thr Pro Ala Asp Arg Cys Asn Asn Gln Lys Ser Cys Pro Asp Gly
305 310 315 320

Ala Asp Glu Lys Asn Cys Phe Ser Cys Gln Pro Gly Thr Phe His Cys
325 330 335

Gly Thr Asn Leu Cys Ile Phe Glu Thr Trp Arg Cys Asp Gly Gln Glu
340 345 350

Asp Cys Gln Asp Gly Ser Asp Glu His Gly Cys Leu Ala Ala Val Pro
355 360 365

Arg Lys Val Ile Thr Ala Ala Leu Ile Gly Ser Leu Val Cys Gly Leu
370 375 380

Leu Leu Val Ile Ala Leu Gly Cys Ala Phe Lys Leu Tyr Ser Leu Arg
385 390 395 400

Thr Gln Glu Tyr Arg Ala Phe Glu Thr Gln Met Thr Arg Leu Glu Ala
405 410 415

Glu Phe Val Arg Arg Glu Ala Pro Pro Ser Tyr Gly Gln Leu Ile Ala

420 425 430
Gln Gly Leu Ile Pro Pro Val Glu Asp Phe Pro Val Tyr Ser Ala Ser
435 440 445
Gln Ala Ser Val Leu Gln Asn Leu Arg Thr Ala Met Arg Arg Gln Met
450 455 460
Arg Arg His Ala Ser Arg Arg Gly Pro Ser Arg Arg Arg Leu Gly Arg
465 470 475 480
Leu Trp Asn Arg Leu Phe His Arg Pro Arg Ala Pro Arg Gly Gln Ile
485 490 495
Pro Leu Leu Thr Ala Ala Arg Pro Ser Gln Thr Val Leu Gly Asp Gly
500 505 510
Phe Leu Gln Pro Ala Pro Gly Ala Ala Pro Asp Pro Pro Ala Pro Leu
515 520 525
Met Asp Thr Gly Ser Thr Arg Ala Ala Gly Asp Arg Pro Pro Ser Ala
530 535 540
Pro Gly Arg Ala Pro Glu Val Gly Pro Ser Gly Pro Pro Leu Pro Ser
545 550 555 560
Gly Leu Arg Asp Pro Glu Cys Arg Pro Val Asp Lys Asp Arg Lys Val
565 570 575
Cys Arg Glu Pro Leu Val Asp Gly Pro Ala Pro Ala Asp Ala Pro Arg
580 585 590
Glu Pro Cys Ser Ala Gln Asp Pro His Pro Gln Val Ser Thr Ala Ser
595 600 605
Ser Thr Leu Gly Pro His Ser Pro Glu Pro Leu Gly Val Cys Arg Asn
610 615 620
Pro Pro Pro Pro Cys Ser Pro Met Leu Glu Ala Ser Asp Asp Glu Ala
625 630 635 640
Leu Leu Val Cys

<210> 2135

<211> 204

<212> PRT

<213> Homo sapiens

<400> 2135

Met Gln Thr Pro Pro His Asp Ser Asn Ile Asn Ile Cys Asn Ser Val

1 5 10 15

Thr Val Lys Phe Ser Pro Trp Ser Thr Tyr Ser Ser Ile Arg Tyr Phe

20 25 30

Leu Leu Leu Leu Phe Cys Phe Phe Phe Phe Phe Leu Arg Trp Ser Leu

35 40 45

Thr Leu Ser Pro Arg Leu Glu Cys Lys Gly Thr Ile Ser Ala His Cys

50 55 60

Arg Leu His Leu Pro Gly Ser Ser Asp Pro Pro Ala Ser Ala Ser Gln

65 70 75 80

Val Ala Gly Ala His His Tyr Trp Cys Pro Pro Gln Cys Pro Ala Asn

85 90 95

Phe Cys Thr Phe Ser Arg Asn Arg Val Ser Val Gly Gln Val Gly Leu

100 105 110

Glu Leu Leu Thr Ser Cys Asp Ala Pro Ala Leu Ala Ser Gln Ser Ala

115 120 125

Gly Ile Thr Gly Val Ser His Arg Thr Gln Pro Ser Ile Arg Tyr Phe

130 135 140

Val Leu Phe Cys Phe Val Phe Val Phe Phe Glu Met Glu Phe Cys Ser

145 150 155 160

Cys Cys Pro Gly Trp Ser Ala Met Ala Thr Gln Pro Pro Leu Pro Val

	165		170		175										
Phe	Lys	Gln	Phe	Ser	Cys	Leu	Ser	Leu	Leu	Ser	Ser	Trp	Asp	Tyr	Arg
	180		185		190										
Arg	Leu	Pro	Pro	Arg	Leu	Ala	Asp	Phe	Leu	Tyr	Phe				
	195		200												

<210> 2136

<211> 819

<212> PRT

<213> Homo sapiens

<400> 2136

Met	Asn	Ala	Thr	Leu	Gln	Cys	Leu	Ser	Asn	Thr	Glu	Leu	Phe	Ala	Glu
1				5					10					15	
Tyr	Leu	Ala	Leu	Gly	Gln	Tyr	Arg	Ala	Gly	Arg	Pro	Glu	Pro	Ser	Pro
			20					25					30		
Asp	Pro	Glu	Gln	Pro	Ala	Gly	Arg	Gly	Ala	Gln	Gly	Gln	Gly	Glu	Val
		35					40				45				
Thr	Glu	Gln	Leu	Ala	His	Leu	Val	Arg	Ala	Leu	Trp	Thr	Leu	Glu	Tyr
	50					55					60				
Thr	Pro	Gln	His	Ser	Arg	Asp	Phe	Lys	Thr	Ile	Val	Ser	Lys	Asn	Ala
65					70				75					80	
Leu	Gln	Tyr	Arg	Gly	Asn	Ser	Gln	His	Asp	Ala	Gln	Glu	Phe	Leu	Leu
				85				90					95		
Trp	Leu	Leu	Asp	Arg	Val	His	Glu	Asp	Leu	Asn	His	Ser	Val	Lys	Gln
		100						105					110		
Ser	Gly	Gln	Pro	Pro	Leu	Lys	Pro	Pro	Ser	Glu	Thr	Asp	Met	Met	Pro
		115					120					125			

Glu Gly Pro Ser Phe Pro Val Cys Ser Thr Phe Val Gln Glu Leu Phe
 130 135 140
 Gln Ala Gln Tyr Arg Ser Ser Leu Thr Cys Pro His Cys Gln Lys Gln
 145 150 155 160
 Ser Asn Thr Phe Asp Pro Phe Leu Cys Ile Ser Leu Pro Ile Pro Leu
 165 170 175
 Pro His Thr Arg Pro Leu Tyr Val Thr Val Val Tyr Gln Gly Lys Cys
 180 185 190
 Ser His Cys Met Arg Ile Gly Val Ala Val Pro Leu Ser Gly Thr Val
 195 200 205
 Ala Arg Leu Arg Glu Ala Val Ser Met Glu Thr Lys Ile Pro Thr Asp
 210 215 220
 Gln Ile Val Leu Thr Glu Met Tyr Tyr Asp Gly Phe His Arg Ser Phe
 225 230 235 240
 Cys Asp Thr Asp Asp Leu Glu Thr Val His Glu Ser Asp Cys Ile Phe
 245 250 255
 Ala Phe Glu Thr Pro Glu Ile Phe Arg Pro Glu Gly Ile Leu Ser Gln
 260 265 270
 Arg Gly Ile His Leu Asn Asn Asn Leu Asn His Leu Lys Phe Gly Leu
 275 280 285
 Asp Tyr His Arg Leu Ser Ser Pro Thr Gln Thr Ala Ala Lys Gln Gly
 290 295 300
 Lys Met Asp Ser Pro Thr Ser Arg Ala Gly Ser Asp Lys Ile Val Leu
 305 310 315 320
 Leu Val Cys Asn Arg Ala Cys Thr Gly Gln Gln Gly Lys Arg Phe Gly
 325 330 335
 Leu Pro Phe Val Leu His Leu Glu Lys Thr Ile Ala Trp Asp Leu Leu
 340 345 350
 Gln Lys Glu Ile Leu Glu Lys Met Lys Tyr Phe Leu Arg Pro Thr Val

355 360 365
Cys Ile Gln Val Cys Pro Phe Ser Leu Arg Val Val Ser Val Val Gly
370 375 380
Ile Thr Tyr Leu Leu Pro Gln Glu Glu Gln Pro Leu Cys His Pro Thr
385 390 395 400
Val Glu Arg Ala Leu Lys Ser Cys Gly Pro Gly Gly Thr Ala His Val
405 410 415
Lys Leu Val Val Glu Trp Asp Lys Glu Thr Arg Asp Phe Leu Phe Val
420 425 430
Asn Thr Glu Asp Glu Tyr Ile Pro Asp Ala Glu Ser Val Arg Leu Gln
435 440 445
Arg Glu Arg His His Gln Pro Gln Thr Cys Thr Leu Ser Gln Cys Phe
450 455 460
Gln Leu Tyr Thr Lys Glu Glu Arg Leu Ala Pro Asp Asp Ala Trp Arg
465 470 475 480
Cys Pro His Cys Lys His Leu Gln Gln Gly Ser Ile Thr Leu Ser Leu
485 490 495
Trp Thr Leu Pro Asp Val Leu Ile Ile His Leu Lys Arg Phe Arg Gln
500 505 510
Glu Gly Asp Arg Arg Met Lys Leu Gln Asn Met Val Lys Phe Pro Leu
515 520 525
Thr Gly Leu Asp Met Thr Pro His Val Val Lys Arg Ser Gln Ser Ser
530 535 540
Trp Ser Leu Pro Ser His Trp Ser Pro Trp Arg Arg Pro Tyr Gly Leu
545 550 555 560
Gly Arg Asp Pro Glu Asp Tyr Ile Tyr Asp Leu Tyr Ala Val Cys Asn
565 570 575
His His Gly Thr Met Gln Gly Gly His Tyr Thr Ala Tyr Cys Lys Asn
580 585 590

Ser Val Asp Gly Leu Trp Tyr Cys Phe Asp Asp Ser Asp Val Gln Gln
595 600 605
Leu Ser Glu Asp Glu Val Cys Thr Gln Thr Ala Tyr Ile Leu Phe Tyr
610 615 620
Gln Arg Arg Thr Ala Ile Pro Ser Trp Ser Ala Asn Ser Ser Val Ala
625 630 635 640
Gly Ser Thr Ser Ser Ser Leu Cys Glu His Trp Val Ser Arg Leu Pro
645 650 655
Gly Ser Lys Pro Ala Ser Val Thr Ser Ala Ala Ser Ser Arg Arg Thr
660 665 670
Ser Leu Ala Ser Leu Ser Glu Ser Val Glu Met Thr Gly Glu Arg Ser
675 680 685
Glu Asp Asp Gly Gly Phe Ser Thr Arg Pro Phe Val Arg Ser Val Gln
690 695 700
Arg Gln Ser Leu Ser Ser Arg Ser Ser Val Thr Ser Pro Leu Ala Val
705 710 715 720
Asn Glu Asn Cys Met Arg Pro Ser Trp Ser Leu Ser Ala Lys Leu Gln
725 730 735
Met Arg Ser Asn Ser Pro Ser Arg Phe Ser Gly Asp Ser Pro Ile His
740 745 750
Ser Ser Ala Ser Thr Leu Glu Lys Ile Gly Glu Ala Ala Asp Asp Lys
755 760 765
Val Ser Ile Ser Cys Phe Gly Ser Leu Arg Asn Leu Ser Ser Ser Tyr
770 775 780
Gln Glu Pro Ser Asp Ser His Ser Arg Arg Glu His Lys Ala Val Gly
785 790 795 800
Arg Ala Leu Trp Leu Ser Trp Lys Ala Cys Ser Lys Thr Asn Arg Thr
805 810 815
Pro Ala Asp

<210> 2137

<211> 187

<212> PRT

<213> Homo sapiens

<400> 2137

Met	Val	Met	His	Ser	Glu	Asp	Glu	Pro	Tyr	Lys	Cys	Lys	Phe	Cys	Gly
1				5					10					15	
Lys	Ala	Phe	Asp	Asn	Leu	His	Leu	Tyr	Leu	Thr	His	Glu	Arg	Thr	His
				20				25					30		
Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys	Asn	Lys	Cys	Gly	Lys	Ala	Phe	Ser
			35				40					45			
Cys	Ser	Ser	Ser	Ile	Arg	Lys	His	Ala	Arg	Ile	His	Thr	Gly	Glu	Lys
	50					55				60					
Pro	Tyr	Ile	Cys	Lys	Gln	Cys	Gly	Lys	Ala	Phe	Arg	Tyr	Ser	Ser	Ser
65					70					75				80	
Ile	Arg	Asn	His	Glu	Asn	Thr	His	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Cys
				85				90					95		
Lys	Gln	Cys	Gly	Lys	Ala	Phe	Ser	Tyr	Ser	Ser	Tyr	Phe	Arg	Ile	His
			100					105				110			
Glu	Arg	Ile	His	Thr	Gly	Glu	Gln	Val	Tyr	Lys	Cys	Lys	Glu	Cys	Gly
		115					120				125				
Lys	Thr	Phe	Thr	Tyr	Pro	Ser	Ala	Phe	His	Lys	His	Lys	Ser	Thr	His
		130					135				140				
Thr	Ser	Gln	Lys	Leu	Tyr	Glu	Cys	Lys	Glu	Cys	Gly	Lys	Ala	Phe	Asp
145					150					155				160	

130

<210> 2139

<211> 463

<212> PRT

<213> Homo sapiens

<400> 2139

Met	Arg	Ala	Leu	Ala	Leu	Asp	Leu	Gly	Ser	Pro	Ala	Ala	Leu	Arg	Glu
1				5					10					15	
Trp	Gly	Arg	Cys	Gln	Ala	Arg	Cys	Gln	Glu	Leu	Glu	Arg	Arg	Ile	Gln
				20				25						30	
Gln	His	Leu	Gly	Glu	Glu	Ala	Ser	Pro	Arg	Gly	Tyr	Arg	Arg	Arg	Arg
				35				40						45	
Ala	Asp	Gly	Ala	Ser	Ser	Gly	Gly	Ala	Gln	Trp	Gly	Pro	Arg	Ser	Pro
				50				55						60	
Ser	Pro	Ser	Leu	Ser	Ser	Leu	Leu	Leu	Pro	Ser	Ser	Pro	Gly	Pro	Arg
				65				70					75		80
Pro	Ala	Pro	Ser	His	Cys	Ser	Leu	Ala	Pro	Cys	Gly	Glu	Asp	Tyr	Glu
				85				90						95	
Glu	Glu	Gly	Pro	Glu	Leu	Ala	Pro	Glu	Ala	Glu	Gly	Arg	Pro	Pro	Arg
				100				105						110	
Ala	Val	Leu	Ile	Arg	Gly	Leu	Glu	Val	Thr	Ser	Thr	Glu	Val	Val	Asp
				115				120						125	
Arg	Thr	Cys	Ser	Pro	Arg	Glu	His	Val	Leu	Leu	Gly	Arg	Ala	Arg	Gly
				130				135						140	
Pro	Asp	Gly	Pro	Trp	Gly	Val	Gly	Thr	Pro	Arg	Met	Glu	Arg	Lys	Arg
				145				150						155	160

Ser Ile Ser Ala Gln Gln Arg Leu Val Ser Glu Leu Ile Ala Cys Glu
165 170 175
Gln Asp Tyr Val Ala Thr Leu Ser Glu Pro Val Pro Pro Pro Gly Pro
180 185 190
Glu Leu Thr Pro Glu Leu Arg Gly Thr Trp Ala Ala Ala Leu Ser Ala
195 200 205
Arg Glu Arg Leu Arg Ser Phe His Arg Thr His Phe Leu Arg Glu Leu
210 215 220
Gln Gly Cys Ala Thr His Pro Leu Arg Ile Gly Ala Cys Phe Leu Arg
225 230 235 240
His Gly Asp Gln Phe Ser Leu Tyr Ala Gln Tyr Val Lys His Arg His
245 250 255
Lys Leu Glu Asn Gly Leu Ala Ala Leu Ser Pro Ser Ser Lys Gly Ser
260 265 270
Met Glu Ala Gly Pro Tyr Leu Pro Arg Ala Leu Gln Gln Pro Leu Glu
275 280 285
Gln Leu Thr Arg Tyr Gly Arg Leu Leu Glu Glu Leu Leu Arg Glu Ala
290 295 300
Gly Pro Glu Leu Ser Ser Glu Cys Arg Ala Leu Gly Ala Ala Val Gln
305 310 315 320
Leu Leu Arg Glu Gln Glu Ala Arg Gly Arg Asp Leu Leu Ala Val Glu
325 330 335
Ala Val Arg Gly Cys Glu Ile Asp Leu Lys Glu Gln Gly Gln Leu Leu
340 345 350
His Arg Asp Pro Phe Thr Val Ile Cys Gly Arg Lys Lys Cys Leu Arg
355 360 365
His Val Phe Leu Phe Glu His Leu Leu Leu Phe Ser Lys Leu Lys Gly
370 375 380
Pro Glu Gly Gly Ser Glu Met Phe Val Tyr Lys Gln Ala Phe Lys Thr

385 390 395 400
Ala Asp Met Gly Leu Thr Glu Asn Ile Gly Asp Ser Gly Leu Cys Phe
 405 410 415
Glu Leu Trp Phe Arg Arg Arg Arg Ala Arg Glu Ala Tyr Thr Leu Gln
 420 425 430
Ala Thr Ser Pro Glu Ile Lys Leu Lys Trp Thr Ser Ser Ile Ala Gln
 435 440 445
Leu Leu Trp Arg Gln Ala Ala His Asn Lys Gly Thr Gly Gln Ser
 450 455 460

<210> 2140

<211> 119

<212> PRT

<213> Homo sapiens

<400> 2140

Met Gly Ala Gly Pro Arg Val Gly Gly Gly Ala Arg Ser Gly Tyr Ile
1 5 10 15
Cys Leu Val Pro Lys Cys Arg Asp Glu Ala Gln Pro Ser Pro Pro Phe
 20 25 30
Gly Ala Pro His Trp Trp Leu Arg Val Arg Gly Asp Asp Arg Asp Pro
 35 40 45
Pro Glu Val Tyr Ser Trp Gly Leu Glu Gly Cys Gly Arg Gly Leu Gly
 50 55 60
Gly His Trp Gly Leu Ala Arg Val Gly Pro Met Arg Gly Gln Ser Leu
65 70 75 80
Ala Cys Ala Leu Thr Ser Leu Leu Cys Val Thr Trp Glu Thr Asn Gly
 85 90 95

Cys Pro Tyr Ser Thr Ala Ser Met Pro His Ala Lys His Arg Pro Cys

100

105

110

Ser Arg Asp Leu Gly Phe Glu

115

<210> 2141

<211> 716

<212> PRT

<213> Homo sapiens

<400> 2141

Met Met Ser Ile Arg Gln Arg Arg Glu Ile Arg Ala Thr Glu Val Ser

1

5

10

15

Glu Asp Phe Pro Ala Gln Glu Glu Asn Val Lys Leu Glu Asn Lys Leu

20

25

30

Pro Ser Gly Cys Thr Ser Arg Arg Leu Trp Lys Ile Leu Ser Leu Thr

35

40

45

Ile Gly Gly Thr Ile Ala Leu Cys Ile Gly Leu Leu Thr Ser Val Tyr

50

55

60

Leu Ala Thr Leu His Glu Asn Asp Leu Trp Phe Ser Asn Ile Lys Glu

65

70

75

80

Val Glu Arg Glu Ile Ser Phe Arg Thr Glu Cys Gly Leu Tyr Tyr Ser

85

90

95

Tyr Tyr Lys Gln Met Leu Gln Ala Pro Thr Leu Val Gln Gly Phe His

100

105

110

Gly Leu Ile Tyr Asp Asn Lys Thr Glu Ser Met Lys Thr Ile Asn Leu

115

120

125

Leu Gln Arg Met Asn Ile Tyr Gln Glu Val Phe Leu Ser Ile Leu Tyr

130 135 140
Arg Val Leu Pro Ile Gln Lys Tyr Leu Glu Pro Val Tyr Phe Tyr Ile
145 150 155 160
Tyr Thr Leu Phe Gly Leu Gln Ala Ile Tyr Val Thr Ala Leu Tyr Ile
165 170 175
Thr Ser Trp Leu Leu Ser Gly Thr Trp Leu Ser Gly Leu Leu Ala Ala
180 185 190
Phe Trp Tyr Val Thr Asn Arg Ile Asp Thr Thr Arg Val Glu Phe Thr
195 200 205
Ile Pro Leu Arg Glu Asn Trp Ala Leu Pro Phe Phe Ala Ile Gln Ile
210 215 220
Ala Ala Ile Thr Tyr Phe Leu Arg Pro Asn Leu Gln Pro Leu Ser Glu
225 230 235 240
Arg Leu Thr Leu Leu Ala Ile Phe Ile Ser Thr Phe Leu Phe Ser Leu
245 250 255
Thr Trp Gln Phe Asn Gln Phe Met Met Leu Met Gln Ala Leu Val Leu
260 265 270
Phe Thr Leu Asp Ser Leu Asp Met Leu Pro Ala Val Lys Ala Thr Trp
275 280 285
Leu Tyr Gly Ile Gln Ile Thr Ser Leu Leu Leu Val Cys Ile Leu Gln
290 295 300
Phe Phe Asn Ser Met Ile Leu Gly Ser Leu Leu Ile Ser Phe Asn Leu
305 310 315 320
Ser Val Phe Ile Ala Arg Lys Leu Gln Lys Asn Leu Lys Thr Gly Ser
325 330 335
Phe Leu Asn Arg Leu Gly Lys Leu Leu Leu His Leu Phe Met Val Leu
340 345 350
Cys Leu Thr Leu Phe Leu Asn Asn Ile Ile Lys Lys Ile Leu Asn Leu
355 360 365

Lys Ser Asp Glu His Ile Phe Lys Phe Leu Lys Ala Lys Phe Gly Leu
370 375 380
Gly Ala Thr Arg Asp Phe Asp Ala Asn Leu Tyr Leu Cys Glu Glu Ala
385 390 395 400
Phe Gly Leu Leu Pro Phe Asn Thr Phe Gly Arg Leu Ser Asp Thr Leu
405 410 415
Leu Phe Tyr Ala Tyr Ile Phe Val Leu Ser Ile Thr Val Ile Val Ala
420 425 430
Phe Val Val Ala Phe His Asn Leu Ser Asp Ser Thr Asn Gln Gln Ser
435 440 445
Val Gly Lys Met Glu Lys Gly Thr Val Asp Leu Lys Pro Glu Thr Ala
450 455 460
Tyr Asn Leu Ile His Thr Ile Leu Phe Gly Phe Leu Ala Leu Ser Thr
465 470 475 480
Met Gly Met Lys Tyr Leu Trp Thr Ser His Met Cys Val Phe Ala Ser
485 490 495
Phe Gly Leu Cys Ser Pro Glu Ile Trp Glu Leu Leu Leu Lys Ser Val
500 505 510
His Leu Tyr Asn Pro Lys Arg Ile Cys Ile Met Arg Tyr Ser Val Pro
515 520 525
Ile Leu Ile Leu Leu Tyr Leu Cys Tyr Lys Phe Trp Pro Gly Met Met
530 535 540
Asp Glu Leu Ser Glu Leu Arg Glu Phe Tyr Asp Pro Asp Thr Val Glu
545 550 555 560
Leu Met Asn Trp Ile Asn Ser Asn Thr Pro Arg Lys Ala Val Phe Ala
565 570 575
Gly Ser Met Gln Leu Leu Ala Gly Val Lys Leu Cys Thr Gly Arg Thr
580 585 590
Leu Thr Asn His Pro His Tyr Glu Asp Ser Ser Leu Arg Glu Arg Thr

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Met Met Ala His Arg Asp Gln Arg Asp Val Ser Leu Ser Ser Leu Arg
50 55 60
Met Leu Ile Val Thr Asp Gly Ala Asn Pro Trp Ser Val Ser Ser Cys
65 70 75 80
Asp Ala Phe Leu Ser Leu Phe Gln Ser His Gly Leu Lys Pro Glu Ala
85 90 95
Ile Cys Pro Cys Ala Thr Ser Ala Glu Ala Met Thr Val Ala Ile Arg
100 105 110
Arg Pro Gly Val Pro Gly Ala Pro Leu Pro Gly Arg Ala Ile Leu Ser
115 120 125
Met Asn Gly Leu Ser Tyr Gly Val Ile Arg Val Asn Thr Glu Asp Lys
130 135 140
Asn Ser Ala Leu Thr Val Gln Asp Val Gly His Val Met Pro Gly Gly
145 150 155 160
Met Met Cys Ile Val Lys Pro Asp Gly Pro Pro Gln Leu Cys Lys Thr
165 170 175
Asp Glu Ile Gly Glu Ile Cys Val Ser Ser Arg Thr Gly Gly Met Met
180 185 190
Tyr Phe Gly Leu Ala Gly Val Thr Lys Asn Thr Phe Glu Val Ile Pro
195 200 205
Val Asn Ser Ala Gly Ser Pro Val Gly Asp Val Pro Phe Ile Arg Ser
210 215 220
Gly Leu Leu Gly Phe Val Gly Pro Gly Ser Leu Val Phe Val Val Gly
225 230 235 240
Lys Met Asp Gly Leu Leu Met Val Ser Gly Arg Arg His Asn Ala Asp
245 250 255
Asp Ile Val Ala Thr Gly Leu Ala Val Glu Ser Ile Lys Thr Val Tyr
260 265 270
Arg Gly Arg Ile Ala Val Phe Ser Val Ser Val Phe Tyr Asp Glu Arg

275	280	285
Ile Val Val Val Ala Glu Gln Arg Pro Asp Ala Ser Glu Glu Asp Ser		
290	295	300
Phe Gln Trp Met Ser Arg Val Leu Gln Ala Ile Asp Ser Ile His Gln		
305	310	315
Val Gly Val Tyr Cys Leu Ala Leu Val Pro Ala Asn Thr Leu Pro Lys		
325	330	335
Thr Pro Leu Gly Gly Ile His Ile Ser Gln Thr Lys Gln Leu Phe Leu		
340	345	350
Glu Gly Ser Leu His Pro Cys Asn Ile Leu Met Cys Pro His Thr Cys		
355	360	365
Val Thr Asn Leu Pro Lys Pro Arg Gln Lys Gln Pro Gly Val Gly Pro		
370	375	380
Ala Pro Val Met Val Gly Asn Leu Val Ala Gly Lys Arg Ile Ala Gln		
385	390	395
Ala Ala Gly Arg Asp Leu Gly Gln Ile Glu Glu Asn Asp Leu Val Arg		
405	410	415
Lys His Gln Phe Leu Ala Glu Ile Leu Gln Trp Arg Ala Gln Ala Thr		
420	425	430
Pro Asp His Val Leu Leu Met Leu Leu Asn Ala Lys Gly Thr Thr Val		
435	440	445
Cys Thr Ala Ser Cys Leu Gln Leu His Lys Arg Ala Glu Arg Ile Ala		
450	455	460
Ser Val Leu Gly Asp Lys Gly His Leu Asn Ala Gly Asp Asn Val Val		
465	470	475
Leu Leu Tyr Pro Pro Gly Ile Glu Leu Ile Ala Ala Phe Tyr Gly Cys		
485	490	495
Leu Tyr Ala Gly Cys Ile Pro Val Thr Val Arg Pro Pro His Ala Gln		
500	505	510

Asn Leu Thr Ala Thr Leu Pro Thr Val Arg Met Ile Val Asp Val Ser
515 520 525
Lys Ala Ala Cys Ile Leu Thr Ser Gln Thr Leu Met Arg Leu Leu Arg
530 535 540
Ser Arg Glu Ala Ala Ala Val Asp Val Lys Thr Trp Pro Thr Ile
545 550 555 560
Ile Asp Thr Asp Asp Leu Pro Arg Lys Arg Leu Pro Gln Leu Tyr Lys
565 570 575
Pro Pro Thr Pro Glu Met Leu Ala Tyr Leu Asp Phe Ser Val Ser Thr
580 585 590
Thr Gly Met Leu Thr Gly Val Lys Met Ser His Ser Ala Val Asn Ala
595 600 605
Leu Cys Arg Ala Ile Lys Leu Gln Cys Glu Leu Tyr Ser Ser Arg Gln
610 615 620
Ile Ala Ile Cys Leu Asp Pro Tyr Cys Gly Leu Gly Phe Ala Leu Trp
625 630 635 640
Cys Leu Cys Ser Val Tyr Ser Gly His Gln Ser Val Leu Ile Pro Pro
645 650 655
Met Glu Leu Glu Asn Asn Leu Phe Leu Trp Leu Ser Thr Val Asn Gln
660 665 670
Tyr Lys Ile Arg Asp Thr Phe Cys Ser Tyr Ser Val Met Glu Leu Cys
675 680 685
Thr Lys Gly Leu Gly Asn Gln Val Glu Val Leu Lys Thr Arg Gly Ile
690 695 700
Asn Leu Ser Cys Val Arg Thr Cys Val Val Val Ala Glu Glu Arg Pro
705 710 715 720
Arg Val Ala Leu Gln Gln Ser Phe Ser Lys Leu Phe Lys Asp Ile Gly
725 730 735
Leu Ser Pro Arg Ala Val Ser Thr Thr Phe Gly Ser Arg Val Asn Val

740 745 750
Ala Ile Cys Leu Gln Gly Thr Ser Gly Pro Asp Pro Thr Thr Val Tyr
755 760 765
Val Asp Leu Lys Ser Leu Arg His Asp Arg Val Arg Leu Val Glu Arg
770 775 780
Gly Ala Pro Gln Ser Leu Leu Leu Ser Glu Ser Gly Lys Ile Leu Pro
785 790 795 800
Gly Val Lys Val Val Ile Val Asn Pro Glu Thr Lys Gly Pro Val Gly
805 810 815
Asp Ser His Leu Gly Glu Ile Trp Val Asn Ser Pro His Thr Ala Ser
820 825 830
Gly Tyr Tyr Thr Ile Tyr Asp Ser Glu Thr Leu Gln Ala Asp His Phe
835 840 845
Asn Thr Arg Leu Ser Phe Gly Asp Ala Ala Gln Thr Leu Trp Ala Arg
850 855 860
Thr Gly Tyr Leu Gly Phe Val Arg Arg Thr Glu Leu Thr Ala Ala Thr
865 870 875 880
Gly Glu Arg His Asp Ala Leu Tyr Val Val Gly Ala Leu Asp Glu Thr
885 890 895
Leu Glu Leu Arg Gly Leu Arg Tyr His Pro Ile Asp Ile Glu Thr Ser
900 905 910
Val Ser Arg Ile His Arg Ser Ile Ala Glu Cys Ala Val Phe Thr Trp
915 920 925
Thr Asn Leu Leu Val Val Val Val Glu Leu Cys Gly Ser Glu Gln Glu
930 935 940
Ala Leu Asp Leu Val Pro Leu Val Thr Asn Val Val Leu Glu Glu His
945 950 955 960
Tyr Leu Ile Val Gly Val Val Val Val Val Asp Pro Gly Val Ile Pro
965 970 975

Ile Asn Ser Arg Gly Glu Lys Gln Arg Met His Leu Arg Asp Ser Phe

980

985

990

Leu Ala Asp Gln Leu Asp Pro Ile Tyr Val Ala Tyr Asn Met

995

1000

1005

<210> 2143

<211> 129

<212> PRT

<213> Homo sapiens

<400> 2143

Met Ala Cys Pro Ser Pro Val Ser Arg Arg Leu Ala Arg Ser Thr Leu

1

5

10

15

Leu Leu Ile Pro Leu Phe Gly Val His Tyr Ile Met Phe Ala Phe Phe

20

25

30

Pro Asp Asn Phe Lys Pro Glu Val Lys Met Val Phe Glu Leu Val Val

35

40

45

Gly Ser Phe Gln Gly Phe Val Val Ala Ile Leu Tyr Cys Phe Leu Asn

50

55

60

Gly Glu Val Gln Ala Glu Leu Arg Arg Lys Trp Arg Arg Trp His Leu

65

70

75

80

Gln Gly Val Leu Gly Trp Asn Pro Lys Tyr Arg His Pro Ser Gly Gly

85

90

95

Ser Asn Gly Ala Thr Cys Ser Thr Gln Val Ser Met Leu Thr Arg Val

100

105

110

Ser Pro Gly Ala Arg Arg Ser Ser Ser Phe Gln Ala Glu Val Ser Leu

115

120

125

Val

<210> 2144

<211> 112

<212> PRT

<213> Homo sapiens

<400> 2144

Met	Tyr	Gln	Ile	Phe	Lys	Lys	Leu	Arg	Trp	Ser	Leu	Thr	Leu	Ser	Pro
1					5				10					15	
Arg	Leu	Glu	Cys	Ser	Asp	Ala	Ile	Leu	Thr	His	Cys	Asn	Leu	Cys	Leu
					20				25					30	
Leu	Gly	Ser	Ser	Asn	Ser	Pro	Ala	Ser	Ala	Ser	Ser	Val	Ala	Gly	Ile
					35				40					45	
Thr	Gly	Met	Cys	His	His	Ala	Trp	Ile	Ile	Phe	Ala	Phe	Leu	Val	Glu
					50				55					60	
Thr	Gly	Phe	Cys	Arg	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Leu
					65				70					75	
Gly	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Asn	Ala	Gly	Ile	Ile	Gly	Val
					85				90					95	
Ser	His	Arg	Thr	Trp	Pro	Ala	Pro	His	Phe	Leu	Tyr	Pro	Val	Tyr	His
					100				105					110	

<210> 2145

<211> 145

<212> PRT

<213> Homo sapiens

<400> 2145

Met Lys Phe Asn Pro Phe Val Thr Ser Asp Arg Ser Lys Asn Arg Lys

1 5 10 15

Arg His Phe Asn Ala Pro Ser His Val Arg Arg Lys Ile Met Ser Ser

20 25 30

Pro Leu Ser Lys Glu Leu Arg Gln Lys Tyr Asn Val Arg Ser Met Pro

35 40 45

Ile Arg Lys Asp Asp Glu Val Gln Val Val Arg Gly His Tyr Lys Gly

50 55 60

Gln Gln Ile Gly Lys Val Val Gln Val Tyr Arg Lys Lys Tyr Val Ile

65 70 75 80

Tyr Ile Glu Arg Val Gln Arg Glu Lys Ala Asn Gly Thr Thr Val His

85 90 95

Val Gly Ile His Pro Ser Lys Val Val Ile Thr Arg Leu Lys Leu Asp

100 105 110

Lys Asp Arg Lys Lys Ile Leu Glu Arg Lys Ala Lys Ser Arg Gln Val

115 120 125

Gly Lys Glu Lys Gly Lys Tyr Lys Glu Glu Leu Ile Glu Lys Met Gln

130 135 140

Glu

145

<210> 2146

<211> 134

<212> PRT

<213> Homo sapiens

<400> 2146

Met Leu Thr Ile Ala Ile Val Leu Trp Val Leu Phe Leu Arg Arg Ser
 1 5 10 15
 Leu Thr Leu Leu Pro Arg Leu Glu Cys Gly Gly Val Ile Ser Val His
 20 25 30
 Cys Asn Leu Arg Pro His Gly Ser Ser Asp Ser Pro Ala Ser Ala Ser
 35 40 45
 Leu Val Ala Gly Ile Ala Gly Ala Cys Arg His Ala Trp Leu Ile Phe
 50 55 60
 Phe Val Phe Leu Val Glu Thr Gly Phe Arg Arg Val Gly His Ala Gly
 65 70 75 80
 Phe Glu Leu Leu Thr Ser Gly Asp Leu Pro Ala Ser Ala Ser Gln Ser
 85 90 95
 Ala Gly Ile Ala Gly Val Ser His Arg Ala Arg Pro Arg Gly Leu Leu
 100 105 110
 Leu Ser Ala Gly Ile Ser Asp Arg Ser Gly Gln Gln Arg Val Arg Leu
 115 120 125
 Tyr Asn Lys Leu Lys Lys
 130

<210> 2147

<211> 754

<212> PRT

<213> Homo sapiens

<400> 2147

Met Asn Phe Glu Ala Val Leu His Tyr Lys His Gln Asn Gln Ala Arg
 1 5 10 15

Asp Glu Lys Lys Lys Leu Arg His Ala Ser Gly Ala Asn Ile Thr Asn
 20 25 30
 Ala Thr Thr Ala Ala Thr Thr Ala Ala Thr Ala Thr Thr Thr Ala Ser
 35 40 45
 Thr Glu Gly Ser Asn Ser Glu Ser Glu Ala Glu Ser Thr Glu Asn Ser
 50 55 60
 Pro Thr Pro Ser Pro Leu Gln Lys Lys Val Thr Glu Asp Leu Ser Lys
 65 70 75 80
 Thr Leu Leu Met Tyr Thr Val Pro Ala Val Gln Gly Phe Phe Arg Ser
 85 90 95
 Ile Ser Leu Ser Arg Gly Asn Asn Leu Gln Asp Thr Leu Arg Val Leu
 100 105 110
 Thr Leu Trp Phe Asp Tyr Gly His Trp Pro Asp Val Asn Glu Ala Leu
 115 120 125
 Val Glu Gly Val Lys Ala Ile Gln Ile Asp Thr Trp Leu Gln Val Ile
 130 135 140
 Pro Gln Leu Ile Ala Arg Ile Asp Thr Pro Arg Pro Leu Val Gly Arg
 145 150 155 160
 Leu Ile His Gln Leu Leu Thr Asp Ile Gly Arg Tyr His Pro Gln Ala
 165 170 175
 Leu Ile Tyr Pro Leu Thr Val Ala Ser Lys Ser Thr Thr Thr Ala Arg
 180 185 190
 His Asn Ala Ala Asn Lys Ile Leu Lys Asn Met Cys Glu His Ser Asn
 195 200 205
 Thr Leu Val Gln Gln Ala Met Met Val Ser Glu Glu Leu Ile Arg Val
 210 215 220
 Ala Ile Leu Trp His Glu Met Trp His Glu Gly Leu Glu Glu Ala Ser
 225 230 235 240
 Arg Leu Tyr Phe Gly Glu Arg Asn Val Lys Gly Met Phe Glu Val Leu

	245		250		255
Glu Pro Leu His Ala Met Met Glu Arg Gly Pro Gln Thr Leu Lys Glu					
	260		265		270
Thr Ser Phe Asn Gln Ala Tyr Gly Arg Asp Leu Met Glu Ala Gln Glu					
	275		280		285
Trp Cys Arg Lys Tyr Met Lys Ser Gly Asn Val Lys Asp Leu Thr Gln					
	290		295		300
Ala Trp Asp Leu Tyr Tyr His Val Phe Arg Arg Ile Ser Lys Gln Leu					
305		310		315	320
Pro Gln Leu Thr Ser Leu Glu Leu Gln Tyr Val Ser Pro Lys Leu Leu					
	325		330		335
Met Cys Arg Asp Leu Glu Leu Ala Val Pro Gly Thr Tyr Asp Pro Asn					
	340		345		350
Gln Pro Ile Ile Arg Ile Gln Ser Ile Ala Pro Ser Leu Gln Val Ile					
	355		360		365
Thr Ser Lys Gln Arg Pro Arg Lys Leu Thr Leu Met Gly Ser Asn Gly					
	370		375		380
His Glu Phe Val Phe Leu Leu Lys Gly His Glu Asp Leu Arg Gln Asp					
385		390		395	400
Glu Arg Val Met Gln Leu Phe Gly Leu Val Asn Thr Leu Leu Ala Asn					
	405		410		415
Asp Pro Thr Ser Leu Arg Lys Asn Leu Ser Ile Gln Arg Tyr Ala Val					
	420		425		430
Ile Pro Leu Ser Thr Asn Ser Gly Leu Ile Gly Trp Val Pro His Cys					
	435		440		445
Asp Thr Leu His Ala Leu Ile Arg Asp Tyr Arg Glu Lys Lys Lys Ile					
	450		455		460
Leu Leu Asn Ile Glu His Arg Ile Met Leu Arg Met Ala Pro Asp Tyr					
465		470		475	480

Asp His Leu Thr Leu Met Gln Lys Val Glu Val Phe Glu His Ala Val			
	485	490	495
Asn Asn Thr Ala Gly Asp Asp Leu Ala Lys Leu Leu Trp Leu Lys Ser			
	500	505	510
Pro Ser Ser Glu Val Trp Phe Asp Arg Arg Thr Asn Tyr Thr Arg Ser			
	515	520	525
Leu Ala Val Met Ser Met Val Gly Tyr Ile Leu Gly Leu Gly Asp Arg			
	530	535	540
His Pro Ser Asn Leu Met Leu Asp Arg Leu Ser Gly Lys Ile Leu His			
	545	550	555
Ile Asp Phe Gly Asp Cys Phe Glu Val Ala Met Thr Arg Glu Lys Phe			
	565	570	575
Pro Glu Lys Ile Pro Phe Arg Leu Thr Arg Met Leu Thr Asn Ala Met			
	580	585	590
Glu Val Thr Gly Leu Asp Gly Asn Tyr Arg Ile Thr Cys His Thr Val			
	595	600	605
Met Glu Val Leu Arg Glu His Lys Asp Ser Val Met Ala Val Leu Glu			
	610	615	620
Ala Phe Val Tyr Asp Pro Leu Leu Asn Trp Arg Leu Met Asp Thr Asn			
	625	630	635
Thr Lys Gly Asn Lys Arg Ser Arg Thr Arg Thr Asp Ser Tyr Ser Ala			
	645	650	655
Gly Gln Ser Val Glu Ile Leu Asp Gly Val Glu Leu Gly Glu Pro Ala			
	660	665	670
His Arg Lys Thr Gly Thr Thr Val Pro Glu Ser Ile His Ser Phe Ile			
	675	680	685
Gly Asp Gly Leu Val Lys Pro Glu Ala Leu Asn Lys Lys Ala Ile Gln			
	690	695	700
Ile Ile Asn Arg Val Arg Asp Lys Leu Thr Gly Arg Asp Phe Ser His			

705 710 715 720
 Asp Asp Thr Leu Asp Val Pro Thr Gln Val Glu Leu Leu Ile Lys Gln
 725 730 735
 Ala Thr Ser His Glu Asn Leu Cys Gln Cys Tyr Ile Gly Trp Cys Pro
 740 745 750
 Phe Trp

<210> 2148

<211> 114

<212> PRT

<213> Homo sapiens

<400> 2148

Met Gln Ala Gln Asn Arg Asp Ser Asp Ile Gly His Pro Ala Ala Glu
 1 5 10 15
 Leu Pro Val Cys Gln Pro Ser Phe Leu His Cys Ser Lys Ala Val Ser
 20 25 30
 Gly Leu His Val Gly Asn Arg Phe Thr Pro Gly Ala Asn Phe Leu Ile
 35 40 45
 Leu Ile Phe Ser Ser Asn Ser Thr Lys Ser Pro Asn Phe Thr Ile Glu
 50 55 60
 Lys Leu Leu Leu Ile Met His Leu Asn Leu Leu Asn Lys Phe Ser Gln
 65 70 75 80
 Ser Trp Ser Leu Ser Asp Ile Ala Ser Glu Arg Glu Ala Ala Leu Ser
 85 90 95
 Gly Leu Gly Gln Asn Cys His Met Asp Glu Ile Leu Ser Val Lys Lys
 100 105 110

Trp Pro

<210> 2149

<211> 225

<212> PRT

<213> Homo sapiens

<400> 2149

Met Met Arg Gly Thr Cys Asp Leu Ala Asp Gly Gly Lys Gln Cys Pro

1 5 10 15

Pro Leu Cys Arg Trp Pro His Pro Thr Cys Trp Arg Pro Lys Gln Asn

20 25 30

Gln Gln Val Arg Gly Asn Ser His Ser Leu Pro Ala Phe Lys Trp Gly

35 40 45

His Arg Ser Ser Pro Pro Phe Arg Leu Arg Val Gly Leu Lys Phe Thr

50 55 60

Pro Leu Ala Leu Leu Gly Leu Arg Pro Leu Thr His Ser Gly Thr His

65 70 75 80

Ala Ile Ser Ser Pro Gly Ser Gln Val Leu Asp Ser His Trp Asn Ser

85 90 95

His His Gly Phe Ser Trp Asp Ser Gly Pro Arg Pro His Trp Asn Ser

100 105 110

His His Gln Leu Ser Trp Val Ser Gly His Arg Leu Thr Leu Glu Leu

115 120 125

Thr Pro Ser Ala Leu Leu Gly Leu Arg Pro Ser Asn Gln Thr Gly Thr

130 135 140

His Thr Ile Ser Ser Pro Gly Ser Gln Thr Phe Lys Ser Asn Trp Asn

145 150 155 160
 Ser His His Trp Leu Ser Trp Val Ser Gly Pro Arg Leu Thr Leu Glu
 165 170 175
 Leu Thr Ser Ser Ala Leu Leu Gly Pro Gln Leu Ala Asn Cys Arg Pro
 180 185 190
 Leu Asp Ser Ser Thr Cys Ile Ala Ala Gly Ala Asn Ser Leu Gln Cys
 195 200 205
 Val Ser Ser Tyr Val Ser Ile Cys Asp Trp Phe Cys Ser Ser Gly Ala
 210 215 220

His

225

<210> 2150

<211> 205

<212> PRT

<213> Homo sapiens

<400> 2150

Met His Leu Gln Met Arg Glu Asp Met Ala Lys Tyr Arg Arg Met Ser
 1 5 10 15
 Gly Val Arg Pro Gln Ser Phe Arg Asp Leu Glu Thr Pro Pro His Trp
 20 25 30
 Ala Ala Tyr Asp Thr Gly Leu Glu Leu Leu Gly Arg Gln Glu Ala Gly
 35 40 45
 Leu Ala Leu Pro Arg Leu Glu Glu Ala Leu Gln Gly Ser Leu Ala Gln
 50 55 60
 Met Glu Ser Cys Arg Ala Asp Cys Glu Gly Pro Glu Glu Gln Gln Gly
 65 70 75 80

Ala Glu Glu Glu Glu Asp Gly Ala Ala Ser Gln Gly Gly Leu Tyr Glu
 85 90 95
 Ala Ile Ala Gly His Trp Ile Gln Val Leu Gln Cys Arg Gln Arg Cys
 100 105 110
 Val Gly Glu Thr Ala Thr Arg Pro Gly Arg Ser Phe Pro Val Pro Asp
 115 120 125
 Phe Leu Pro Asn Gln Leu Arg Arg Leu His Glu Ala His Ala Gln Val
 130 135 140
 Ser Leu Ser Gly Leu His Gly Asn His His Phe Thr Arg Thr Leu Ile
 145 150 155 160
 Cys Pro Pro Leu Ala Pro Val Thr Ser Ser Gly Asp Gly Leu Pro Ser
 165 170 175
 Ala Leu Leu Leu Leu Thr Phe Leu Tyr Phe Pro Pro Ser Cys Ser Ser
 180 185 190
 Leu Asn Ser Pro Ala Lys Trp Ala Ile Cys Pro Arg Leu
 195 200 205

<210> 2151

<211> 167

<212> PRT

<213> Homo sapiens

<400> 2151

Met Phe Asp Phe Ser Phe Pro Thr Pro Ala Ser Ala Gly Thr Arg Met
 1 5 10 15
 Gly Pro Ala Ser Cys Gly Gly Arg Ser Leu His Leu Pro Gln Leu Arg
 20 25 30
 Phe Ser Arg Val Asp Ala Thr Ala Val Thr Asp Val Pro Phe Gln Arg

35 40 45
 Met His Ala Pro His Arg Ala Pro Glu Val Phe Cys Ser Arg Ser Ser
 50 55 60
 Arg Gly Ala Gly Arg Gly His Pro Thr Pro Thr Pro Arg Val Arg Trp
 65 70 75 80
 Ala Leu Ala Gly Asn Gln Pro Arg Cys Cys Ala Gln Leu Leu Ser Gly
 85 90 95
 Arg Arg Gly Ser Gly Ala Gln Leu Arg Ala Gly Trp Val Arg Gly Pro
 100 105 110
 Ala Val Gly Asn Leu Phe Ile Leu Leu Leu Gly Lys Glu Asp Gly Glu
 115 120 125
 Glu Glu Gly Thr Val Leu Ser Tyr Ser Ser Met Val His Ile Ser Asn
 130 135 140
 Ile Thr Gly Ile Val Gly Thr Thr Val Ser Lys Thr Lys Pro Ala Leu
 145 150 155 160
 Val Leu Met Glu Leu Thr Phe
 165

<210> 2152

<211> 104

<212> PRT

<213> Homo sapiens

<400> 2152

Met Arg Pro Gly Pro Gly Phe Glu Gly Pro Gly Ser Trp Asp Leu Gly
 1 5 10 15
 Val Ala Gly Leu Arg Ser Pro Glu Gly Leu Gly Asp Pro Gly Val Trp
 20 25 30

Gly Ser Trp Val Ala Ala Ser Pro Ala Lys Glu Glu Glu Ala Ala Arg
 35 40 45
 Ala Gly Arg Ala Gln Pro Leu Gly Val Glu Gln Met Thr Pro Leu Pro
 50 55 60
 Arg Pro Arg Ala Trp Asp Leu Ile Pro Gly Arg Gly Glu Glu Ala Leu
 65 70 75 80
 Ala Ala Ser Leu Gln Pro Cys Phe Leu Val Leu Val Lys Ser Gln Asn
 85 90 95
 Gly Arg Arg Arg Glu Ser Leu Ile
 100

<210> 2153

<211> 114

<212> PRT

<213> Homo sapiens

<400> 2153

Met Phe Thr Ser Lys Ser Asn Ser Val Ser Pro Ser Pro Ser Leu Glu
 1 5 10 15
 Gln Ala Asp Ser Asp Ala Leu Asp Ile Ser Thr Lys Val Gln Leu Tyr
 20 25 30
 Gly Val Leu Trp Lys Arg Pro Phe Gly Arg Pro Ser Ala Lys Trp Ser
 35 40 45
 Arg Arg Phe Phe Ile Ile Lys Glu Ser Phe Leu Leu Tyr Tyr Ser Glu
 50 55 60
 Ser Glu Lys Lys Ser Phe Glu Thr Asn Lys Tyr Phe Asn Ile His Pro
 65 70 75 80
 Lys Val Arg Arg Pro Leu Pro Gly Pro Gln Gln Gly Arg Ala Gln Cys

	85	90	95
Gly His Gln Ser Leu His Leu Val Arg Gly Gly Asp Cys Ala Leu Ala			
100	105	110	
Leu Ala			

<210> 2154

<211> 122

<212> PRT

<213> Homo sapiens

<400> 2154

Met Ser Arg His Ala Ala Met Gly Leu Arg Pro Glu Ser Ala Gly Cys			
1	5	10	15
Leu Cys Leu Ala Leu Pro Leu Pro Asp Arg Ala Leu Ser Phe Gln Lys			
20	25	30	
Gln Lys Lys Gly Gln Pro Gln Arg Val Ala Glu Arg Gln Gln Ser Pro			
35	40	45	
Pro Gly Gln Gly Gln Leu Gly Val Pro Pro Ser Pro Leu Arg Arg Gly			
50	55	60	
Ala Thr Arg Ala Leu Val Thr Ser Gly His Ser Pro Ala Pro Ser Pro			
65	70	75	80
Cys Gly Ala Ala Gly Thr Gly Gly Ser Leu Leu Arg Ala Gly Gly Thr			
85	90	95	
Ala Lys Glu Ala Pro Asp Ser Leu Phe Phe Phe Phe Glu Thr Glu Ser			
100	105	110	
Leu Cys His Pro Gly Trp Ser Ala Val Ala			
115	120		

<210> 2155

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2155

Met Ala Ala Thr Gly Phe Ser Ala Pro Asn Gly Ser Cys His Gly Thr

1 5 10 15

Ser Arg Thr Val Asn Ser Asp Ala Pro Met Ser Pro Glu Leu Pro Lys

20 25 30

Pro His Leu Pro Asp Gln Leu Val Ile Val Asn Glu Thr Glu Ala Asp

35 40 45

Ser Lys Pro Ser Lys Asn Val Ala Arg Ser Ala Ala Val Glu Thr Ala

50 55 60

Ser Leu Ser Pro Ser Leu Val Pro Ala Arg Gln Pro Thr Ile Ser Leu

65 70 75 80

Leu Cys Glu Asp Thr Ala Asp Thr Leu Ser Val Glu Ser Leu Thr Leu

85 90 95

Val Pro Pro Val Asp Pro His Ser Leu Arg Ser Leu Thr Gly Met Pro

100 105 110

Pro Leu Ser Thr Pro Ala Ala Ala Cys Thr Glu Pro Val Gly Glu Glu

115 120 125

Ala Ala Cys Ala Glu Pro Val Gly Thr Ala Glu Asp

130 135 140

<210> 2156

<211> 149

<212> PRT

<213> Homo sapiens

<400> 2156

Met Leu Val Val Ser Ile Phe Ile Ile Ile Lys Ile Phe Pro Cys Ser

1 5 10 15

Leu Phe Pro Ala Ser Lys Phe Pro Lys Pro Tyr Ile Gly Thr Pro Phe

20 25 30

Val Lys Gln Ile Lys Ala Lys Gly Leu Trp Leu Lys Ser Trp Gly Arg

35 40 45

Asp Pro Gly Met Thr Ser Ser Met Trp Phe Pro Ile His Thr Ser Gln

50 55 60

Gly Pro Leu Arg Asn Pro Gly Ala Leu Pro Lys Gln Phe Glu Pro Leu

65 70 75 80

Val Trp Thr Leu Gly Asn Thr Gly Trp Gln Val Pro Phe Val Cys Leu

85 90 95

Ser Thr Cys Ser Pro Trp Leu Pro Asp Ser Pro Pro Ser Val Ser Gly

100 105 110

Ser His Ser Val Thr Ser Gln Leu Ser Arg Glu Cys Phe Gly Ala Thr

115 120 125

Val Pro Val Ala Gly Ser Thr His Ser His Ser Ser Phe Phe Phe Ala

130 135 140

Asn Arg Ile Gln Leu

145

<210> 2157

<211> 399

<212> PRT

<213> Homo sapiens

<400> 2157

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Met Ser Arg Arg Asp Ser Glu Ser Thr Arg His Asp Ser Glu Thr Glu
  1              5              10              15
Asp Met Leu Trp Asp Asp Leu Leu His Gly Pro Glu Cys Arg Ser Ser
      20              25              30
Val Thr Ser Asp Ser Glu Gly Ala His Val Asn Thr Leu His Ser Gly
      35              40              45
Thr Lys Arg Asp Pro Lys Glu Asp Val Phe Gln Gln Asn His Leu Phe
      50              55              60
Trp Leu Gln Asn Ser Ser Pro Ser Ser Asp Arg Val Ser Ala Ile Ile
      65              70              75              80
Trp Glu Gly Asn Glu Cys Lys Lys Met Asp Met Ser Val Leu Glu Ile
      85              90              95
Ser Gly Ile Ile Met Ser Arg Val Asn Ala Tyr Gln Gln Gly Val Gly
      100              105              110
Tyr Gln Met Leu Gly Asn Val Val Thr Ile Gly Leu Ala Phe Phe Pro
      115              120              125
Phe Leu His Arg Leu Phe Arg Glu Lys Ser Leu Asp Gln Leu Lys Ser
      130              135              140
Ile Ser Ala Glu Glu Ile Leu Thr Leu Phe Cys Gly Ala Pro Pro Val
      145              150              155              160
Thr Pro Ile Ile Val Leu Ser Ile Ile Asn Phe Phe Glu Arg Leu Cys
      165              170              175
Leu Thr Trp Met Phe Phe Phe Met Met Cys Val Ala Glu Arg Thr Tyr
      180              185              190
Lys Gln Arg Phe Leu Phe Ala Lys Leu Phe Ser His Ile Thr Ser Ala

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195	200	205
Arg Lys Ala Arg Lys Tyr Glu Ile Pro His Phe Arg Leu Lys Lys Val		
210	215	220
Glu Asn Ile Lys Ile Trp Leu Ser Leu Arg Ser Tyr Leu Lys Arg Arg		
225	230	235
Gly Pro Gln Arg Ser Val Asp Val Val Val Ser Ser Val Phe Leu Leu		
245	250	255
Thr Leu Ser Ile Ala Phe Ile Cys Cys Ala Gln Val Leu Gln Gly His		
260	265	270
Lys Thr Phe Leu Asn Asp Ala Tyr Asn Trp Glu Phe Leu Ile Trp Glu		
275	280	285
Thr Ala Leu Leu Leu Phe Leu Leu Arg Leu Ala Ser Leu Gly Ser Lys		
290	295	300
Thr Asn Lys Lys Tyr Ser Asn Val Ser Ile Leu Leu Thr Glu Gln Ile		
305	310	315
Asn Leu Tyr Leu Lys Met Glu Lys Lys Pro Asn Lys Lys Glu Gln Leu		
325	330	335
Thr Leu Val Asn Asn Val Leu Lys Leu Ser Thr Lys Leu Leu Lys Glu		
340	345	350
Leu Asp Thr Pro Phe Arg Leu Tyr Gly Leu Thr Met Asn Pro Leu Ile		
355	360	365
Tyr Asn Ile Thr Arg Val Val Ile Leu Ser Ala Val Ser Gly Val Ile		
370	375	380
Ser Asp Leu Leu Gly Phe Asn Ile Arg Leu Trp Lys Ile Lys Ser		
385	390	395

<210> 2158

<211> 129

<212> PRT

<213> Homo sapiens

<400> 2158

Met	Ser	Pro	Val	Phe	Leu	Ile	Ser	Lys	Asn	Ser	Glu	Leu	Pro	Val	Arg
1				5				10					15		
Ala	Gln	Glu	Leu	Ser	Glu	Leu	Pro	Thr	Thr	Leu	Pro	Thr	Pro	His	Ser
			20					25					30		
Val	Ala	Ser	Pro	Leu	Ser	Ser	Leu	Arg	Arg	Arg	Ser	Glu	Ser	Trp	Ser
			35					40					45		
Leu	Cys	Phe	His	Cys	Asn	Leu	Ser	Gln	Gly	Lys	Ser	Ser	Pro	Gly	Tyr
	50					55				60					
Leu	Trp	Asp	Ala	Leu	Ala	Ala	Cys	Glu	Ala	Gln	Met	Ala	Ser	Gly	Thr
65				70						75				80	
Arg	Ile	Leu	Thr	His	Ser	Ala	Val	His	Phe	Ser	Lys	Leu	Glu	Phe	Ala
				85						90				95	
Ile	Gly	Phe	Phe	Arg	Cys	Pro	Thr	Ile	Ile	Tyr	His	Tyr	Leu	Ser	Tyr
			100					105					110		
Ser	Leu	Ser	Ser	Pro	Asn	Pro	Lys	Glu	Arg	Ile	Leu	Ile	Val	Phe	Ile
			115					120					125		

Asn

<210> 2159

<211> 952

<212> PRT

<213> Homo sapiens

<400> 2159

Met	Ala	Met	Glu	Pro	Gly	Ala	Leu	Trp	Thr	Phe	Leu	Gly	His	Leu	Trp
1				5					10					15	
Leu	Leu	Ala	Gly	Pro	Thr	Cys	Glu	Glu	Asp	Val	Asp	Glu	Cys	Leu	Ser
			20					25					30		
Asp	Pro	Cys	Leu	His	Gly	Gly	Thr	Cys	Ser	Asp	Thr	Val	Ala	Gly	Tyr
		35					40						45		
Ile	Cys	Arg	Cys	Pro	Glu	Thr	Trp	Gly	Gly	Arg	Asp	Cys	Ser	Val	Gln
	50						55					60			
Leu	Thr	Gly	Cys	Gln	Gly	His	Thr	Cys	Pro	Leu	Ala	Ala	Thr	Cys	Ile
	65					70				75				80	
Pro	Ile	Phe	Glu	Ser	Gly	Val	His	Ser	Tyr	Val	Cys	His	Cys	Pro	Pro
						85				90				95	
Gly	Ala	His	Gly	Pro	Phe	Cys	Gly	Gln	Asn	Thr	Thr	Phe	Ser	Val	Met
			100					105					110		
Ala	Gly	Ser	Pro	Ile	Gln	Ala	Ser	Val	Pro	Ala	Gly	Gly	Pro	Leu	Gly
		115					120					125			
Leu	Ala	Leu	Arg	Phe	Arg	Thr	Thr	Leu	Pro	Ala	Gly	Thr	Leu	Ala	Thr
		130					135					140			
Arg	Asn	Asp	Thr	Lys	Glu	Ser	Leu	Glu	Leu	Ala	Leu	Val	Ala	Ala	Thr
	145					150				155				160	
Leu	Gln	Ala	Thr	Leu	Trp	Ser	Tyr	Ser	Thr	Thr	Val	Leu	Val	Leu	Arg
						165				170				175	
Leu	Pro	Asp	Leu	Ala	Leu	Asn	Asp	Gly	His	Trp	His	Gln	Val	Glu	Val
			180						185				190		
Val	Leu	His	Leu	Ala	Thr	Leu	Glu	Leu	Arg	Leu	Trp	His	Glu	Gly	Cys
			195						200				205		
Pro	Ala	Arg	Leu	Cys	Val	Ala	Ser	Gly	Pro	Val	Ala	Leu	Ala	Ser	Thr
			210						215					220	

Ala Ser Ala Thr Pro Leu Pro Ala Gly Ile Ser Ser Ala Gln Leu Gly
225 230 235 240
Asp Ala Thr Phe Ala Gly Cys Leu Gln Asp Val Arg Val Asp Gly His
245 250 255
Leu Leu Leu Pro Glu Asp Leu Gly Glu Asn Val Leu Leu Gly Cys Glu
260 265 270
Arg Arg Glu Gln Cys Arg Pro Leu Pro Cys Val His Gly Gly Ser Cys
275 280 285
Val Asp Leu Trp Thr His Phe Arg Cys Asp Cys Ala Arg Pro His Arg
290 295 300
Gly Pro Thr Cys Ala Asp Glu Ile Pro Ala Ala Thr Phe Gly Leu Gly
305 310 315 320
Gly Ala Pro Ser Ser Ala Ser Phe Leu Leu Gln Glu Leu Pro Gly Pro
325 330 335
Asn Leu Thr Val Ser Phe Leu Leu Arg Thr Arg Glu Ser Ala Gly Leu
340 345 350
Leu Leu Gln Phe Ala Asn Asp Ser Ala Ala Gly Leu Thr Val Phe Leu
355 360 365
Ser Glu Gly Arg Ile Arg Ala Glu Ala Pro Gly Ser Pro Ala Val Val
370 375 380
Leu Pro Gly Arg Trp Asp Asp Gly Leu Arg His Leu Val Met Leu Ser
385 390 395 400
Phe Gly Pro Asp Gln Leu Gln Asp Leu Gly Gln His Val His Val Gly
405 410 415
Gly Arg Leu Leu Ala Ala Asp Ser Gln Pro Trp Gly Gly Pro Phe Arg
420 425 430
Gly Cys Leu Gln Asp Leu Arg Leu Asp Gly Cys His Leu Pro Phe Phe
435 440 445
Pro Leu Pro Leu Asp Asn Ser Ser Gln Pro Ser Glu Leu Gly Gly Arg

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Gly Leu Pro Leu Pro Leu Ala Arg Pro Arg Pro Gly Ala Ala Pro Gly
690 695 700
Ala Arg Glu His Phe Ala Ser Trp Pro Gly Thr Pro Ala Pro Ile Leu
705 710 715 720
Gly Cys Arg Gly Ala Pro Val Cys Ala Pro Ser Pro Cys Leu His Asp
725 730 735
Gly Ala Cys Arg Asp Leu Phe Asp Ala Phe Ala Cys Ala Cys Gly Pro
740 745 750
Gly Trp Glu Gly Pro Arg Cys Glu Ala His Val Asp Pro Cys His Ser
755 760 765
Ala Pro Cys Ala Arg Gly Arg Cys His Thr His Pro Asp Gly Arg Phe
770 775 780
Glu Cys Arg Cys Pro Pro Gly Phe Gly Gly Pro Arg Cys Arg Leu Pro
785 790 795 800
Val Pro Ser Lys Glu Cys Ser Leu Asn Val Thr Cys Leu Asp Gly Ser
805 810 815
Pro Cys Glu Gly Arg Ser Pro Ala Ala Asn Cys Ser Cys Leu Glu Gly
820 825 830
Leu Ala Gly Gln Arg Cys Gln Val Pro Thr Leu Pro Cys Glu Ala Asn
835 840 845
Pro Cys Leu Asn Gly Gly Thr Cys Arg Ala Ala Gly Gly Val Ser Glu
850 855 860
Cys Ile Cys Asn Ala Arg Phe Ser Gly Gln Phe Cys Glu Val Ala Lys
865 870 875 880
Gly Leu Pro Leu Pro Leu Pro Phe Pro Leu Leu Glu Val Ala Val Pro
885 890 895
Ala Ala Cys Ala Cys Leu Leu Leu Leu Leu Gly Leu Leu Ser Gly Ile
900 905 910
Leu Ala Ala Arg Lys Arg Arg Gln Ser Glu Gly Thr Tyr Ser Pro Ser

915 920 925
 Gln Gln Glu Val Ala Gly Ala Arg Leu Glu Met Asp Ser Val Leu Lys
 930 935 940
 Val Pro Pro Glu Glu Arg Leu Ile
 945 950

<210> 2160

<211> 749

<212> PRT

<213> Homo sapiens

<400> 2160

Met Gln Arg Pro Ser Val Ser Arg Ala Glu Asn Tyr Gln Leu Leu Trp
 1 5 10 15
 Asp Thr Ile Ala Ser Leu Lys Gln Cys Glu Gln Ala Met Gln His Ala
 20 25 30
 Phe Ile Pro Val Asn Gly Thr Glu Ile Glu Tyr Glu Phe Glu Glu Ile
 35 40 45
 Thr Leu Glu Arg Gly Asn Ser Gly Leu Gly Phe Ser Ile Ala Gly Gly
 50 55 60
 Thr Asp Asn Pro His Ile Gly Asp Asp Pro Gly Ile Phe Ile Thr Lys
 65 70 75 80
 Ile Ile Pro Gly Gly Ala Ala Ala Glu Asp Gly Arg Leu Arg Val Asn
 85 90 95
 Asp Cys Ile Leu Arg Val Asn Glu Val Asp Val Ser Glu Val Ser His
 100 105 110
 Ser Lys Ala Val Glu Ala Leu Lys Glu Ala Gly Ser Ile Val Arg Leu
 115 120 125

Tyr Val Arg Arg Arg Arg Pro Ile Leu Glu Thr Val Val Glu Ile Lys
130 135 140
Leu Phe Lys Gly Pro Lys Gly Leu Gly Phe Ser Ile Ala Gly Gly Val
145 150 155 160
Gly Asn Gln His Ile Pro Gly Asp Asn Ser Ile Tyr Val Thr Lys Ile
165 170 175
Ile Asp Gly Gly Ala Ala Gln Lys Asp Gly Arg Leu Gln Val Gly Asp
180 185 190
Arg Leu Leu Met Val Asn Asn Tyr Ser Leu Glu Glu Val Thr His Glu
195 200 205
Glu Ala Val Ala Ile Leu Lys Asn Thr Ser Glu Val Val Tyr Leu Lys
210 215 220
Val Gly Lys Pro Thr Thr Ile Tyr Met Thr Asp Pro Tyr Gly Pro Pro
225 230 235 240
Asp Ile Thr His Ser Tyr Ser Pro Pro Met Glu Asn His Leu Leu Ser
245 250 255
Gly Asn Asn Gly Thr Leu Glu Tyr Lys Thr Ser Leu Pro Pro Ile Ser
260 265 270
Pro Gly Arg Tyr Ser Pro Ile Pro Lys His Met Leu Val Asp Asp Asp
275 280 285
Tyr Thr Ser His Ser Gln His Ser Thr Ala Thr Arg Gln Pro Ser Met
290 295 300
Thr Leu Gln Arg Ala Val Ser Leu Glu Gly Glu Pro Arg Lys Val Val
305 310 315 320
Leu His Lys Gly Ser Thr Gly Leu Gly Phe Asn Ile Val Gly Gly Glu
325 330 335
Asp Gly Glu Gly Ile Phe Val Ser Phe Ile Leu Ala Gly Gly Pro Ala
340 345 350
Asp Leu Ser Gly Glu Leu Gln Arg Gly Asp Gln Ile Leu Ser Val Asn

355	360	365
Gly Ile Asp Leu Arg Gly Ala Ser His Glu Gln Ala Ala Ala Ala Leu		
370	375	380
Lys Gly Ala Gly Gln Thr Val Thr Ile Ile Ala Gln Tyr Gln Pro Glu		
385	390	395
Asp Tyr Ala Arg Phe Glu Ala Lys Ile His Asp Leu Arg Glu Gln Met		
405	410	415
Met Asn His Ser Met Ser Ser Gly Ser Gly Ser Leu Arg Thr Asn Gln		
420	425	430
Lys Arg Ser Leu Tyr Val Arg Ala Met Phe Asp Tyr Asp Lys Ser Lys		
435	440	445
Asp Ser Gly Leu Pro Ser Gln Gly Leu Ser Phe Lys Tyr Gly Asp Ile		
450	455	460
Leu His Val Ile Asn Ala Ser Asp Asp Glu Trp Trp Gln Ala Arg Arg		
465	470	475
Val Met Leu Glu Gly Asp Ser Glu Glu Met Gly Val Ile Pro Ser Lys		
485	490	495
Arg Arg Val Glu Arg Lys Glu Arg Ala Arg Leu Lys Thr Val Lys Phe		
500	505	510
Asn Ala Lys Pro Gly Val Ile Asp Ser Lys Gly Asp Ile Pro Gly Leu		
515	520	525
Gly Asp Asp Gly Tyr Gly Thr Lys Thr Leu Arg Gly Gln Glu Asp Leu		
530	535	540
Ile Leu Ser Tyr Glu Pro Val Thr Arg Gln Glu Ile Asn Tyr Thr Arg		
545	550	555
Pro Val Ile Ile Leu Gly Pro Met Lys Asp Arg Ile Asn Asp Asp Leu		
565	570	575
Ile Ser Glu Phe Pro Asp Lys Phe Gly Ser Cys Val Pro His Thr Thr		
580	585	590

Arg Pro Lys Arg Asp Tyr Glu Val Asp Gly Arg Asp Tyr His Phe Val
595 600 605

Ile Ser Arg Glu Gln Met Glu Lys Asp Ile Gln Glu His Lys Phe Ile
610 615 620

Glu Ala Gly Gln Tyr Asn Asp Asn Leu Tyr Gly Thr Ser Val Gln Ser
625 630 635 640

Val Arg Phe Val Ala Glu Arg Gly Lys His Cys Ile Leu Asp Val Ser
645 650 655

Gly Asn Ala Ile Lys Arg Leu Gln Val Ala Gln Leu Tyr Pro Ile Ala
660 665 670

Ile Phe Ile Lys Pro Arg Ser Leu Glu Pro Leu Met Glu Met Asn Lys
675 680 685

Arg Leu Thr Glu Glu Gln Ala Lys Lys Thr Tyr Asp Arg Ala Ile Lys
690 695 700

Leu Glu Gln Glu Phe Gly Glu Tyr Phe Thr Ala Ile Val Gln Gly Asp
705 710 715 720

Thr Leu Glu Asp Ile Tyr Asn Gln Cys Lys Leu Val Ile Glu Glu Gln
725 730 735

Ser Gly Pro Phe Ile Trp Ile Pro Ser Lys Glu Lys Leu
740 745

<210> 2161

<211> 304

<212> PRT

<213> Homo sapiens

<400> 2161

Met Gln Glu Trp Val Val Leu Glu Ile Tyr Ser Pro Leu Ile Ser Gln

1	5	10	15
Gln Asp Phe Ile Gln Ile Arg Leu Arg Glu Asp Leu Lys Pro Trp Glu			
20	25	30	
Lys Ser Pro Ile Leu Lys Ile Ser Ala Pro Gln Pro Ile Pro Ser Asn			
35	40	45	
Arg Ile Asp Thr Thr Ser Ser Ala Ser Trp Val Ala Gly Ser Phe Ser			
50	55	60	
Pro Val Ser Pro Pro Val Val Asp Leu Arg Thr Ile Met Glu Ile Glu			
65	70	75	80
Glu Ser Arg Gln Lys Cys Gly Ala Thr Pro Lys Ser His Leu Gly Lys			
85	90	95	
Thr Val Ser His Gly Val Lys Leu Ser Gln Lys Gln Arg Lys Met Ile			
100	105	110	
Ala Leu Thr Thr Lys Glu Asn Asn Ser Gly Met Asn Ser Met Glu Thr			
115	120	125	
Val Leu Phe Thr Pro Ser Lys Ala Pro Lys Pro Val Asn Ala Trp Ala			
130	135	140	
Ser Ser Leu His Ser Val Ser Ser Lys Ser Phe Arg Asp Phe Leu Leu			
145	150	155	160
Glu Glu Lys Lys Ser Val Thr Ser His Ser Ser Gly Asp His Val Lys			
165	170	175	
Lys Val Ser Phe Lys Gly Ile Glu Asn Ser Gln Ala Pro Lys Ile Val			
180	185	190	
Arg Cys Ser Thr His Gly Thr Pro Gly Pro Glu Gly Asn His Ile Ser			
195	200	205	
Asp Leu Pro Leu Leu Asp Ser Pro Asn Pro Trp Leu Ser Ser Ser Val			
210	215	220	
Thr Ala Pro Ser Met Val Ala Pro Val Thr Phe Ala Ser Ile Val Glu			
225	230	235	240

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	100		105		110										
Asn	Pro	Phe	Tyr	Asn	Pro	Gly	Asp	Arg	Ile	Gln	Ser	Arg	Trp	Ala	Leu
	115		120		125										
Leu	Ser	Val	Ser	Ala	Ser	Ser	Pro	Gly	Gly	Pro	Tyr	Phe	Leu	Cys	Leu
	130		135		140										
His	Pro	Val	Gln	Val	Gly	Leu	Thr	Phe	Cys	Val	Leu	Pro	Pro	Ser	Phe
145			150		155						160				
Cys	Arg	Thr	Cys	Leu	Ala	Ile	Leu	Val	Ala	Lys	Met	Gln	Pro	Phe	Gly
			165		170						175				
Lys															

<210> 2163

<211> 170

<212> PRT

<213> Homo sapiens

<400> 2163

Met	Pro	Leu	His	Ser	Ser	Leu	Ala	Thr	Glu	Arg	Asp	Ser	Ile	Ser	Lys
1				5					10					15	
Lys	Gln	Lys	Ile	Glu	Met	Ala	Ser	Arg	Cys	Val	Ala	Trp	Val	Gly	Leu
			20					25				30			
Glu	Leu	Leu	Ser	Ser	Asn	Asp	Pro	Leu	Thr	Ser	Ala	Ser	Glu	Ser	Ala
			35					40				45			
Gly	Ile	Ile	Gly	Val	Ser	His	Gly	Ala	Arg	Pro	Pro	Arg	Gly	Val	Leu
	50						55				60				
Ser	Pro	Pro	Gly	Ile	Ala	Val	Trp	Cys	Glu	Val	Gly	Ser	Gly	Leu	Val
65					70					75				80	

Ser His Leu Gly Cys Glu Pro Ala Cys Leu Ala Ser Trp Ser Gln Ala
 85 90 95
 Ser Cys Asp Leu Asp Leu Gly Pro Pro Ser Ser Phe Val Leu Ser Leu
 100 105 110
 Ser Leu Arg Leu Gly Gly His Pro Leu Ser Pro Glu Trp Ser Trp Arg
 115 120 125
 Val Arg Ser Leu Val Arg Pro Cys Thr Val Gly Gly Thr Leu Ser Pro
 130 135 140
 Glu Arg Ser Trp Arg Val Arg Ser Leu Val Arg Leu Cys Thr Trp Ala
 145 150 155 160
 Ala Pro Cys Leu Gln Asn Gly Pro Gly Val
 165 170

<210> 2164

<211> 146

<212> PRT

<213> Homo sapiens

<400> 2164

Met His Phe Leu Gly Leu Pro Ile Ile Lys Tyr Pro Lys Leu Gly Gly
 1 5 10 15
 Arg Lys Gln His Thr Tyr Ser Leu Pro Val Leu Glu Thr Gly Ser Leu
 20 25 30
 Gln Ser Arg Cys Arg Gln Asp Cys Cys Leu Phe Glu Val Pro Leu Gly
 35 40 45
 Arg Thr Leu Leu Ser Pro Pro Asp Arg Pro Gly Ser Trp Trp Pro Leu
 50 55 60
 Ala Ser Ile Ser Pro Ser Ser Leu Pro Pro Phe Ser Cys Gly Leu Leu

65 70 75 80
 Cys Leu Cys Leu Ser Arg Thr Pro Val Val Leu Asp Gln Gly Pro Thr
 85 90 95
 Leu Leu Gln Leu Ser Ser Ser Phe Phe Phe Phe Phe Phe Phe Trp Arg
 100 105 110
 Arg Ser Leu Ala Leu Ser Pro Arg Leu Glu Phe Ser Gly Thr Ile Ser
 115 120 125
 Ala His Cys Lys Leu Cys Leu Pro Gly Ser His His Ser Pro Ala Ser
 130 135 140
 Ala Ser
 145

<210> 2165

<211> 179

<212> PRT

<213> Homo sapiens

<400> 2165

Met Gly Lys Tyr Leu Ser Phe Leu Phe Met Ser Val Ser Arg Ser Ala
 1 5 10 15
 Lys His Cys Phe Phe Ser Leu Ser Leu Leu Ala Ser Val Asn Lys Lys
 20 25 30
 Glu Met Leu Asn Phe Ser Ser Ile His Glu Asn Lys Glu Ile Ser Val
 35 40 45
 Ser Pro Gln Val Arg Gly Pro Phe Gly Gly Gln Met Val Lys Thr Arg
 50 55 60
 Ala Cys Met Gly Leu Ser Met Ala Trp Gly Ser Cys Cys Ser Pro Gly
 65 70 75 80

Gly Cys Leu Pro Arg Gln Gly Lys Leu Arg Ser Pro Leu Glu Leu Gln
 85 90 95
 Gly His Gln Ala His Gly Pro Leu Ser Asp Ser Ser Leu Ser Val Cys
 100 105 110
 Lys Arg Gly Thr Cys His Gln Leu Ile Pro Cys Ser Ser Ser Gln Ala
 115 120 125
 Ser Thr Pro Lys Glu Glu Glu Val Leu Arg Gln Gly Pro Gly Leu Thr
 130 135 140
 Ser Gly Glu Ala Gly Gly Trp Pro Leu Ser Ala Ser Phe Leu Gln His
 145 150 155 160
 Arg Ser Ser Ala Thr His Arg His Pro Ala Gln Trp Pro Glu Arg Ser
 165 170 175
 Pro Arg Val

<210> 2166

<211> 756

<212> PRT

<213> Homo sapiens

<400> 2166

Met Glu Glu Glu Leu Lys Cys Pro Val Cys Gly Ser Leu Phe Arg Glu
 1 5 10 15
 Pro Ile Ile Leu Pro Arg Ser His Asn Val Cys Leu Pro Cys Ala Arg
 20 25 30
 Thr Ile Ala Val Gln Thr Pro Asp Gly Glu Gln His Leu Pro Gln Pro
 35 40 45
 Leu Leu Leu Ser Arg Gly Ser Gly Leu Gln Ala Gly Ala Ala Ala Ala

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Ala Gly Ala Thr Gly Gly Ser Thr Ala Arg Lys Phe Pro Thr Cys Pro
 290 295 300
 Glu His Glu Met Glu Asn Tyr Ser Met Tyr Cys Val Ser Cys Arg Thr
 305 310 315 320
 Pro Val Cys Tyr Leu Cys Leu Glu Glu Gly Arg His Ala Lys His Glu
 325 330 335
 Val Lys Pro Leu Gly Ala Met Trp Lys Gln His Lys Ala Gln Leu Ser
 340 345 350
 Gln Ala Leu Asn Gly Val Ser Asp Lys Ala Lys Glu Ala Lys Glu Phe
 355 360 365
 Leu Val Gln Leu Lys Asn Ile Leu Gln Gln Ile Gln Glu Asn Gly Leu
 370 375 380
 Asp Tyr Glu Ala Cys Leu Val Ala Gln Cys Asp Ala Leu Val Asp Ala
 385 390 395 400
 Leu Thr Arg Gln Lys Ala Lys Leu Leu Thr Lys Val Thr Lys Glu Arg
 405 410 415
 Glu His Lys Leu Lys Met Val Trp Asp Gln Ile Asn His Cys Thr Leu
 420 425 430
 Lys Leu Arg Gln Ser Thr Gly Leu Met Glu Tyr Cys Leu Glu Val Ile
 435 440 445
 Lys Glu Asn Asp Pro Ser Gly Phe Leu Gln Ile Ser Asp Ala Leu Ile
 450 455 460
 Lys Arg Val Gln Val Ser Gln Glu Gln Trp Val Lys Gly Ala Leu Glu
 465 470 475 480
 Pro Lys Val Ser Ala Glu Phe Asp Leu Thr Leu Asp Ser Glu Pro Leu
 485 490 495
 Leu Gln Ala Ile His Gln Leu Asp Phe Ile Gln Met Lys Cys Arg Val
 500 505 510
 Pro Pro Val Pro Leu Leu Gln Leu Glu Lys Cys Cys Thr Arg Asn Asn

515 520 525
Ser Val Thr Leu Ala Trp Arg Met Pro Pro Phe Thr His Ser Pro Val
530 535 540
Asp Gly Tyr Ile Leu Glu Leu Asp Asp Gly Ala Gly Gly Gln Phe Arg
545 550 555 560
Glu Val Tyr Val Gly Lys Glu Thr Leu Cys Thr Ile Asp Gly Leu His
565 570 575
Phe Asn Ser Thr Tyr Asn Ala Arg Val Lys Ala Phe Asn Ser Ser Gly
580 585 590
Val Gly Pro Tyr Ser Lys Thr Val Val Leu Gln Thr Ser Asp Val Ala
595 600 605
Trp Phe Thr Phe Asp Pro Asn Ser Gly His Arg Asp Ile Ile Leu Ser
610 615 620
Asn Asp Asn Gln Thr Ala Thr Cys Ser Ser Tyr Asp Asp Arg Val Val
625 630 635 640
Leu Gly Thr Ala Ala Phe Ser Lys Gly Val His Tyr Trp Glu Leu His
645 650 655
Val Asp Arg Tyr Asp Asn His Pro Asp Pro Ala Phe Gly Val Ala Arg
660 665 670
Ala Ser Val Val Lys Asp Val Met Leu Gly Lys Asp Asp Lys Ala Trp
675 680 685
Ala Met Tyr Val Asp Asn Asn Arg Ser Trp Phe Met His Cys Asn Ser
690 695 700
His Thr Asn Arg Thr Glu Gly Gly Val Cys Lys Gly Ala Thr Val Gly
705 710 715 720
Val Leu Leu Asp Leu Asn Lys His Thr Leu Thr Phe Phe Ile Asn Gly
725 730 735
Gln Gln Gln Gly Pro Thr Ala Phe Arg His Gln Val Gln Pro Ser Val
740 745 750

Thr Ser Leu Phe

755

<210> 2167

<211> 1246

<212> PRT

<213> Homo sapiens

<400> 2167

Met Val Pro Ala Gly Asp Gln Asp Arg Ala Pro His Arg Gly Lys Pro

1 5 10 15

Ala Gln Ala Gly Ala Arg Thr Ser Arg Ala Ser Arg Ala Leu Arg Ser

20 25 30

Trp Arg Arg Ser Gln Ala Ala Arg Ala Thr Val Thr His Pro Arg Gly

35 40 45

Gly His Asp Arg Gly Ser His Gly Gly Tyr Arg Glu Gly His Arg Gly

50 55 60

Cys Arg Arg Asp Pro Gln Trp Ala Ser Ala Gly Pro Pro Pro Leu Ser

65 70 75 80

Phe Thr Glu Glu Val Lys Phe Glu Leu Arg Ala Leu Lys Asp Trp Asp

85 90 95

Phe Lys Met Ser Val Pro Asp Tyr Met Gln Cys Ala Glu Asp His Gln

100 105 110

Thr Leu Leu Val Val Val Gln Pro Val Gly Ile Val Ser Glu Glu Asn

115 120 125

Phe Phe Arg Ile Tyr Lys Arg Ile Cys Ser Val Ser Gln Ile Ser Val

130 135 140

Arg Asp Ser Gln Arg Val Leu Tyr Ile Arg Tyr Arg His His Tyr Pro

145	150	155	160
Pro Glu Asn Asn Glu Trp Gly Asp Phe Gln Thr His Arg Lys Val Val			
	165	170	175
Gly Leu Ile Thr Ile Thr Asp Cys Phe Ser Ala Lys Asp Trp Pro Gln			
	180	185	190
Thr Phe Glu Lys Phe His Val Gln Lys Glu Ile Tyr Gly Ser Thr Leu			
	195	200	205
Tyr Asp Ser Arg Leu Phe Val Phe Gly Leu Gln Gly Glu Ile Val Glu			
	210	215	220
Gln Pro Arg Thr Asp Val Ala Phe Tyr Pro Asn Tyr Glu Asp Cys Gln			
	225	230	235
Thr Val Glu Lys Arg Ile Glu Asp Phe Ile Glu Ser Leu Phe Ile Val			
	245	250	255
Leu Glu Ser Lys Arg Leu Asp Arg Ala Thr Asp Lys Ser Gly Asp Lys			
	260	265	270
Ile Pro Leu Leu Cys Val Pro Phe Glu Lys Lys Asp Phe Val Gly Leu			
	275	280	285
Asp Thr Asp Ser Arg His Tyr Lys Lys Arg Cys Gln Gly Arg Met Arg			
	290	295	300
Lys His Val Gly Asp Leu Cys Leu Gln Ala Gly Met Leu Gln Asp Ser			
	305	310	315
Leu Val His Tyr His Met Ser Val Glu Leu Leu Arg Ser Val Asn Asp			
	325	330	335
Phe Leu Trp Leu Gly Ala Ala Leu Glu Gly Leu Cys Ser Ala Ser Val			
	340	345	350
Ile Tyr His Tyr Pro Gly Gly Thr Gly Gly Lys Ser Gly Ala Arg Arg			
	355	360	365
Phe Gln Gly Ser Thr Leu Pro Ala Glu Ala Ala Asn Arg His Arg Pro			
	370	375	380

Gly Ala Gln Glu Val Leu Ile Asp Pro Gly Ala Leu Thr Thr Asn Gly
 385 390 395 400
 Ile Asn Pro Asp Thr Ser Thr Glu Ile Gly Arg Ala Lys Asn Cys Leu
 405 410 415
 Ser Pro Glu Asp Ile Ile Asp Lys Tyr Lys Glu Ala Ile Ser Tyr Tyr
 420 425 430
 Ser Lys Tyr Lys Asn Ala Gly Val Ile Glu Leu Glu Ala Cys Ile Lys
 435 440 445
 Ala Val Arg Val Leu Ala Ile Gln Lys Arg Ser Met Glu Ala Ser Glu
 450 455 460
 Phe Leu Gln Asn Ala Val Tyr Ile Asn Leu Arg Gln Leu Ser Glu Glu
 465 470 475 480
 Glu Lys Ile Gln Arg Tyr Ser Ile Leu Ser Glu Leu Tyr Glu Leu Ile
 485 490 495
 Gly Phe His Arg Lys Ser Ala Phe Phe Lys Arg Val Ala Ala Met Gln
 500 505 510
 Cys Val Ala Pro Ser Ile Ala Glu Pro Gly Trp Arg Ala Cys Tyr Lys
 515 520 525
 Leu Leu Leu Glu Thr Leu Pro Gly Tyr Ser Leu Ser Leu Asp Pro Lys
 530 535 540
 Asp Phe Ser Arg Gly Thr His Arg Gly Trp Ala Ala Val Gln Met Arg
 545 550 555 560
 Leu Leu His Glu Leu Val Tyr Ala Ser Arg Arg Met Gly Asn Pro Ala
 565 570 575
 Leu Ser Val Arg His Leu Ser Phe Leu Leu Gln Thr Met Leu Asp Phe
 580 585 590
 Leu Ser Asp Gln Glu Lys Lys Asp Val Ala Gln Ser Leu Glu Asn Tyr
 595 600 605
 Thr Ser Lys Cys Pro Gly Thr Met Glu Pro Ile Ala Leu Pro Gly Gly

610 615 620
Leu Thr Leu Pro Pro Val Pro Phe Thr Lys Leu Pro Val Val Arg His
625 630 635 640
Val Lys Leu Leu Asn Leu Pro Ala Ser Leu Arg Pro His Lys Met Lys
645 650 655
Ser Leu Leu Gly Gln Asn Val Ser Thr Lys Ser Pro Phe Ile Tyr Ser
660 665 670
Pro Ile Ile Ala His Asn Arg Gly Glu Glu Arg Asn Lys Lys Ile Asp
675 680 685
Phe Gln Trp Val Gln Gly Asp Val Cys Glu Val Gln Leu Met Val Tyr
690 695 700
Asn Pro Met Pro Phe Glu Leu Arg Val Glu Asn Met Gly Leu Leu Thr
705 710 715 720
Ser Gly Val Glu Phe Glu Ser Leu Pro Ala Ala Leu Ser Leu Pro Ala
725 730 735
Glu Ser Gly Leu Tyr Pro Val Thr Leu Val Gly Val Pro Gln Thr Thr
740 745 750
Gly Thr Ile Thr Val Asn Gly Tyr His Thr Thr Val Phe Gly Val Phe
755 760 765
Ser Asp Cys Leu Leu Asp Asn Leu Pro Gly Ile Lys Thr Ser Gly Ser
770 775 780
Thr Val Glu Val Ile Pro Ala Leu Pro Arg Leu Gln Ile Ser Thr Ser
785 790 795 800
Leu Pro Arg Ser Ala His Ser Leu Gln Pro Ser Ser Gly Asp Glu Ile
805 810 815
Ser Thr Asn Val Ser Val Gln Leu Tyr Asn Gly Glu Ser Gln Gln Leu
820 825 830
Ile Ile Lys Leu Glu Asn Ile Gly Met Glu Pro Leu Glu Lys Leu Glu
835 840 845

Val Thr Ser Lys Val Leu Thr Thr Lys Glu Lys Leu Tyr Gly Asp Phe
850 855 860
Leu Ser Trp Lys Leu Glu Glu Thr Leu Ala Gln Phe Pro Leu Gln Pro
865 870 875 880
Gly Lys Val Ala Thr Phe Thr Ile Asn Ile Lys Val Lys Leu Asp Phe
885 890 895
Ser Cys Gln Glu Asn Leu Leu Gln Asp Leu Ser Asp Asp Gly Ile Ser
900 905 910
Val Ser Gly Phe Pro Leu Ser Ser Pro Phe Arg Gln Val Val Arg Pro
915 920 925
Arg Val Glu Gly Lys Pro Val Asn Pro Pro Glu Ser Asn Lys Ala Gly
930 935 940
Asp Tyr Ser His Val Lys Thr Leu Glu Ala Val Leu Asn Phe Lys Tyr
945 950 955 960
Ser Gly Gly Pro Gly His Thr Glu Gly Tyr Tyr Arg Asn Leu Ser Leu
965 970 975
Gly Leu His Val Glu Val Glu Pro Ser Val Phe Phe Thr Arg Val Ser
980 985 990
Thr Leu Pro Ala Thr Ser Thr Arg Gln Cys His Leu Leu Leu Asp Val
995 1000 1005
Phe Asn Ser Thr Glu His Glu Leu Thr Val Ser Thr Arg Ser Ser Glu
1010 1015 1020
Ala Leu Ile Leu His Ala Gly Glu Cys Gln Arg Met Ala Ile Gln Val
1025 1030 1035 1040
Asp Lys Phe Asn Phe Glu Ser Phe Pro Glu Ser Pro Gly Glu Lys Gly
1045 1050 1055
Gln Phe Ala Asn Pro Lys Gln Leu Glu Glu Glu Arg Arg Glu Ala Arg
1060 1065 1070
Gly Leu Glu Ile His Ser Lys Leu Gly Ile Cys Trp Arg Ile Pro Ser

1075 1080 1085
Leu Lys Arg Ser Gly Glu Ala Ser Val Glu Gly Leu Leu Asn Gln Leu
1090 1095 1100
Val Leu Glu His Leu Gln Leu Ala Pro Leu Gln Trp Asp Val Leu Val
1105 1110 1115 1120
Asp Gly Gln Pro Cys Asp Arg Glu Ala Val Ala Ala Cys Gln Val Gly
1125 1130 1135
Asp Pro Val Arg Leu Glu Val Arg Leu Thr Asn Arg Ser Pro Arg Ser
1140 1145 1150
Val Gly Pro Phe Ala Leu Thr Val Val Pro Phe Gln Asp His Gln Asn
1155 1160 1165
Gly Val His Asn Tyr Asp Leu His Asp Thr Val Ser Phe Val Gly Ser
1170 1175 1180
Ser Thr Phe Tyr Leu Asp Ala Val Gln Pro Ser Gly Gln Ser Ala Cys
1185 1190 1195 1200
Leu Gly Ala Leu Leu Phe Leu Tyr Thr Gly Asp Phe Phe Leu His Ile
1205 1210 1215
Arg Phe His Glu Asp Ser Thr Ser Lys Glu Leu Pro Pro Ser Trp Phe
1220 1225 1230
Cys Leu Pro Ser Val His Val Cys Ala Leu Glu Ala Gln Ala
1235 1240 1245

<210> 2168

<211> 110

<212> PRT

<213> Homo sapiens

<400> 2168

Met Trp Ala Val Trp Arg Leu Val Pro Glu Asp Lys Ser Lys Gly Val
 1 5 10 15
 Ala Ser Ser Leu Gly His Gly Asn His Trp Leu Lys Tyr Pro Ile Lys
 20 25 30
 Gln Glu Glu Pro Lys Ser Ser Lys Phe Arg Asp Trp Gln Met Asp Asn
 35 40 45
 Leu His Asn Ser Gly Arg Ala Val Trp Asp Glu Ser Leu Cys Thr Arg
 50 55 60
 Met Leu Ala Ser Pro Ser Pro Asn Thr Val Leu Tyr Ala Gln Glu Thr
 65 70 75 80
 Glu Lys Thr Arg Ser Thr Ile Arg Arg Trp Gly Ser Gln Gln Gly Asn
 85 90 95
 Thr Gly Ala Gln Asp Ile Ser Leu Gly Ser Leu Phe Pro Ser
 100 105 110

<210> 2169

<211> 120

<212> PRT

<213> Homo sapiens

<400> 2169

Met Leu Pro Leu Phe Leu Lys Asp Ile Phe Ala Leu Tyr Glu Ile Leu
 1 5 10 15
 Gly Ser Pro Phe Tyr Phe Ile Leu Phe Leu Arg Pro Ser Leu Thr Leu
 20 25 30
 Ser Pro Arg Leu Glu Cys Ser Gly Thr Ile Leu Ala His Cys Asn Leu
 35 40 45
 His Leu Leu Gly Ser Ser Asp Ser Cys Val Ser Ala Ser Gln Val Ala

50	55	60	
Gly Ile Thr Gly Met His His His Ala Trp Leu Ile Phe Val Phe Leu			
65	70	75	80
Val Glu Met Gly Leu His His Ile Ser Glu Ala Gly Leu Lys Leu Leu			
85	90	95	
Thr Ser Ser Asp Leu Pro Thr Ser Ala Ser Gln Ser Ala Gly Ile Thr			
100	105	110	
Gly Val Ser Tyr Trp Arg Pro Ala			
115	120		

<210> 2170

<211> 125

<212> PRT

<213> Homo sapiens

<400> 2170

Met Leu Ala Val Ala Val Ala Ser Ser Arg Thr Leu Glu Val Leu Asp			
1	5	10	15
Leu Glu Gly Thr Gly Leu Thr Asn Gln Ser Ala Gln Thr Leu Leu Asp			
20	25	30	
Met Val Glu Asn Tyr Pro Thr Ala Leu Arg Ser Leu Val Leu Ala Glu			
35	40	45	
Asn Ser Ile Ser Pro Glu Leu Gln Gln Gln Ile Cys Asp Leu Leu Ser			
50	55	60	
Glu Gly Glu Glu Glu Glu Glu Val Ala Gly Gly Ala Gly Asp Thr Gln			
65	70	75	80
Glu Trp Glu Arg Gly Arg Glu Pro Ala Ala His Gln Arg Gly Ser Ser			
85	90	95	

Ser Trp Met Cys Pro Ser Asp Pro Ser Ser Gln Met Val Leu Met Thr

100

105

110

Ser Gly Leu Gly Asp Ser Leu Leu Ala Glu Thr Glu Met

115

120

125

<210> 2171

<211> 164

<212> PRT

<213> Homo sapiens

<400> 2171

Met Ser Pro Ser Gly Asn Ala Gly Gly Ser Gly Glu Val Ser Cys Lys

1

5

10

15

Cys Ala Ser Thr Gln His Gln Glu Gly Met His Leu Cys Trp Gln Arg

20

25

30

Arg Met Gly Val Ser Asp Ser Thr Ala Gly Ser Thr Cys Ser Val Pro

35

40

45

Gln Val Arg Asp Leu Pro Gly Gln Ala Glu His Leu Gly Ala Gln Val

50

55

60

His Ser Leu Glu Gln Asp Leu Gly Val Gly Asp Leu Gln Val Gln Ala

65

70

75

80

Gly His Leu Glu Ala Gln Ile Asn Ser Gln Glu Gln Asp Leu Ala Thr

85

90

95

Ala Val Ser Pro Ala Leu Ser Pro Ser Ser Trp Arg Asp Thr Pro Ile

100

105

110

Gln Ser Asp Ala Glu Glu Glu Val Pro Pro Leu Leu Asp His Pro Val

115

120

125

Ile His Gln Lys Val Glu His Glu Gln Pro Met Gly Pro Gln Ala Arg

130 135 140
 Ser Gln Asp Pro Ser Gln Trp Trp His Ile Pro Leu Ile Val Leu Ile
 145 150 155 160
 Pro Pro Leu Ile

<210> 2172

<211> 189

<212> PRT

<213> Homo sapiens

<400> 2172

Met Cys Ala Lys Arg Leu Arg Gly Pro Phe Arg Ile Phe Leu Pro Leu
 1 5 10 15
 Arg Lys Tyr Ser Phe Phe Pro Ser Gln Val Ala Gln Pro Phe Ala Ser
 20 25 30
 Ala Ala Val Ala Gln Ala Leu Leu Ser Ser Pro Gly Thr Asn Leu Gln
 35 40 45
 Gln Thr Leu Val Gly Gly Leu Arg Leu Arg His Gly Ser Val Gly Gly
 50 55 60
 Ala Gln Trp Val Val Lys Ala Ala Cys Pro Trp Glu Pro Gln Asp Val
 65 70 75 80
 Ala Cys Cys Gly Gly Phe Thr Val Thr Ala Arg Ile Ala Ala Cys Val
 85 90 95
 Leu Leu Cys Leu Cys Glu His Met Tyr Thr Pro Ser Ala His Ala Arg
 100 105 110
 Met Thr Phe Gly Thr Glu His Leu Leu Leu Trp Pro Ala Gln Arg Arg
 115 120 125

Ala Asp Pro Arg Thr Ala Ala Pro Ile Arg Leu His Gln Gly Gln Leu
 130 135 140
 Asp Pro Ser Arg Asp Pro Glu Asn Leu Arg Ala Trp Ala Val Gly Ser
 145 150 155 160
 Cys Arg Ala Gly Val Glu Leu His Gly Ser Pro Val His Leu His Met
 165 170 175
 Arg Ala Gly Gln His Ile Ser Met Phe Ala Gly Val Ala
 180 185

<210> 2173

<211> 176

<212> PRT

<213> Homo sapiens

<400> 2173

Met Tyr Gly Asn Ser Pro Lys Cys Thr Tyr Ser Arg Ser Ile Ile His
 1 5 10 15
 Tyr Phe Arg Asp Ala Phe Ser Ser Val Ser Gly Tyr Arg Ser Val Gly
 20 25 30
 Met Ala Ser Ser Arg Leu Met Phe Leu Leu Ser Gln Ala Pro Ser Leu
 35 40 45
 Thr Phe Ser Phe Phe Cys Phe Cys Phe Phe Glu Thr Val Ser His Cys
 50 55 60
 Arg Pro Gly Trp Thr Ala Val Ala Arg Ser Leu Leu Thr Ala Pro Ser
 65 70 75 80
 Asp Cys Trp Ile Gln Val Ile Leu Leu Leu Ser Leu Pro Ser Asn Trp
 85 90 95
 Asp His Arg Cys Leu Pro Pro His Pro Ala Asn Phe Phe Val Phe Leu

100	105	110	
Val Glu Thr Gly Ser Cys His	Val Ala Gln Ala Gly Leu Glu Leu Leu		
115	120	125	
Ala Ser Ser His Arg Leu Thr Ser Ala Ser Gln Ser Ala Gly Ile Thr			
130	135	140	
Gly Met Ser His His Ala Gln Pro Phe Gln Pro Phe Leu Leu Leu Pro			
145	150	155	160
Ser Gly Tyr His Asn Asn Phe Asp Glu Leu Leu Phe Lys Gly Ile Leu			
165	170	175	

<210> 2174

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2174

Met Trp Thr Arg Asp Ser Lys Arg Leu Ala Thr Thr Pro Arg His Pro			
1	5	10	15
Ala Glu Lys Trp Trp Val Gly Ile Gln Thr Gln Val Trp Ala Met Ser			
20	25	30	
Trp Pro Ser Phe Leu His Cys Ser Ala Arg Thr Ser Glu Lys Gly Phe			
35	40	45	
Gln Tyr His Ile Ser Gln Glu Ser Ser Thr Asn Asp Arg Val Leu Ile			
50	55	60	
Cys Trp Gln Arg Leu Pro Ser Pro Arg His Leu His Ser Ser Phe Leu			
65	70	75	80
Tyr Leu Leu Gln Ser Leu Ser Ser His Pro Leu Leu Pro Glu Ala Phe			
85	90	95	

Pro Glu His Phe Ile

100

<210> 2175

<211> 137

<212> PRT

<213> Homo sapiens

<400> 2175

Met Pro Gln Phe Gly Thr Leu Cys Phe Gly Glu Pro Leu Glu Arg Met

1 5 10 15

Val Pro Leu Arg Asn Ala Arg Gly Gly Leu Gln Ile Ser Gly Pro Leu

20 25 30

Arg Glu Glu Ser Trp Val Gly Lys Pro His Leu Phe Leu Ala Gly Ile

35 40 45

Pro Gly Arg Lys Cys Cys Pro Leu Leu Val Glu Arg Asn Met Val Ile

50 55 60

Val Ser Gln Pro Glu Ser Leu Gly Asp Ser Arg Glu Ala Ala Thr Arg

65 70 75 80

Ser Cys Ser Leu Ser Gln Arg Gly Trp Arg Arg Lys Gln Leu Val Trp

85 90 95

Asp Glu Gly Met Pro Arg Pro His His Val Ser Lys Gly Val Thr Gly

100 105 110

Met Ile Asn His Ser Ala Cys Glu Lys Pro Val Pro Pro Ser Leu Thr

115 120 125

Gly Thr Cys His Pro Cys Ile Ala Leu

130 135

<210> 2176

<211> 887

<212> PRT

<213> Homo sapiens

<400> 2176

Met Pro Ser Leu Pro Gln Glu Gly Val Ile Gln Gly Pro Ser Pro Leu

1 5 10 15

Asp Leu Asn Thr Glu Leu Pro Tyr Gln Ser Thr Met Lys Arg Lys Val

20 25 30

Arg Lys Lys Lys Lys Lys Gly Thr Ile Thr Ala Asn Val Ala Gly Ala

35 40 45

Lys Phe Glu Ile Val Arg Leu Val Ile Asp Glu Met Gly Phe Met Lys

50 55 60

Thr Pro Asp Glu Asp Glu Thr Ser Asn Leu Ile Trp Cys Asp Ser Ala

65 70 75 80

Val Gln Gln Glu Lys Ile Ser Glu Leu Gln Asn Tyr Gln Arg Ile Asn

85 90 95

His Phe Pro Gly Met Gly Glu Ile Cys Arg Lys Asp Phe Leu Ala Arg

100 105 110

Asn Met Thr Lys Met Ile Lys Ser Arg Pro Leu Asp Tyr Thr Phe Val

115 120 125

Pro Arg Thr Trp Ile Phe Pro Ala Glu Tyr Thr Gln Phe Gln Asn Tyr

130 135 140

Val Lys Glu Leu Lys Lys Lys Arg Lys Gln Lys Thr Phe Ile Val Lys

145 150 155 160

Pro Ala Asn Gly Ala Met Gly His Gly Ile Ser Leu Ile Arg Asn Gly

165 170 175

Asp Lys Leu Pro Ser Gln Asp His Leu Ile Val Gln Glu Tyr Ile Glu
 180 185 190
 Lys Pro Phe Leu Met Glu Gly Tyr Lys Phe Asp Leu Arg Ile Tyr Ile
 195 200 205
 Leu Val Thr Ser Cys Asp Pro Leu Lys Ile Phe Leu Tyr His Asp Gly
 210 215 220
 Leu Val Arg Met Gly Thr Glu Lys Tyr Ile Pro Pro Asn Glu Ser Asn
 225 230 235 240
 Leu Thr Gln Leu Tyr Met His Leu Thr Asn Tyr Ser Val Asn Lys His
 245 250 255
 Asn Glu His Phe Glu Arg Asp Glu Thr Glu Asn Lys Gly Ser Lys Arg
 260 265 270
 Ser Ile Lys Trp Phe Thr Glu Phe Leu Gln Ala Asn Gln His Asp Val
 275 280 285
 Ala Lys Phe Trp Ser Asp Ile Ser Glu Leu Val Val Lys Thr Leu Ile
 290 295 300
 Val Ala Glu Pro His Val Leu His Ala Tyr Arg Met Cys Arg Pro Gly
 305 310 315 320
 Gln Pro Pro Gly Ser Glu Ser Val Cys Phe Glu Val Leu Gly Phe Asp
 325 330 335
 Ile Leu Leu Asp Arg Lys Leu Lys Pro Trp Leu Leu Glu Ile Asn Arg
 340 345 350
 Ala Pro Ser Phe Gly Thr Asp Gln Lys Ile Asp Tyr Asp Val Lys Arg
 355 360 365
 Gly Val Leu Leu Asn Ala Leu Lys Leu Leu Asn Ile Arg Thr Ser Asp
 370 375 380
 Lys Arg Arg Asn Leu Ala Lys Gln Lys Ala Glu Ala Gln Arg Arg Leu
 385 390 395 400
 Tyr Gly Gln Asn Ser Ile Lys Arg Leu Leu Pro Gly Ser Ser Asp Trp

405	410	415
Glu Gln Gln Arg His Gln Leu Glu Arg Arg Lys Glu Glu Leu Lys Glu		
420	425	430
Arg Leu Ala Gln Val Arg Lys Gln Ile Ser Arg Glu Glu His Glu Asn		
435	440	445
Arg His Met Gly Asn Tyr Arg Arg Ile Tyr Pro Pro Glu Asp Lys Ala		
450	455	460
Leu Leu Glu Lys Tyr Glu Asn Leu Leu Ala Val Ala Phe Gln Thr Phe		
465	470	475
Leu Ser Gly Arg Ala Ala Ser Phe Gln Arg Glu Leu Asn Asn Pro Leu		
485	490	495
Lys Arg Met Lys Glu Glu Asp Ile Leu Asp Leu Leu Glu Gln Cys Glu		
500	505	510
Ile Asp Asp Glu Lys Leu Met Gly Lys Thr Thr Lys Thr Arg Gly Pro		
515	520	525
Lys Pro Leu Cys Ser Met Pro Glu Ser Thr Glu Ile Met Lys Arg Pro		
530	535	540
Lys Tyr Cys Ser Ser Asp Ser Ser Tyr Asp Ser Ser Ser Ser Ser Ser		
545	550	555
Glu Ser Asp Glu Asn Glu Lys Glu Glu Tyr Gln Asn Lys Lys Arg Glu		
565	570	575
Lys Gln Val Thr Tyr Asn Leu Lys Pro Ser Asn His Tyr Lys Leu Ile		
580	585	590
Gln Gln Pro Ser Ser Ile Arg Arg Ser Val Ser Cys Pro Arg Ser Ile		
595	600	605
Ser Ala Gln Ser Pro Ser Ser Gly Asp Thr Arg Pro Phe Ser Ala Gln		
610	615	620
Gln Met Ile Ser Val Ser Arg Pro Thr Ser Ala Ser Arg Ser His Ser		
625	630	635
		640

Leu Asn Arg Ala Ser Ser Tyr Met Arg His Leu Pro His Ser Asn Asp
645 650 655
Ala Cys Ser Thr Asn Ser Gln Val Ser Glu Ser Leu Arg Gln Leu Lys
660 665 670
Thr Lys Glu Gln Glu Asp Asp Leu Thr Ser Gln Thr Leu Phe Val Leu
675 680 685
Lys Asp Met Lys Ile Arg Phe Pro Gly Lys Ser Asp Ala Glu Ser Glu
690 695 700
Leu Leu Ile Glu Asp Ile Ile Asp Asn Trp Lys Tyr His Lys Thr Lys
705 710 715 720
Val Ala Ser Tyr Trp Leu Ile Lys Leu Asp Ser Val Lys Gln Arg Lys
725 730 735
Val Leu Asp Ile Val Lys Thr Ser Ile Arg Thr Val Leu Pro Arg Ile
740 745 750
Trp Lys Val Pro Asp Val Glu Glu Val Asn Leu Tyr Arg Ile Phe Asn
755 760 765
Arg Val Phe Asn Arg Leu Leu Trp Ser Arg Gly Gln Gly Leu Trp Asn
770 775 780
Cys Phe Cys Asp Ser Gly Ser Ser Trp Glu Ser Ile Phe Asn Lys Ser
785 790 795 800
Pro Glu Val Val Thr Pro Leu Gln Leu Gln Cys Cys Gln Arg Leu Val
805 810 815
Glu Leu Cys Lys Gln Cys Leu Leu Val Val Tyr Lys Tyr Ala Thr Asp
820 825 830
Lys Arg Gly Ser Leu Ser Gly Ile Gly Pro Asp Trp Gly Asn Ser Arg
835 840 845
Tyr Leu Leu Pro Gly Ser Thr Gln Phe Phe Leu Arg Thr Pro Thr Tyr
850 855 860
Asn Leu Lys Tyr Asn Ser Pro Gly Met Thr Arg Ser Asn Val Leu Phe

865 870 875 880
Thr Ser Arg Tyr Gly His Leu
885

<210> 2177

<211> 188

<212> PRT

<213> Homo sapiens

<400> 2177

Met Thr Lys Thr His Met Ile Ile Ser Ile Asp Ala Glu Lys Ala Phe
1 5 10 15
Asp Glu Ile Gln His His Phe Met Leu Lys Ile Leu Asp Lys Leu Gly
20 25 30
Ile Asp Gly Thr Tyr Leu Lys Ile Val Arg Ala Ile Tyr Asp Lys Pro
35 40 45
Thr Ala Asn Ile Ile Leu Asn Gly His Lys Leu Glu Val Phe Pro Leu
50 55 60
Lys Thr Gly Thr Arg Gln Glu Cys Pro Leu Leu Pro Leu Leu Phe Asn
65 70 75 80
Thr Val Leu Glu Val Leu Ala Arg Ala Ile Thr Gln Glu Lys Glu Ile
85 90 95
Gln Gly Ile Gln Ile Gly Ser Glu Lys Val Lys Leu Ser Leu Phe Ala
100 105 110
Asp Gly Met Ile Val Tyr Leu Glu Asn Pro Ile Val Pro Ala Gln Ser
115 120 125
Leu Leu Lys Leu Ile Ser Asn Phe Ser Lys Val Ser Gly Tyr Lys Ile
130 135 140

Asn Val Gln Lys Ser Gln Ala Phe Leu Tyr Thr Asn Asn Arg Gln Thr
 145 150 155 160
 Glu Gly Gln Ile Met Ser Glu Leu Pro Val Thr Ile Ala Thr Lys Arg
 165 170 175
 Ile Lys Tyr Leu Gly Ile Gln Leu Thr Arg Asp Val
 180 185

<210> 2178

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2178

Met Thr Met Asn Gln Thr Glu His Asn Leu Thr Val Ser Gln Ile Pro
 1 5 10 15
 Ser Pro Gln Thr Trp His Val Phe Tyr Ala Asp Lys Tyr Thr Cys Gln
 20 25 30
 Asp Asp Lys Glu Asn Ser Gln Val Glu Asp Ile Pro Phe Glu Met Val
 35 40 45
 Leu Leu Asn Pro Asp Ala Glu Gly Asn Pro Phe Asp His Phe Ser Ala
 50 55 60
 Gly Glu Ser Gly Leu His Glu Phe Phe Phe Leu Leu Val Leu Val Tyr
 65 70 75 80
 Phe Val Ile Ala Cys Ile Tyr Ala Gln Ser Leu Trp Gln Ala Ile Lys
 85 90 95
 Lys Gly Gly Pro Met His Met Ile Leu Lys Val Leu Thr Thr Ala Leu
 100 105 110
 Leu Leu Gln Ala Gly Ser Ala Leu Ala Asn Tyr Ile His Phe Ser Ser

115	120	125
Tyr Ser Lys Asp Gly Ile Gly Val Pro Phe Met Gly Ser Leu Ala Glu		
130	135	140
Phe Phe Asp Ile Ala Ser Gln Ile Gln Met Leu Tyr Leu Leu Leu Ser		
145	150	155
Leu Cys Met Gly Trp Thr Ile Val Arg Met Lys Lys Ser Gln Ser Arg		
165	170	175
Pro Leu Gln Trp Asp Ser Thr Pro Ala Ser Thr Gly Ile Ala Val Phe		
180	185	190
Ile Val Met Thr Gln Ser Val Leu Leu Leu Trp Glu Gln Phe Glu Asp		
195	200	205
Ile Ser His His Ser Tyr His Ser His His Asn Leu Ala Gly Ile Leu		
210	215	220
Leu Ile Val Leu Arg Ile Cys Leu Ala Leu Ser Leu Gly Cys Arg Leu		
225	230	235
Tyr Gln Ile Ile Thr Val Glu Arg Ser Thr Leu Lys Arg Glu Phe Tyr		
245	250	255
Ile Thr Phe Ala Lys Gly Cys Ile Leu Trp Phe Leu Cys His Pro Val		
260	265	270
Leu Ala Cys Ile Ser Val Ile Phe Ser Asp Tyr Gln Arg Asp Lys Val		
275	280	285
Ile Thr Ile Gly Val Ile Leu Cys Gln Ser Val Ser Met Val Ile Leu		
290	295	300
Tyr Arg Leu Phe Leu Ser His Ser Leu Tyr Trp Glu Val Ser Ser Leu		
305	310	315
Ser Ser Val Thr Leu Pro Leu Thr Ile Ser Ser Gly His Lys Ser Arg		
325	330	335
Pro His Phe		

<210> 2179

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2179

Met Ala Val Cys Leu Trp Val Ser Leu Ser Val Cys Gly Cys Leu Ser
 1 5 10 15
 Pro Ser Val Gly Ile Ser Leu Cys Leu Trp Val Ser Leu Pro Ser Val
 20 25 30
 Gly Val His Leu Cys Leu Trp Val Ser Leu Phe Val Ser Val Ser Val
 35 40 45
 Cys Gly Cys Leu Cys Leu Trp Val Ser Leu Cys Glu Cys Pro Cys Glu
 50 55 60
 Cys Leu Cys Leu Trp Val Ser Leu Leu Val Cys Gly Tyr Leu Ser Leu
 65 70 75 80
 Ser Val Gly Val Ser Val Gly Phe Pro Thr Cys Gly Ser Cys Arg Ser
 85 90 95
 Val Thr Leu Gln Thr Phe Arg Pro Gln Pro Ala Ser Leu Gln Thr Ala
 100 105 110
 Val Ala Trp Gly Ser Arg His Ala Leu Gln Gly Gln Met Val Val Ile
 115 120 125
 Ala Glu Ile Leu Asp Pro His Val Gly Glu Val Pro Val Glu Met Ser
 130 135 140
 Pro Gly Lys Leu Leu Pro Ala Thr Ser Gly Pro Glu Arg Leu Pro Gly
 145 150 155 160
 Leu His Asp Val Lys Val Gly His Ile Leu Ile Cys Gln Leu Arg Val

165 170 175
 Leu Gly Arg Trp Thr Phe Phe Leu Ala Thr Val Thr Pro Ser Leu Lys
 180 185 190
 Arg Ser Ser
 195

<210> 2180

<211> 556

<212> PRT

<213> Homo sapiens

<400> 2180

Met Pro Leu Val Pro Glu Ala Asp Ala Ala Gln Ala Gly Gly His Asp
 1 5 10 15
 Ala His Pro Ala Gly Arg Asp His Arg Gly His Arg Asp Ala His Arg
 20 25 30
 His Arg Arg Gln His Pro Gln His His Arg Arg Pro His Pro Pro Gly
 35 40 45
 Gln Leu Arg Arg Ala Gly Thr Thr Ala Leu Arg Ala Gly Ser Arg Val
 50 55 60
 Thr Ile Ala Asp Gly Gly Val Pro Gly Leu Gln Pro Glu Pro Tyr Leu
 65 70 75 80
 Ala Val Tyr Leu His Ser Glu Pro Arg Pro Asn Glu Arg Asn Cys Ser
 85 90 95
 Ala Ser Arg Arg Ile Arg Pro Glu Ser Leu Gln Gly Ala Asp His Arg
 100 105 110
 Pro Tyr Thr Phe Phe Ile Ser Pro Gly Thr Arg Asp Pro Val Gly Ser
 115 120 125

Tyr Arg Leu Asn Leu Ser Ser His Phe Arg Trp Ser Ala Leu Glu Val
 130 135 140
 Ser Val Gly Leu Tyr Thr Ser Leu Cys Gln Tyr Phe Ser Glu Glu Asp
 145 150 155 160
 Val Val Trp Arg Thr Glu Gly Leu Leu Pro Leu Glu Glu Thr Ser Pro
 165 170 175
 Arg Gln Ala Val Cys Leu Thr Arg His Leu Thr Ala Phe Gly Thr Ser
 180 185 190
 Leu Phe Met Pro Pro Ser His Val Arg Phe Val Phe Pro Glu Pro Thr
 195 200 205
 Ala Asp Val Asn Tyr Ile Val Met Leu Thr Cys Ala Val Cys Leu Val
 210 215 220
 Thr Tyr Met Val Met Ala Ala Ile Leu His Lys Leu Asp Gln Leu Asp
 225 230 235 240
 Ala Ser Arg Gly Cys Ala Ile Pro Phe Cys Gly Gln Arg Gly Arg Phe
 245 250 255
 Lys Tyr Glu Ile Leu Val Lys Thr Gly Trp Gly Arg Gly Ser Gly Thr
 260 265 270
 Thr Ala His Val Gly Ile Met Leu Tyr Gly Val Asp Ser Arg Ser Gly
 275 280 285
 His Arg His Leu Asp Gly Asp Arg Ala Phe His Arg Asn Ser Leu Asp
 290 295 300
 Ile Phe Gln Ile Ala Thr Pro His Ser Leu Gly Ser Met Trp Lys Ile
 305 310 315 320
 Arg Val Trp His Asp Asn Lys Gly Leu Ser Pro Ala Trp Phe Leu Gln
 325 330 335
 His Ile Ile Val Arg Asp Leu Gln Thr Ala Arg Ser Thr Phe Phe Leu
 340 345 350
 Val Asn Asp Trp Leu Ser Val Glu Thr Glu Ala Asn Gly Gly Leu Val

355 360 365
Glu Lys Glu Val Leu Ala Ala Ser His Ala Ala Leu Leu Arg Phe Arg
370 375 380
Arg Leu Leu Val Ala Glu Leu Gln Arg Gly Phe Phe Asp Lys His Ile
385 390 395 400
Trp Leu Ser Ile Trp Asp Arg Pro Pro Arg Ser Cys Phe Thr Arg Ile
405 410 415
Gln Arg Ala Thr Cys Cys Val Leu Leu Ile Cys Leu Phe Leu Gly Ala
420 425 430
Asn Ala Val Trp Tyr Gly Ala Val Gly Asp Ser Ala Tyr Ser Thr Gly
435 440 445
Arg Val Ser Arg Leu Asn Pro Leu Ser Val Asp Thr Val Ala Val Gly
450 455 460
Leu Val Ser Ser Val Val Val Tyr Pro Val Tyr Leu Ala Ile Leu Phe
465 470 475 480
Leu Phe Arg Met Ser Arg Ser Lys Val Ala Gly Ser Pro Ser Pro Thr
485 490 495
Pro Ala Gly Gln Gln Val Leu Asp Val Asp Ser Cys Leu Asp Ser Ser
500 505 510
Val Leu Asp Ser Ser Phe Leu Thr Phe Ser Gly Leu His Ala Glu Val
515 520 525
Arg Ala Leu Leu Gly Val Leu Pro Pro Trp Arg Ser Leu Asp Ser Arg
530 535 540
Pro Cys Ala Pro Leu Ser Arg Pro Leu Leu Asp Arg
545 550 555

<210> 2181

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2181

Met	Asn	Leu	Tyr	Glu	Ser	Phe	Ala	Gln	Ala	Thr	Gln	Leu	Gly	Asp	Leu
1				5					10					15	
His	Thr	Cys	Leu	Met	Met	Asp	Met	Lys	Ala	Cys	Gln	Glu	Asp	Asp	Val
			20					25					30		
Arg	Leu	Leu	Cys	His	Leu	Thr	Pro	Ser	Ile	Tyr	Thr	Glu	Phe	Pro	Asp
			35					40					45		
Glu	Thr	Leu	Arg	Ser	Gly	Glu	Leu	Leu	Asn	Met	Ile	Val	Ala	Val	Ile
		50				55					60				
Asp	Ser	Ala	Gln	Leu	Gln	Glu	Leu	Val	Cys	His	Val	Met	Met	Gly	Asn
		65			70					75				80	
Leu	Val	Met	Phe	Arg	Lys	Asp	Ser	Val	Leu	Asn	Ile	Leu	Ile	Gln	Ser
				85					90					95	
Leu	Asp	Trp	Glu	Thr	Phe	Glu	Gln	Tyr	Cys	Ala	Trp	Gln	Leu	Phe	Leu
			100						105				110		
Ala	His	Asn	Ile	Pro	Leu	Glu	Thr	Ile	Ile	Pro	Ile	Leu	Gln	His	Leu
		115						120					125		
Lys	Tyr	Lys	Glu	His	Pro	Glu	Ala	Leu	Ser	Cys	Leu	Leu	Leu	Gln	Leu
		130						135					140		
Arg	Arg	Glu	Lys	Pro	Ser	Glu	Glu	Met	Val	Lys	Met	Val	Leu	Ser	Arg
		145				150				155				160	
Pro	Cys	His	Pro	Asp	Asp	Gln	Phe	Thr	Thr	Ser	Ile	Leu	Arg	His	Trp
				165					170					175	
Cys	Met	Lys	His	Asp	Glu	Leu	Leu	Ala	Glu	His	Ile	Lys	Ser	Leu	Leu
			180						185					190	
Ile	Lys	Asn	Asn	Ser	Leu	Pro	Arg	Lys	Arg	Gln	Ser	Leu	Arg	Ser	Ser

[illegible]

<210> 2182

<211> 124

<212> PRT

<213> Homo sapiens

<400> 2182

Met Leu His Leu Glu Glu Thr Gly Glu Ala Gly Phe Thr Ser Leu Cys

1

5

10

15

Ile Val Trp Leu His Cys Ser Phe Gly Ile Lys Lys Phe Phe Thr Ser
 20 25 30
 Leu Val Cys Pro Arg Thr Asn Pro Ser Leu Ser Cys Cys Ser Val Ile
 35 40 45
 Leu Gln Cys Trp Phe Arg Ser Leu Gln Ser Leu Glu Leu Pro Leu Ala
 50 55 60
 Phe Ala Pro Lys Ile Cys Ser Phe Thr Gln Gln Ile Phe Thr Lys Phe
 65 70 75 80
 Leu Leu Tyr Ala Gly Pro Cys Gly Glu Leu Lys Asp Glu Ser Asp Val
 85 90 95
 Gly Pro Val His Lys Cys Cys Gln Ser Ser Val Gly His Arg Ala Ser
 100 105 110
 Thr Arg Glu Leu Leu Leu Leu Cys Pro Arg Ile Ala
 115 120

<210> 2183

<211> 932

<212> PRT

<213> Homo sapiens

<400> 2183

Met Thr Asn Leu Lys Ser Thr Ala Pro His Phe Val Arg Cys Ile Asn
 1 5 10 15
 Pro Asn Val Asn Lys Ile Pro Gly Ile Leu Asp Pro Tyr Leu Val Leu
 20 25 30
 Gln Gln Leu Cys Cys Asn Gly Val Leu Glu Gly Thr Arg Ile Cys Arg
 35 40 45
 Glu Gly Phe Pro Asn Arg Leu Gln Tyr Ala Asp Phe Lys Gln Arg Tyr

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Cys Phe Glu Leu Lys Lys Glu Ile Asp Asp Leu Glu Thr Met Leu Val
 290 295 300
 Lys Ser Glu Lys Glu Lys Arg Thr Thr Glu His Lys Val Lys Asn Leu
 305 310 315 320
 Thr Glu Glu Val Glu Phe Leu Asn Glu Asp Ile Ser Lys Leu Asn Arg
 325 330 335
 Ala Ala Lys Val Val Gln Glu Ala His Gln Gln Thr Leu Asp Asp Leu
 340 345 350
 His Met Glu Glu Glu Lys Leu Ser Ser Leu Ser Lys Ala Asn Leu Lys
 355 360 365
 Leu Glu Gln Gln Val Asp Glu Leu Glu Gly Ala Leu Glu Gln Glu Arg
 370 375 380
 Lys Ala Arg Met Asn Cys Glu Arg Glu Leu His Lys Leu Glu Gly Asn
 385 390 395 400
 Leu Lys Leu Asn Arg Glu Ser Met Glu Asn Leu Glu Ser Ser Gln Arg
 405 410 415
 His Leu Ala Glu Glu Leu Arg Lys Lys Glu Leu Glu Leu Ser Gln Met
 420 425 430
 Asn Ser Lys Val Glu Asn Glu Lys Gly Leu Val Ala Gln Leu Gln Lys
 435 440 445
 Thr Val Lys Glu Leu Gln Ala Gln Ile Lys Asp Leu Lys Glu Lys Leu
 450 455 460
 Glu Ala Glu Arg Thr Thr Arg Ala Lys Met Glu Arg Glu Arg Ala Asp
 465 470 475 480
 Leu Thr Gln Asp Leu Ala Asp Leu Asn Glu Arg Leu Glu Glu Val Gly
 485 490 495
 Gly Ser Ser Leu Ala Gln Leu Glu Ile Thr Lys Lys Gln Glu Thr Lys
 500 505 510
 Phe Gln Lys Leu His Arg Asp Met Glu Glu Ala Thr Leu His Phe Glu

515	520	525
Thr Thr Ser Ala Ser Leu Lys Lys Arg His Ala Asp Ser Leu Ala Glu		
530	535	540
Leu Glu Gly Gln Val Glu Asn Leu Gln Gln Val Lys Gln Lys Leu Glu		
545	550	555
Lys Asp Lys Ser Asp Leu Gln Leu Glu Val Asp Asp Leu Leu Thr Arg		
565	570	575
Val Glu Gln Met Thr Arg Ala Lys Ala Asn Ala Glu Lys Leu Cys Thr		
580	585	590
Leu Tyr Glu Glu Arg Leu His Glu Ala Thr Ala Lys Leu Asp Lys Val		
595	600	605
Thr Gln Leu Ala Asn Asp Leu Ala Ala Gln Lys Thr Lys Leu Trp Ser		
610	615	620
Glu Ser Gly Glu Phe Leu Arg Arg Leu Glu Glu Lys Glu Ala Leu Ile		
625	630	635
Asn Gln Leu Ser Arg Glu Lys Ser Asn Phe Thr Arg Gln Ile Glu Asp		
645	650	655
Leu Arg Gly Gln Leu Glu Lys Glu Thr Lys Ser Gln Ser Ala Leu Ala		
660	665	670
His Ala Leu Gln Lys Ala Gln Arg Asp Cys Asp Leu Leu Arg Glu Gln		
675	680	685
Tyr Glu Glu Glu Gln Glu Val Lys Ala Glu Leu His Arg Thr Leu Ser		
690	695	700
Lys Val Asn Ala Glu Met Val Gln Trp Arg Met Lys Tyr Glu Asn Asn		
705	710	715
Val Ile Gln Arg Thr Glu Asp Leu Glu Asp Ala Lys Lys Glu Leu Ala		
725	730	735
Ile Arg Leu Gln Glu Ala Ala Glu Ala Met Gly Val Ala Asn Ala Arg		
740	745	750

Asn Ala Ser Leu Glu Arg Ala Arg His Gln Leu Gln Leu Glu Leu Gly
755 760 765
Asp Ala Leu Ser Asp Leu Gly Lys Val Arg Ser Ala Ala Ala Arg Leu
770 775 780
Asp Gln Lys Gln Leu Gln Ser Gly Lys Ala Leu Ala Asp Trp Lys Gln
785 790 795 800
Lys His Glu Glu Ser Gln Ala Leu Leu Asp Ala Ser Gln Lys Glu Val
805 810 815
Gln Ala Leu Ser Thr Glu Leu Leu Lys Leu Lys Asn Thr Tyr Glu Glu
820 825 830
Ser Ile Val Gly Gln Glu Thr Leu Arg Arg Glu Asn Lys Asn Leu Gln
835 840 845
Glu Glu Ile Ser Asn Leu Thr Asn Gln Val Arg Glu Gly Thr Lys Asn
850 855 860
Leu Thr Glu Met Glu Lys Val Lys Lys Leu Ile Glu Glu Glu Lys Thr
865 870 875 880
Glu Val Gln Val Thr Leu Glu Glu Thr Glu Gly Ala Leu Glu Arg Asn
885 890 895
Glu Ser Lys Ile Leu His Phe Gln Leu Glu Leu Leu Glu Ala Lys Ala
900 905 910
Glu Leu Glu Arg Lys Leu Ser Glu Lys Asp Glu Glu Ile Glu Asn Phe
915 920 925
Arg Tyr Leu Arg
930

<210> 2184

<211> 108

<212> PRT

<213> Homo sapiens

<400> 2184

Met	Gln	Ser	Ile	Ser	Leu	Thr	Glu	Glu	Gly	His	Ser	Arg	Met	Arg	Asn
1				5					10					15	
Val	Trp	Arg	His	Ser	Pro	Glu	Asp	Arg	Asn	Ser	Pro	Gly	Leu	Ser	Val
				20				25					30		
Ala	Arg	Gly	Gln	Ala	Trp	Gln	Gln	Lys	Ser	Asn	Val	Arg	Leu	Leu	Ala
				35				40					45		
Lys	Ala	Arg	His	Arg	Lys	Gly	Val	Pro	Trp	Ser	Ala	Leu	Leu	Gly	Val
				50				55					60		
Pro	Leu	Lys	Asp	Val	Pro	Gln	Arg	Gly	Val	Trp	Ser	Asn	Met	Arg	Phe
				65				70					75		80
Lys	Lys	Ser	Ser	Leu	Cys	Leu	Asn	Arg	Trp	Asn	Tyr	Glu	Arg	Pro	Arg
				85				90					95		
Leu	Lys	Met	Glu	Val	Lys	Val	Gly	Gly	Met	Ala	Phe				
				100				105							

<210> 2185

<211> 496

<212> PRT

<213> Homo sapiens

<400> 2185

Met	Ala	Glu	Leu	Gln	Met	Leu	Leu	Glu	Glu	Glu	Ile	Pro	Ser	Gly	Lys
1				5						10				15	
Arg	Ala	Leu	Ile	Glu	Ser	Tyr	Gln	Asn	Leu	Thr	Arg	Val	Ala	Asp	Tyr
				20				25					30		

Cys Glu Asn Asn Tyr Ile Gln Arg His Gly Phe Ala Val Leu Leu Cys
 35 40 45
 Leu Leu Ser Asn Ser Trp Pro Gln Ala Thr Asp Lys Arg Lys Ala Leu
 50 55 60
 Glu Glu Thr Lys Ala Tyr Thr Thr Gln Ser Leu Ala Ser Val Ala Tyr
 65 70 75 80
 Gln Ile Asn Ala Leu Ala Asn Asn Val Leu Gln Leu Leu Asp Ile Gln
 85 90 95
 Ala Ser Gln Leu Arg Arg Met Glu Ser Ser Ile Asn His Ile Ser Gln
 100 105 110
 Thr Val Asp Ile His Lys Glu Lys Val Ala Arg Arg Glu Ile Gly Ile
 115 120 125
 Leu Thr Thr Asn Lys Asn Thr Ser Arg Thr His Lys Ile Ile Ala Pro
 130 135 140
 Ala Asn Met Glu Arg Pro Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr
 145 150 155 160
 Thr Val Leu Asp Asp Val Gly His Gly Val Lys Trp Leu Lys Ala Lys
 165 170 175
 His Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr Leu Ser Arg Thr Asn
 180 185 190
 Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro Met Ser Gly Arg Gly Thr
 195 200 205
 Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu Pro Val Lys Pro Pro
 210 215 220
 Thr Val Pro Asn Asp Tyr Met Thr Ser Pro Ala Arg Leu Gly Ser Gln
 225 230 235 240
 His Ser Pro Gly Arg Thr Ala Ser Leu Asn Gln Arg Pro Arg Thr His
 245 250 255
 Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu Asn Ser Gly Ser Ser

260 265 270
Ser Ile Gly Ile Pro Ile Ala Val Pro Thr Pro Ser Pro Pro Thr Ile
275 280 285
Gly Pro Glu Asn Ile Ser Val Pro Pro Pro Ser Gly Ala Pro Pro Ala
290 295 300
Pro Pro Leu Ala Pro Leu Leu Pro Val Ser Thr Val Ile Ala Ala Pro
305 310 315 320
Gly Ser Ala Pro Gly Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser
325 330 335
Arg His Asn Ser Thr Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg
340 345 350
Thr Pro Ser Val Thr Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly
355 360 365
Gly Pro Leu Tyr Ser Gln Asn Ser Ile Ala Asp Ser Pro Thr Pro Pro
370 375 380
Pro Pro Pro Pro Pro Asp Asp Ile Pro Met Phe Asp Asp Ser Pro Pro
385 390 395 400
Pro Pro Pro Pro Pro Pro Val Asp Tyr Glu Asp Glu Glu Ala Ala Val
405 410 415
Val Gln Tyr Asn Asp Pro Tyr Ala Gly Gly Asp Pro Ala Trp Ala Pro
420 425 430
Lys Asn Tyr Ile Glu Lys Val Val Ala Ile Tyr Asp Tyr Thr Lys Asp
435 440 445
Lys Asp Asp Glu Leu Ser Phe Met Glu Gly Ala Ile Ile Tyr Val Ile
450 455 460
Lys Lys Asn Asp Asp Gly Trp Tyr Glu Gly Val Cys Asn Arg Val Thr
465 470 475 480
Gly Leu Phe Pro Gly Asn Tyr Val Glu Ser Ile Met His Tyr Thr Asp
485 490 495

<210> 2186

<211> 969

<212> PRT

<213> Homo sapiens

<400> 2186

Met His Ser Ser Pro Ala Ser Ser Asn Tyr Gln Gln Thr Thr Ile Ser

1 5 10 15

His Ser Pro Ser Ser Arg Phe Val Pro Pro Gln Thr Ser Ser Gly Asn

20 25 30

Arg Phe Met Pro Gln Gln Asn Ser Pro Val Pro Ser Pro Tyr Ala Pro

35 40 45

Gln Ser Pro Ala Gly Tyr Met Pro Tyr Ser His Pro Ser Ser Tyr Thr

50 55 60

Thr His Pro Gln Met Gln Gln Ala Ser Val Ser Ser Pro Ile Val Ala

65 70 75 80

Gly Gly Leu Arg Asn Ile His Asp Asn Lys Val Ser Gly Pro Leu Ser

85 90 95

Gly Asn Ser Ala Asn His His Ala Asp Asn Pro Arg His Gly Ser Ser

100 105 110

Glu Asp Tyr Leu His Met Val His Arg Leu Ser Ser Asp Asp Gly Asp

115 120 125

Ser Ser Thr Met Arg Asn Ala Ala Ser Phe Pro Leu Arg Ser Pro Gln

130 135 140

Pro Val Cys Ser Pro Ala Gly Ser Glu Gly Thr Pro Lys Gly Ser Arg

145 150 155 160

Pro Pro Leu Ile Leu Gln Ser Gln Ser Leu Pro Cys Ser Ser Pro Arg

165 170 175
Asp Val Pro Pro Asp Ile Leu Leu Asp Phe Pro Glu Arg Lys Gln Lys
180 185 190
Lys Gln Lys Lys Met Lys Leu Gly Lys Asp Glu Lys Glu Gln Ser Glu
195 200 205
Lys Ala Ala Met Tyr Asp Ile Ile Ser Ser Pro Ser Lys Asp Ser Thr
210 215 220
Lys Leu Thr Leu Arg Leu Ser Arg Val Arg Ser Ser Asp Met Asp Gln
225 230 235 240
Gln Glu Asp Met Ile Ser Gly Val Glu Asn Ser Asn Val Ser Glu Asn
245 250 255
Asp Ile Pro Phe Asn Val Gln Tyr Pro Gly Gln Thr Ser Lys Thr Pro
260 265 270
Ile Thr Pro Gln Asp Ile Asn Arg Pro Leu Asn Ala Ala Gln Cys Leu
275 280 285
Ser Gln Gln Glu Gln Thr Ala Phe Leu Pro Ala Asn Gln Val Pro Val
290 295 300
Leu Gln Gln Asn Thr Ser Val Ala Ala Lys Gln Pro Gln Thr Ser Val
305 310 315 320
Val Gln Asn Gln Gln Gln Ile Ser Gln Gln Gly Pro Ile Tyr Asp Glu
325 330 335
Val Glu Leu Asp Ala Leu Ala Glu Ile Glu Arg Ile Glu Arg Glu Ser
340 345 350
Ala Ile Glu Arg Glu Arg Phe Ser Lys Glu Val Gln Asp Lys Asp Lys
355 360 365
Pro Leu Lys Lys Arg Lys Gln Asp Ser Tyr Pro Gln Glu Ala Gly Gly
370 375 380
Ala Thr Gly Gly Asn Arg Pro Ala Ser Gln Glu Thr Gly Ser Thr Gly
385 390 395 400

Asn Gly Ser Arg Pro Ala Leu Met Val Ser Ile Asp Leu His Gln Ala
 405 410 415
 Gly Arg Val Asp Ser Gln Ala Ser Ile Thr Gln Asp Ser Asp Ser Ile
 420 425 430
 Lys Lys Pro Glu Glu Ile Lys Gln Cys Asn Asp Ala Pro Val Ser Val
 435 440 445
 Leu Gln Glu Asp Ile Val Gly Ser Leu Lys Ser Thr Pro Glu Asn His
 450 455 460
 Pro Glu Thr Pro Lys Lys Lys Ser Asp Pro Glu Leu Ser Lys Ser Glu
 465 470 475 480
 Met Lys Gln Ser Glu Ser Arg Leu Ala Glu Ser Lys Pro Asn Glu Asn
 485 490 495
 Arg Leu Val Glu Thr Lys Ser Ser Glu Asn Lys Leu Glu Thr Lys Val
 500 505 510
 Glu Thr Gln Thr Glu Glu Leu Lys Gln Asn Glu Ser Arg Thr Thr Glu
 515 520 525
 Cys Lys Gln Asn Glu Ser Thr Ile Val Glu Pro Lys Gln Asn Glu Asn
 530 535 540
 Arg Leu Ser Asp Thr Lys Pro Asn Asp Asn Lys Gln Asn Asn Gly Arg
 545 550 555 560
 Ser Glu Thr Thr Lys Ser Arg Pro Glu Thr Pro Lys Gln Lys Gly Glu
 565 570 575
 Ser Arg Pro Glu Thr Pro Lys Gln Lys Ser Asp Gly His Pro Glu Thr
 580 585 590
 Pro Lys Gln Lys Gly Asp Gly Arg Pro Glu Thr Pro Lys Gln Lys Gly
 595 600 605
 Glu Ser Arg Pro Glu Thr Pro Lys Gln Lys Asn Glu Gly Arg Pro Glu
 610 615 620
 Thr Pro Lys His Arg His Asp Asn Arg Arg Asp Ser Gly Lys Pro Ser

625 630 635 640
Thr Glu Lys Lys Pro Glu Val Ser Lys His Lys Gln Asp Thr Lys Ser
 645 650 655
Asp Ser Pro Arg Leu Lys Ser Glu Arg Ala Glu Ala Leu Lys Gln Arg
 660 665 670
Pro Asp Gly Arg Ser Val Ser Glu Ser Leu Arg Arg Asp His Asp Asn
 675 680 685
Lys Gln Lys Ser Asp Asp Arg Gly Glu Ser Glu Arg His Arg Gly Asp
 690 695 700
Gln Ser Arg Val Arg Arg Pro Glu Thr Leu Arg Ser Ser Ser Arg Asn
705 710 715 720
Glu His Gly Ile Lys Ser Asp Ser Ser Lys Thr Asp Lys Leu Glu Arg
 725 730 735
Lys His Arg His Glu Ser Gly Asp Ser Arg Glu Arg Pro Ser Ser Gly
 740 745 750
Glu Gln Lys Ser Arg Pro Asp Ser Pro Arg Val Lys Gln Gly Asp Ser
 755 760 765
Asn Lys Ser Arg Ser Asp Lys Leu Gly Phe Lys Ser Pro Thr Ser Lys
 770 775 780
Asp Asp Lys Arg Thr Glu Gly Asn Lys Ser Lys Val Asp Thr Asn Lys
785 790 795 800
Ala His Pro Asp Asn Lys Ala Glu Phe Pro Ser Tyr Leu Leu Gly Gly
 805 810 815
Arg Ser Gly Ala Leu Lys Asn Phe Val Ile Pro Lys Ile Lys Arg Asp
 820 825 830
Lys Asp Gly Asn Val Thr Gln Glu Thr Lys Lys Met Glu Met Lys Gly
 835 840 845
Glu Pro Lys Asp Lys Val Glu Lys Ile Gly Leu Val Glu Asp Leu Asn
 850 855 860

Lys Gly Ala Lys Pro Val Val Val Leu Gln Lys Leu Ser Leu Asp Asp
 865 870 875 880
 Val Gln Lys Leu Ile Lys Asp Arg Glu Asp Lys Ser Arg Ser Ser Leu
 885 890 895
 Lys Pro Ile Lys Asn Lys Pro Ser Lys Ser Asn Lys Gly Ser Ile Asp
 900 905 910
 Gln Ser Val Leu Lys Glu Leu Pro Pro Glu Leu Leu Ala Glu Ile Glu
 915 920 925
 Ser Thr Met Pro Leu Cys Glu Arg Val Lys Met Asn Lys Arg Lys Arg
 930 935 940
 Ser Thr Val Asn Glu Lys Pro Lys Tyr Ala Glu Ile Ser Ser Asp Glu
 945 950 955 960
 Asp Asn Asp Ser Asp Glu Ala Phe Glu
 965

<210> 2187

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2187

Met Arg Leu Asn Thr Glu Ser Ala Glu Ala Gln Ala Glu Pro Pro Phe
 1 5 10 15
 Phe Arg Glu Val Gly Glu Arg Ile Ser Glu Leu Gly Glu Lys Gly Ser
 20 25 30
 Phe Val Lys Tyr Ser Gln Lys Thr Val Phe Lys Phe Leu Ser Phe Cys
 35 40 45
 Ile Met Leu Asp Ile Ser Ser Asp His Lys Leu Asp Ser Asn Ile Asn

50 55 60
 Lys Gln Phe Cys Leu Tyr Phe Val Ser Gly Phe Ser Cys Gln Ala Leu
 65 70 75 80
 Trp Cys Val Gln Thr Thr Ser Glu Val Glu Ala Gly Gly Ser Leu Asp
 85 90 95
 Pro Arg Ser Leu Ser Ser Ala Trp Val Ala
 100 105

<210> 2188

<211> 246

<212> PRT

<213> Homo sapiens

<400> 2188

Met Asn Ser Phe Asp Asp Glu Asp Ala Gly Asp Ser Arg Arg Leu Lys
 1 5 10 15
 Gly Ala Ile Gln Arg Ser Thr Glu Thr Gly Leu Ala Val Glu Met Pro
 20 25 30
 Ser Arg Thr Leu Arg Gln Ala Ser His Glu Ser Ile Glu Asp Ser Met
 35 40 45
 Asn Ser Tyr Gly Ser Glu Gly Asn Leu Asn Tyr Gly Gly Val Cys Leu
 50 55 60
 Ala Ser Asp Ala Gln Phe Ser Asp Phe Leu Gly Ser Met Gly Pro Ala
 65 70 75 80
 Gln Phe Val Gly Arg Gln Thr Leu Ala Thr Thr Pro Met Gly Asp Val
 85 90 95
 Glu Ile Gly Leu Gln Glu Arg Asn Gly Gln Leu Glu Val Asp Ile Ile
 100 105 110

Gln Ala Arg Gly Leu Thr Ala Lys Pro Gly Ser Lys Thr Leu Pro Ala
 115 120 125
 Ala Tyr Ile Lys Ala Tyr Leu Leu Glu Asn Gly Ile Cys Ile Ala Lys
 130 135 140
 Lys Lys Thr Lys Val Ala Arg Lys Ser Leu Asp Pro Leu His Asn Gln
 145 150 155 160
 Val Leu Leu Phe Pro Glu Ser Pro Gln Gly Lys Val Leu Gln Val Ile
 165 170 175
 Val Trp Gly Asn Tyr Gly Arg Met Glu Arg Lys Gln Phe Met Gly Val
 180 185 190
 Ala Arg Val Leu Leu Glu Glu Leu Asp Leu Thr Thr Leu Ala Val Gly
 195 200 205
 Trp Tyr Lys Leu Phe Pro Thr Ser Ser Met Val Asp Pro Ala Thr Gly
 210 215 220
 Pro Leu Leu Arg Gln Ala Ser Gln Leu Ser Leu Glu Ser Thr Val Gly
 225 230 235 240
 Pro Cys Gly Glu Arg Ser
 245

<210> 2189

<211> 493

<212> PRT

<213> Homo sapiens

<400> 2189

Met Ala Leu Ser Ser Trp Ala Gln Gly Thr Ser Trp Ala Ala Lys Gly
 1 5 10 15
 Phe Ser Arg Ser Phe Ser Leu Ala Glu Phe Ser Leu Leu Lys Pro Arg

20	25	30
Ala Gly Ser Cys Arg Thr Gln Glu Pro Arg Lys Pro Ala Asp Gly Gln		
35	40	45
Pro Trp Leu Arg Cys Ser Pro Cys Thr Gly Gly Gln Arg Ile Trp Val		
50	55	60
His Gly Ala His Pro Ala Thr Ser Pro Pro Ile Arg Gln Lys Gly Lys		
65	70	75
Leu Arg Pro Arg Gly Arg Glu Ser Phe Pro Gln Gly His Thr Ala Gln		
85	90	95
Glu Ser Gln Leu Gly Ala Pro Pro Leu Thr Pro Cys Pro Val Leu Leu		
100	105	110
Met Pro Pro Gly Arg Leu Ala Val Gly Val Ser Glu Gly Gly Val Ala		
115	120	125
Met Gly Arg Trp Gln Gly Glu Ala Gln Pro Pro Leu Gln Thr Pro His		
130	135	140
Ser Gln His Ser Phe Leu Thr Pro Arg Pro Leu Ala Ser His Pro Asp		
145	150	155
Met Ser Thr Ser Leu Gln Glu Gly Gln Glu Asp Gly Pro Ala Gly Trp		
165	170	175
Arg Ala Asn Leu Lys Pro Val Asp Arg Arg Ser Pro Ala Glu Arg Thr		
180	185	190
Leu Lys Pro Lys Glu Pro Arg Ala Leu Ala Glu Pro Arg Ala Gly Glu		
195	200	205
Ala Pro Arg Lys Val Ser Gly Ser Phe Ala Gly Ser Val His Ile Thr		
210	215	220
Leu Thr Pro Val Arg Pro Asp Arg Thr Pro Arg Pro Ala Ser Pro Gly		
225	230	235
Pro Ser Leu Pro Ala Arg Ser Pro Ser Pro Pro Arg Arg Arg Arg Leu		
245	250	255

Ala Val Pro Ala Ser Leu Asp Val Cys Asp Asn Trp Leu Arg Pro Glu
260 265 270
Pro Pro Gly Gln Glu Ala Arg Val Gln Ser Trp Lys Glu Glu Glu Lys
275 280 285
Lys Pro His Leu Gln Gly Lys Pro Gly Arg Pro Leu Ser Pro Ala Asn
290 295 300
Val Pro Ala Leu Pro Gly Glu Thr Val Thr Ser Pro Val Arg Leu His
305 310 315 320
Pro Asp Tyr Leu Ser Pro Glu Glu Ile Gln Arg Gln Leu Gln Asp Ile
325 330 335
Glu Arg Arg Leu Asp Ala Leu Glu Leu Arg Gly Val Glu Leu Glu Lys
340 345 350
Arg Leu Arg Ala Ala Glu Gly Asp Asp Ala Glu Asp Ser Leu Met Val
355 360 365
Asp Trp Phe Trp Leu Ile His Glu Lys Gln Leu Leu Leu Arg Gln Glu
370 375 380
Ser Glu Leu Met Tyr Lys Ser Lys Ala Gln Arg Leu Glu Glu Gln Gln
385 390 395 400
Leu Asp Ile Glu Gly Glu Leu Arg Arg Leu Met Ala Lys Pro Glu Ala
405 410 415
Leu Lys Ser Leu Gln Glu Arg Arg Arg Glu Gln Glu Leu Leu Glu Gln
420 425 430
Tyr Val Ser Thr Val Asn Asp Arg Ser Asp Ile Val Asp Ser Leu Asp
435 440 445
Glu Asp Arg Leu Arg Glu Gln Glu Glu Asp Gln Met Leu Arg Asp Met
450 455 460
Ile Glu Lys Leu Gly Leu Gln Arg Lys Lys Ser Lys Phe Arg Leu Ser
465 470 475 480
Lys Ile Trp Ser Pro Lys Ser Lys Ser Ser Pro Ser Gln

485

490

<210> 2190

<211> 195

<212> PRT

<213> Homo sapiens

<400> 2190

Met Pro Arg Pro Ala Pro Glu Ser Pro Gly Arg Lys Ser Cys Thr Leu

1 5 10 15

Gly Leu Gln Pro His Arg Gly Pro Ser Val Cys Pro Arg Ala Ser Pro

20 25 30

Leu Arg Ala Trp Pro Ala Leu Leu Pro Val Thr Pro Cys Ser Ser Gly

35 40 45

Leu Arg Thr Pro His Pro Pro Gln His Leu Arg Lys Pro Gln Lys Ala

50 55 60

Ala Lys Ser Arg Ser Pro Gln Pro Leu Ala Arg Pro Trp Leu Ala Ser

65 70 75 80

Gly Thr Phe Arg Pro Pro Ser Thr Gly Ser Val Leu Pro Pro Ala Pro

85 90 95

Arg Thr Val Gln Pro Glu Thr Pro Leu Pro Leu Ser Gln Pro Pro Gly

100 105 110

Pro Thr Ser Pro Pro Arg Pro Gln Lys Gly Arg Arg Ala Gln Ser Pro

115 120 125

Trp Gly Phe Pro Lys Ala Arg Val Pro Arg Pro Ser Arg Leu Leu Arg

130 135 140

Tyr Pro Met Ala Leu Pro Arg Lys Gly Leu His Pro Gln Ala Pro Asn

145 150 155 160

Ser Cys Leu Val Arg Gln Arg Arg Pro Asn Leu Pro Ser Ser Arg Gly

165

170

175

Ser Pro Gly Val Gly Ala Gly Arg Val Pro Arg Trp Pro Pro Leu Pro

180

185

190

Ser Ser Pro

195

<210> 2191

<211> 254

<212> PRT

<213> Homo sapiens

<400> 2191

Met Glu Ser Leu Asn Pro Ser Trp Leu Thr Pro Pro Thr Pro Pro Arg

1

5

10

15

Ala Leu Ser Leu Arg Pro Thr Leu Leu Asp Thr Arg Gly Pro Arg Arg

20

25

30

Pro Ser Val Pro Gln Leu Pro Val Pro Trp Arg Gln Pro Arg Ser His

35

40

45

Asp His Ala Gly Asp Ala Ser Pro Gln Ala Glu Ala Gly Phe Glu Ala

50

55

60

Ala Gly Ser Arg Pro Pro Thr Pro Cys Pro Leu Gly Gly Thr Cys Ala

65

70

75

80

Gly Gly Val Gly Val Ala Gly Phe Ala His Arg Pro Ala Pro Val Pro

85

90

95

Cys Cys Asp Ser His Glu Gly Arg Thr Trp Leu Ser Leu His Leu Pro

100

105

110

Trp Thr Val Pro Gly Leu Gly Arg Pro Gly Thr Ala Lys Gly Gln Ser

115					120					125						
Ala	Gln	Thr	Ser	Val	Asp	Thr	Pro	Ser	Ala	Cys	Glu	Pro	Leu	Gly	Ala	
130					135					140						
Ala	Arg	Ala	Arg	Leu	Glu	Cys	Arg	Gly	Gly	Ala	Arg	Thr	Ala	Ala	Ala	
145					150					155					160	
Pro	Arg	Cys	Lys	Gln	Ala	Cys	Arg	Tyr	Lys	Ser	Trp	Ser	Pro	Trp	Ala	
165					170					175						
Ser	Pro	His	Pro	Ser	Leu	Thr	His	Leu	Pro	Glu	Leu	Ser	Lys	Glu	Ala	
180					185					190						
Arg	Gln	Ser	Arg	Ile	Gln	His	His	Ala	Ala	Ser	Thr	Ser	Ala	Leu	Ala	
195					200					205						
Gln	Ala	Ala	Pro	Pro	Ile	Arg	Ala	Cys	Thr	Pro	Arg	Ile	Asp	Ser	Leu	
210					215					220						
Ser	Thr	Glu	Asp	Gln	Asp	Gly	Gly	Gly	Leu	Leu	Leu	Pro	Asp	Glu	Glu	
225					230					235					240	
Asp	Gly	Leu	Gly	His	Gly	His	Val	Pro	Ile	Arg	Gln	Gly	His			
245					250											

<210> 2192

<211> 291

<212> PRT

<213> Homo sapiens

<400> 2192

Met Gly Ser Phe Gln Leu Glu Asp Phe Ala Ala Gly Trp Ile Gly Gly
1 5 10 15
Ala Ala Ser Val Ile Val Gly His Pro Leu Asp Thr Val Lys Thr Arg
20 25 30

Leu Gln Ala Gly Val Gly Tyr Gly Asn Thr Leu Ser Cys Ile Arg Val
 35 40 45
 Val Tyr Arg Arg Glu Ser Met Phe Gly Phe Phe Lys Gly Met Ser Phe
 50 55 60
 Pro Leu Ala Ser Ile Ala Val Tyr Asn Ser Val Val Phe Gly Val Phe
 65 70 75 80
 Ser Asn Thr Gln Arg Phe Leu Ser Gln His Arg Cys Gly Glu Pro Glu
 85 90 95
 Ala Ser Pro Pro Arg Thr Leu Ser Asp Leu Leu Leu Ala Ser Met Val
 100 105 110
 Ala Gly Val Val Ser Val Gly Leu Gly Gly Pro Val Asp Leu Ile Lys
 115 120 125
 Ile Arg Leu Gln Met Gln Thr Gln Pro Phe Arg Asp Ala Asn Leu Gly
 130 135 140
 Leu Lys Ser Arg Ala Val Ala Pro Ala Glu Gln Pro Ala Tyr Gln Gly
 145 150 155 160
 Pro Val His Cys Ile Thr Thr Ile Val Arg Asn Glu Gly Leu Ala Gly
 165 170 175
 Leu Tyr Arg Gly Ala Ser Ala Met Leu Leu Arg Asp Val Pro Gly Tyr
 180 185 190
 Cys Leu Tyr Phe Ile Pro Tyr Val Phe Leu Ser Glu Trp Ile Thr Pro
 195 200 205
 Glu Ala Cys Thr Gly Pro Ser Pro Cys Ala Val Trp Leu Ala Gly Gly
 210 215 220
 Met Ala Gly Lys Gly Ser Ser Ser Trp Ser Arg Thr Pro Val Gln Ala
 225 230 235 240
 Thr Ala Val Gly Gln Leu Gly Asn Cys His Ala Leu Leu Ser Pro Gly
 245 250 255
 Gly Gly Gln Asp Thr Phe Arg Tyr Ser Pro Asn Asn Ser Leu Leu Gly

260 265 270
 Thr Tyr Ser Val Pro Gly Pro Leu Pro Pro Gln Ser His Pro Phe Pro
 275 280 285
 Met Gln Leu
 290

<210> 2193

<211> 100

<212> PRT

<213> Homo sapiens

<400> 2193

Met Leu Ser Ser Ala Ser Asp Leu Ser Asp Leu Leu Phe Ser Ser Ser
 1 5 10 15
 Ser Asp Leu Ile Glu Leu Leu Trp Trp Leu Cys Gln Trp Leu Ala Val
 20 25 30
 Ala Ile Ser Pro His Pro Ala Ile Gly Gly Leu Val Arg Trp His Leu
 35 40 45
 Val Val Ala Ser Ser Pro Glu Gly Asp Gly Ala Gly His Arg His Leu
 50 55 60
 Ser Leu Ala Ala Gly Leu Arg Thr Gly Leu Leu Leu Gly Lys Leu Gln
 65 70 75 80
 Val Gln Pro Val Asp Cys Thr Cys Leu Arg Lys Ser Thr Thr Leu Leu
 85 90 95
 Pro Glu Asn Leu
 100

<210> 2194

<211> 120

<212> PRT

<213> Homo sapiens

<400> 2194

Met Leu Ser Ile Ser Ala Asp Ile Glu Thr Val Gly Glu Thr Leu Lys

1 5 10 15

Lys Ile Ile Pro Thr Leu Glu Glu Tyr His His Tyr Lys Gly Ser Asn

20 25 30

Phe Asp Cys Glu Leu Arg Leu Leu Thr His Gln Ser Leu Ala Gly Gly

35 40 45

Ile Ile Glu Val Lys Asp Ala Lys Ile Lys Glu Leu Gln Gly Asn Thr

50 55 60

Gln Thr Thr Ile Lys Leu Phe Arg Glu Cys Cys Pro His Ser Thr Asp

65 70 75 80

Gly Val Val Leu Ile Gly Glu Arg Leu Trp Ser Cys Arg Val His Lys

85 90 95

Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Thr Glu Asp Val His Arg

100 105 110

Leu Ile Ile Pro Ile Phe Met Met

115 120

<210> 2195

<211> 106

<212> PRT

<213> Homo sapiens

<400> 2195

Met Asn Phe Ser Lys Phe Thr Gln Leu Phe Gly His His Tyr Asn Leu
 1 5 10 15
 Val Leu Glu Gln Phe His Leu Ser Gln Val Ile Pro His Ala His Leu
 20 25 30
 Gln Ile Ile Cys Ile Pro Thr His Cys Cys Gly Gln Leu Gln Phe Tyr
 35 40 45
 Thr Leu Leu Leu Glu Ile Cys Leu Phe Trp Thr Phe Arg Ile Ser Gly
 50 55 60
 Ile Leu Gln Phe Val Val Phe Cys Ile Trp Leu Leu Ser Leu Ser Met
 65 70 75 80
 Val Leu Arg Cys Ile Arg Val Val Ala Cys Ile Asn Met His Ser Ile
 85 90 95
 Cys Ile Cys Phe Phe Phe Phe Phe Ala Glu
 100 105

<210> 2196

<211> 235

<212> PRT

<213> Homo sapiens

<400> 2196

Met Ala Arg Glu Lys His Gln Ala Ser Gln Lys Glu Asn Lys Gln Leu
 1 5 10 15
 Ser Leu Lys Val Asp Glu Leu Glu Arg Leu Glu Ala Leu Gly Pro Ile
 20 25 30
 Ser Val Leu Phe Leu Gly Pro Glu Thr Phe Ser His Leu Ala Val Phe
 35 40 45

Cys Leu Val Cys Gly Ser Val Glu Gly Leu Glu Ala Leu Glu Gly Thr
50 55 60
Arg Gln Thr Ser Glu Glu Lys Leu Leu Pro Phe Gln Trp Lys Leu Glu
65 70 75 80
Ala Thr Ser Ala Gln Asn Ile Glu Phe Leu Gln Val Ile Ala Lys Arg
85 90 95
Glu Glu Ala Ile His Gln Ser Gln Leu Arg Leu Glu Glu Lys Thr Arg
100 105 110
Glu Cys Gly Thr Leu Ala Arg Gln Leu Glu Ser Ala Ile Glu Asp Ala
115 120 125
Arg Arg Gln Val Glu Gln Thr Lys Glu His Ala Leu Ser Lys Glu Arg
130 135 140
Ala Ala Gln Asn Lys Ile Leu Asp Leu Glu Thr Gln Leu Ser Arg Thr
145 150 155 160
Lys Thr Glu Leu Ser Gln Leu Arg Arg Ser Arg Asp Asp Ala Asp Arg
165 170 175
Arg Tyr Gln Ser Arg Leu Gln Asp Leu Lys Asp Arg Leu Glu Gln Ser
180 185 190
Glu Ser Thr Asn Arg Ser Met Gln Asn Tyr Val Gln Phe Leu Lys Ser
195 200 205
Ser Tyr Ala Asn Val Phe Gly Asp Gly Pro Tyr Ser Thr Phe Leu Thr
210 215 220
Ser Ser Pro Ile Arg Ser Arg Ser Pro Pro Ala
225 230 235

<210> 2197

<211> 181

<212> PRT

<213> Homo sapiens

<400> 2197

Met Thr Leu Pro Trp Pro Ser Pro Gly Pro Ser Leu Ile Leu Pro Cys

1 5 10 15

Pro Ser Met Pro Trp Pro Cys Pro His Pro Ala Leu Ala Leu His Trp

20 25 30

Ser Cys Pro Ala Leu Ala Leu Pro Trp Pro Trp Pro Cys Leu Leu Pro

35 40 45

Gly Leu Ala Phe Ala Leu Pro Trp Pro Asp Pro Arg Pro Thr Glu Ser

50 55 60

Met Lys Trp Pro Trp Thr Cys Leu Ala Ile Leu Cys Pro Gly Pro Ile

65 70 75 80

Leu Ser Pro Pro Cys Ser Gly Pro Ala Leu Ala Leu Ala Leu Leu Leu

85 90 95

Val Leu Pro Leu Leu Trp Pro Cys Ser Val Phe Gly Arg Ala Leu Cys

100 105 110

Tyr Pro Ser Pro Ala Leu Pro Trp Pro Trp Pro Tyr His Gly Leu Leu

115 120 125

Leu Pro Trp Pro Gly Pro Thr Leu Ala Phe Ser Thr Leu Ala Leu Pro

130 135 140

Phe Pro Gly Val Ala Leu Pro Trp Pro Cys Pro Ala Leu Ala Leu Ala

145 150 155 160

Leu Pro Tyr Pro Gly Pro Gly Ser Ala Leu Thr Leu Ala Leu Val Leu

165 170 175

Ser Cys Pro Trp Leu

180

<210> 2198

<211> 126

<212> PRT

<213> Homo sapiens

<400> 2198

Met	Glu	Phe	Arg	Phe	Cys	Cys	Pro	Gly	Trp	Ser	Ala	Met	Val	Arg	Ser
1				5					10					15	
Leu	Leu	Ile	Ala	Thr	Ser	Ala	Ser	Trp	Val	Gln	Val	Ile	Leu	Leu	Pro
				20					25					30	
Gln	Pro	Leu	Phe	Gln	Met	Gly	Ala	Tyr	Tyr	Gly	Ser	Pro	Ala	Ser	Ser
				35				40						45	
Pro	Leu	Leu	Tyr	Met	Glu	Gly	Arg	Pro	Ile	Phe	Leu	Trp	Phe	Ile	Gly
				50				55						60	
Leu	Gln	Thr	His	Asn	Lys	Pro	Asn	Lys	Gln	Thr	Ile	Phe	His	Leu	Tyr
				65				70						75	
Leu	Met	Glu	Arg	Leu	His	Ile	Ser	His	Ser	Thr	Tyr	Ile	Leu	Ser	Trp
								85						90	
Met	Gln	Glu	Met	Gln	Glu	Pro	Leu	Arg	Leu	Ser	His	Leu	Glu	Cys	Ser
				100				105						110	
Leu	Glu	Arg	Asn	Leu	Gly	Ser	Asp	Lys	Cys	Leu	Thr	Thr	Ser		
				115				120						125	

<210> 2199

<211> 551

<212> PRT

<213> Homo sapiens

<400> 2199

Met Ala Ala Pro Val Arg Leu Gly Arg Lys Arg Pro Leu Pro Ala Cys

1 5 10 15

Pro Asn Pro Leu Phe Val Arg Trp Leu Thr Glu Trp Arg Asp Glu Ala

20 25 30

Thr Arg Ser Arg His Arg Thr Arg Phe Val Phe Gln Lys Ala Leu Arg

35 40 45

Ser Leu Arg Arg Tyr Pro Leu Pro Leu Arg Ser Gly Lys Glu Ala Lys

50 55 60

Ile Leu Gln His Phe Gly Asp Gly Leu Cys Arg Met Leu Asp Glu Arg

65 70 75 80

Leu Gln Arg His Arg Thr Ser Gly Gly Asp His Ala Pro Asp Ser Pro

85 90 95

Ser Gly Glu Asn Ser Pro Ala Pro Gln Gly Arg Leu Ala Glu Val Gln

100 105 110

Asp Ser Ser Met Pro Val Pro Ala Gln Pro Lys Ala Gly Gly Ser Gly

115 120 125

Ser Tyr Trp Pro Ala Arg His Ser Gly Ala Arg Val Ile Leu Leu Val

130 135 140

Leu Tyr Arg Glu His Leu Asn Pro Asn Gly His His Phe Leu Thr Lys

145 150 155 160

Glu Glu Leu Leu Gln Arg Cys Ala Gln Lys Ser Pro Arg Val Ala Pro

165 170 175

Gly Ser Ala Pro Pro Trp Pro Ala Leu Arg Ser Leu Leu His Arg Asn

180 185 190

Leu Val Leu Arg Thr His Gln Pro Ala Arg Tyr Ser Leu Thr Pro Glu

195 200 205

Gly Leu Glu Leu Ala Gln Lys Leu Ala Glu Ser Glu Gly Leu Ser Leu

210 215 220

Leu Asn Val Gly Ile Gly Pro Lys Glu Pro Pro Gly Glu Glu Thr Ala
225 230 235 240
Val Pro Gly Ala Ala Ser Ala Glu Leu Ala Ser Glu Ala Gly Val Gln
245 250 255
Gln Gln Pro Leu Glu Leu Arg Pro Gly Glu Tyr Arg Val Leu Leu Cys
260 265 270
Val Asp Ile Gly Glu Thr Arg Gly Gly Gly His Arg Pro Glu Leu Leu
275 280 285
Arg Glu Leu Gln Arg Leu His Val Thr His Thr Val Arg Lys Leu His
290 295 300
Val Gly Asp Phe Val Trp Val Ala Gln Glu Thr Asn Pro Arg Asp Pro
305 310 315 320
Ala Asn Pro Gly Glu Leu Val Leu Asp His Ile Val Glu Arg Lys Arg
325 330 335
Leu Asp Asp Leu Cys Ser Ser Ile Ile Asp Gly Arg Phe Arg Glu Gln
340 345 350
Lys Phe Arg Leu Lys Arg Cys Gly Leu Glu Arg Arg Val Tyr Leu Val
355 360 365
Glu Glu His Gly Ser Val His Asn Leu Ser Leu Pro Glu Ser Thr Leu
370 375 380
Leu Gln Ala Val Thr Asn Thr Gln Val Ile Asp Gly Phe Phe Val Lys
385 390 395 400
Arg Thr Ala Asp Ile Lys Glu Ser Ala Ala Tyr Leu Ala Leu Leu Thr
405 410 415
Arg Gly Leu Gln Arg Leu Tyr Gln Gly His Thr Leu Arg Ser Arg Pro
420 425 430
Trp Gly Thr Pro Gly Asn Pro Glu Ser Gly Ala Met Thr Ser Pro Asn
435 440 445
Pro Leu Cys Ser Leu Leu Thr Phe Ser Asp Phe Asn Ala Gly Ala Ile

450. 455 460
 Lys Asn Lys Ala Gln Ser Val Arg Glu Val Phe Ala Arg Gln Leu Met
 465 470 475 480
 Gln Val Arg Gly Val Ser Gly Glu Lys Ala Ala Ala Leu Val Asp Arg
 485 490 495
 Tyr Ser Thr Pro Ala Ser Leu Leu Ala Ala Tyr Asp Ala Cys Ala Thr
 500 505 510
 Pro Lys Glu Gln Glu Thr Leu Leu Ser Thr Ile Lys Cys Gly Arg Leu
 515 520 525
 Gln Arg Asn Leu Gly Pro Ala Leu Ser Arg Thr Leu Ser Gln Leu Tyr
 530 535 540
 Cys Ser Tyr Gly Pro Leu Thr
 545 550

<210> 2200

<211> 696

<212> PRT

<213> Homo sapiens

<400> 2200

Met Ser Ala His Leu Ala Met Ile Asp Thr Leu Met Met Ala Tyr Thr
 1 5 10 15
 Val Glu Met Val Ser Ile Glu Lys Val Ile Ala Cys Ala Gln Gln Tyr
 20 25 30
 Ser Ala Phe Phe Gln Ala Thr Asp Leu Pro Tyr Asp Ile Glu Asp Ala
 35 40 45
 Val Met Tyr Trp Ile Asn Lys Val Asn Glu His Leu Lys Asp Ile Met
 50 55 60

出証特 2 0 0 4 - 3 0 5 9 6 6 1

290 295 300
Gly Val Ser Phe Asp Ile Ser Phe Asp Lys Glu Asp Ser Val Gln Arg
305 310 315 320
Ser Thr Pro Asn Arg Gly Ile Thr Arg Ser Ile Ser Asn Glu Gly Leu
325 330 335
Thr Leu Asn Asn Ser His Val Ser Lys His Ile Arg Lys Asn Leu Ser
340 345 350
Phe Lys Pro Ile Asn Gly Glu Glu Glu Ala Glu Ser Ile Glu Glu Glu
355 360 365
Leu Asn Ile Asp Ser His Ser Asp Leu Lys Ser Cys Val Pro Leu Asn
370 375 380
Thr Asn Glu Leu Asn Ser Asn Glu Asn Ile His Tyr Lys Leu Pro Asn
385 390 395 400
Gly Ala Leu Gln Asn Arg Ile Leu Leu Asp Glu Phe Gly Asn Gln Ile
405 410 415
Glu Thr Pro Ser Ile Glu Glu Ala Leu Gln Ile Ile His Asp Thr Glu
420 425 430
Lys Ser Pro His Thr Pro Gln Pro Asp Gln Ile Ala Asn Gly Phe Phe
435 440 445
Leu His Ser Gln Glu Met Ser Ile Leu Asn Ser Asn Ile Lys Leu Asn
450 455 460
Gln Ser Ser Pro Asp Asn Val Thr Asp Thr Lys Gly Ala Leu Ser Pro
465 470 475 480
Ile Thr Asp Asn Thr Glu Val Asp Thr Gly Ile His Val Pro Ser Glu
485 490 495
Asp Ile Pro Glu Thr Met Asp Glu Asp Ser Ser Leu Arg Asp Tyr Thr
500 505 510
Val Ser Leu Asp Ser Asp Met Asp Asp Ala Ser Lys Phe Leu Gln Asp
515 520 525

Tyr Asp Ile Arg Thr Gly Asn Thr Arg Glu Ala Leu Ser Pro Cys Pro
530 535 540
Ser Thr Val Ser Thr Lys Ser Gln Pro Gly Ser Ser Ala Ser Ser Ser
545 550 555 560
Ser Gly Val Lys Met Thr Ser Phe Ala Glu Gln Lys Phe Arg Lys Leu
565 570 575
Asn His Thr Asp Gly Lys Ser Ser Gly Ser Ser Ser Gln Lys Thr Thr
580 585 590
Pro Glu Gly Ser Glu Leu Asn Ile Pro His Val Val Ala Trp Ala Gln
595 600 605
Ile Pro Glu Glu Thr Gly Leu Pro Gln Gly Arg Asp Thr Thr Gln Leu
610 615 620
Leu Ala Ser Glu Met Val His Leu Arg Met Lys Leu Glu Glu Lys Arg
625 630 635 640
Arg Ala Ile Glu Ala Gln Lys Lys Lys Met Glu Ala Ala Phe Thr Lys
645 650 655
Gln Arg Gln Lys Met Gly Arg Thr Ala Phe Leu Thr Val Val Lys Lys
660 665 670
Lys Gly Asp Gly Ile Ser Pro Leu Arg Glu Glu Ala Ala Gly Ala Glu
675 680 685
Asp Glu Lys Val Tyr Thr Asp Arg
690 695

<210> 2201

<211> 159

<212> PRT

<213> Homo sapiens

<400> 2201

Met Leu Leu Phe Thr Leu Gly Lys Tyr Cys Leu Ser Ile Ser Ser Ala
 1 5 10 15
 Ile Glu Asn Leu Gly Gln Pro Val Leu Pro Thr Cys Leu His Asn Ser
 20 25 30
 Gln Val Ile Gln Phe Gly Phe Pro Thr Asn Leu Pro Ala Ser Ala Ser
 35 40 45
 Ser Cys Ser Lys Gly Glu Arg Leu Lys Gly Lys Leu Ser Gly Gln Thr
 50 55 60
 Pro Ala Leu Thr Gln Pro Trp Glu Glu Met Leu Leu Trp Pro Pro Arg
 65 70 75 80
 Thr Thr Gly Thr Leu Met Thr Glu Thr Ser Leu Thr Leu Asp Leu Leu
 85 90 95
 Ser Leu His Pro Ile Thr Ser Ile Val Val Val Ile Met Leu Leu Cys
 100 105 110
 Asn Val Leu Ile Ile Ala Gly Leu Leu His Trp Thr Val Ser Thr Leu
 115 120 125
 Ile Leu Leu Thr Ala Ser His Pro Ser Phe Pro Met Pro Asn Thr Ile
 130 135 140
 Asn Trp Met Ser Glu Phe Leu Lys Ile Val His Gly Ile His Val
 145 150 155

<210> 2202

<211> 524

<212> PRT

<213> Homo sapiens

<400> 2202

Met Glu Asn Leu Glu Glu Glu Val Ser Gln Ala Glu Asn Ser Leu Leu
 1 5 10 15
 Gln Ala Ala Ala Ala Phe Pro Met Tyr Gly Arg Val His Cys Ile Thr
 20 25 30
 Gly Ala Leu Gln Lys Leu Ser Leu Asn Ser Leu Gln Leu Val Ser Glu
 35 40 45
 Trp Arg Pro Val Val Glu Lys Leu Leu Leu Met Ser Tyr Arg Leu Ser
 50 55 60
 Thr Val Val Ser Pro Val Ile Gln Ser Ser Ser Pro Glu Gly Leu Ile
 65 70 75 80
 Pro Met Asp Thr Asp Ser Glu Ser Ala Ser Arg Leu Gln Met Ile Leu
 85 90 95
 Asn Glu Ile Gln Pro Arg Asp Thr Asn Asp Tyr Phe Asn Gln Ala Lys
 100 105 110
 Ile Leu Lys Glu His Asp Ser Phe Asp Met Lys Asp Leu Asn Ala Ser
 115 120 125
 Val Val Asn Ile Asp Thr Ser Thr Glu Ile Lys Gly Lys Glu Val Lys
 130 135 140
 Thr Cys Asp Val Thr Ala Gln Met Val Leu Val Cys Cys Trp Arg Ser
 145 150 155 160
 Met Lys Glu Val Ala Leu Leu Leu Gly Met Leu Cys Gln Leu Leu Pro
 165 170 175
 Met Gln Pro Val Pro Glu Ser Ser Asp Gly Leu Leu Thr Val Glu Gln
 180 185 190
 Val Lys Glu Ile Gly Asp Tyr Phe Lys Gln His Leu Leu Gln Ser Arg
 195 200 205
 His Arg Gly Ala Phe Glu Leu Ala Tyr Thr Gly Phe Val Lys Leu Thr
 210 215 220
 Glu Val Leu Asn Arg Cys Pro Asn Val Ser Leu Gln Lys Leu Pro Glu

225 230 235 240
Gln Trp Leu Trp Ser Val Leu Glu Glu Ile Lys Cys Ser Asp Pro Ser
 245 250 255
Ser Lys Leu Cys Ala Thr Arg Arg Ser Ala Gly Ile Pro Phe Tyr Ile
 260 265 270
Gln Ala Leu Leu Ala Ser Glu Pro Lys Lys Gly Arg Met Asp Leu Leu
 275 280 285
Lys Ile Thr Met Lys Glu Leu Ile Ser Leu Ala Gly Pro Thr Asp Asp
 290 295 300
Ile Gln Ser Thr Val Pro Gln Val His Ala Leu Asn Ile Leu Arg Ala
305 310 315 320
Leu Phe Arg Asp Thr Arg Leu Gly Glu Asn Ile Ile Pro Tyr Val Ala
 325 330 335
Asp Gly Ala Lys Ala Ala Ile Leu Gly Phe Thr Ser Pro Val Trp Ala
 340 345 350
Val Arg Asn Ser Ser Thr Leu Leu Phe Ser Ala Leu Ile Thr Arg Ile
 355 360 365
Phe Gly Val Lys Arg Ala Lys Asp Glu His Ser Lys Thr Asn Arg Met
 370 375 380
Thr Gly Arg Glu Phe Phe Ser Arg Phe Pro Glu Leu Tyr Pro Phe Leu
385 390 395 400
Leu Lys Gln Leu Glu Thr Val Ala Asn Thr Val Asp Arg Cys Gly His
 405 410 415
Ser Pro Val Tyr His Ser Arg Glu Met Ala Ala Arg Ala Leu Val Pro
 420 425 430
Phe Val Met Ile Asp His Ile Pro Asn Thr Ile Arg Ser Leu Leu Ser
 435 440 445
Thr Leu Pro Ser Cys Thr Asp Gln Cys Phe Arg Gln Asn His Ile His
 450 455 460

Gly Thr Leu Leu Gln Val Phe His Leu Leu Gln Ala Tyr Ser Asp Ser
 465 470 475 480
 Lys His Gly Thr Asn Ser Asp Phe Gln His Glu Leu Thr Asp Ile Thr
 485 490 495
 Val Cys Thr Lys Ala Lys Leu Trp Leu Ala Lys Ser Phe Thr Thr Cys
 500 505 510
 Ala Ser Leu Lys Ile Lys Tyr Phe Cys Leu Phe Phe
 515 520

<210> 2203

<211> 118

<212> PRT

<213> Homo sapiens

<400> 2203

Met His Pro Tyr Asp Val Lys Leu Gly Leu Ile Ala Ser Cys Trp Trp
 1 5 10 15
 Gln Ser Ser Glu Asp Glu Asp Trp Leu Ser Tyr Trp Arg Ala Gly Pro
 20 25 30
 Trp Thr Arg His Leu Leu Leu Arg Pro Asp Glu Asn Gly Pro Gly Pro
 35 40 45
 Leu Ala Thr Arg Cys His Ser Gln Glu Arg Trp Ser Lys Ala Met Gln
 50 55 60
 Cys Gln Leu Arg Phe Glu Lys Gly Val Arg Ser Lys Cys Trp Lys Asp
 65 70 75 80
 Ser Pro Ser Leu Ser Ser Leu Pro Ser Thr Gln Leu Gln Ser Arg Ala
 85 90 95
 Glu Val Thr Thr His Pro Glu Ala Thr Val Glu Glu Thr Gln His Gln

100 105 110
Ala Leu Ser Thr Leu Ser
115

<210> 2204

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2204

Met Met Gly Gln Gly Leu Leu Ser Phe Leu Gln Pro Lys Tyr Cys Pro
1 5 10 15
Ala Pro Glu Ala Pro Ile Pro Pro Gly Ala Gly Ile Thr Gln Ile Phe
20 25 30
Pro Lys Asp His Val Val Pro Ala Glu Trp Thr Thr Pro Ser Thr Leu
35 40 45
Ser Gln Arg Pro Arg Val Pro Trp Gly Arg Glu Thr Gly Lys Asp Gly
50 55 60
Ala Pro Arg Gly Ala Asp Lys Arg Leu Ser Pro Ser Gln Gly Leu Ala
65 70 75 80
Gln Asp Gly Asp Ser Pro Trp Val Trp Ser Trp Val Phe Leu Ser Cys
85 90 95
Pro Gly Gly Arg Gly Arg Gly Thr Arg Met Gly Ala Glu Leu Gln Leu
100 105 110
Ser Arg Val Lys Gly Ser Val Ser Thr Arg His Leu Cys Met Gly Glu
115 120 125
Leu Leu Gly Lys His Trp Pro Leu Pro Ser Val Leu Pro Gln Gly Ser
130 135 140

Ser Arg Gly Pro Glu His Leu Trp Ser Arg Ile Glu Val Cys
 145 150 155

<210> 2205

<211> 130

<212> PRT

<213> Homo sapiens

<400> 2205

Met Gly Ala Leu Asn Ser Ile Ser Leu Glu Thr Asn Lys Ser Ser Phe
 1 5 10 15
 Ser Met Ser Trp Thr Pro Ser Val Glu His Ser Ser Gly Thr Ala Arg
 20 25 30
 Thr Leu Arg Ser Cys Lys Leu Ala Leu Val Gly Phe Ser Ser Met Ser
 35 40 45
 Glu Phe Leu Phe Arg Ala Ser Lys Thr Gln Pro Val Thr Leu Phe Val
 50 55 60
 Pro Asn Val Asn Ser Ala Leu Cys Asp Gln Pro Val Val Arg Gly Val
 65 70 75 80
 Gly Ile His Glu Gln Arg Lys Arg Asn Ile Ser Ser Leu Ile Ser Val
 85 90 95
 Phe Asn His Trp Leu Pro Pro Leu Gln Leu His Leu Gly Arg Ala Leu
 100 105 110
 Ile Cys Arg Phe Asn Ser Arg Gly Asn Phe Thr Cys Leu Met Thr Ala
 115 120 125
 Val Lys
 130

<210> 2206

<211> 160

<212> PRT

<213> Homo sapiens

<400> 2206

Met Ala Ser Pro Ala Pro Leu Val Ala Ser Ile Ser His Gln Met Val

1 5 10 15

Ala Leu Gln Thr Leu Gln Leu Leu Gln Gln Glu Trp Gly Trp Gly Asp

20 25 30

Gly Pro Val Ala Pro Gly Asn Pro Arg Asp Pro Asp His Val Ser Thr

35 40 45

Ala Pro Ala Arg Arg Ser Gly Pro Pro Arg Ala Arg Pro Gly Pro Gly

50 55 60

Arg Glu Glu Arg Gly Gly Gly Val Gly Thr Arg Ser Arg Arg Thr Ala

65 70 75 80

Ala Arg Val Asn Ser Pro Glu Glu Glu Val Val Arg Gly Ala Glu Gly

85 90 95

Gly Ala Glu Leu Leu Pro Phe Pro Arg Asp Arg Gly Pro Cys Thr Leu

100 105 110

Ala Gln Met Ala Met Arg Ser Ala Leu Ala Arg Val Val Asp Ser Thr

115 120 125

Ser Glu Leu Val Ser Val Glu Gln Thr Leu Leu Gly Pro Leu Gln Gln

130 135 140

Glu Arg Ser Phe Pro Ile His Leu Lys Leu Gln Leu Leu Ala Asn Glu

145 150 155 160

<210> 2207

<211> 226

<212> PRT

<213> Homo sapiens

<400> 2207

Met Gln Ala Tyr Asn Pro Leu Ile His Pro Ala Phe Ser Ile Met Ala

1 5 10 15

Leu Phe Phe Ser Ser Lys Val Gln Asn His His Asp Phe Ser Pro Thr

20 25 30

Lys Lys Lys Lys Lys Arg Lys Arg Lys Leu Thr Leu Asn His Lys Ser

35 40 45

Trp Leu Pro Asn Ile Gly His Asn Trp Val Gly Glu Met Tyr Leu Val

50 55 60

Cys Leu Gly Gly Arg Gly Ser Phe Leu Pro Gly Asp Ser Phe Ser Glu

65 70 75 80

His Thr Ala Ile Leu Pro Met Ala Leu Ser Phe Thr Ser Pro Pro Glu

85 90 95

Arg Pro Ala Ser Phe Phe Leu Phe Val Cys Leu Ser Thr Ala Ile Met

100 105 110

Leu Leu Pro Gly Leu Trp Leu Leu Gly Thr His Ser Pro Phe Asn Met

115 120 125

Ala Cys Ser Leu Gln Phe Ser Leu Ser Lys Cys Ser Gln Ser Pro Gly

130 135 140

Leu Cys Ala Lys Gly Asp Ser Ala Leu Ala His Arg Leu Trp Ser Glu

145 150 155 160

Cys Leu Cys Leu Pro Gln Ile Asn Met Leu Lys Phe Asn His Lys Cys

165 170 175

Asp Gly Val Ile Arg Trp Gly Leu Trp Asp Phe Ile Arg Ser Trp Arg

180 185 190
 Gly Ser Leu Ile Lys Lys Ala Ala Leu Pro Pro Pro Ser Cys Lys Ser
 195 200 205
 Pro Ser Val Asn Gln Glu Met Gly Pro His Gln Thr Pro Asn Leu Pro
 210 215 220
 Val Pro
 225

<210> 2208

<211> 140

<212> PRT

<213> Homo sapiens

<400> 2208

Met Lys Lys Val Lys Pro Val Phe Gln Trp Gly Pro Glu Val Gly Glu
 1 5 10 15
 Leu Glu Asp Arg Val Ala Ala Phe Leu Ser Ala Val Pro Lys Arg Gly
 20 25 30
 Pro Ser Pro Ser Arg His Gly Pro Lys Leu Leu Leu Gly Ala Pro Ala
 35 40 45
 Cys Leu Phe Asn Val Cys Leu Ala Pro Phe Pro Gly Glu Ala Thr Pro
 50 55 60
 Gly Thr Ile Ser Gly Leu Arg Arg Thr Thr Ser Leu Lys Gln Pro Leu
 65 70 75 80
 Gly Trp Glu Arg Ser Lys Pro Ser Ala Pro Arg Pro Ser Leu Ser Thr
 85 90 95
 Gly His Glu His Thr Gln Thr Pro Arg Pro Cys Pro Cys Ala Arg Met
 100 105 110

Ala Ala Arg Val Ser Arg His Asp Ala Pro Phe His Glu Cys Thr Glu
115 120 125
Pro Trp Ala Glu Leu Gly Ala Glu Leu His Ala Leu
130 135 140

<210> 2209

<211> 630

<212> PRT

<213> Homo sapiens

<400> 2209

Met Gln Gln Asp Gly Leu Gly Val Gly Thr Arg Asn Gly Ser Gly Lys
1 5 10 15
Gly Arg Ser Val His Pro Ser Trp Pro Trp Cys Ala Pro Arg Pro Leu
20 25 30
Arg Tyr Phe Gly Arg Asp Ala Arg Ala Arg Arg Ala Gln Thr Ala Ala
35 40 45
Met Ala Leu Leu Ala Gly Gly Leu Ser Arg Gly Leu Gly Ser His Pro
50 55 60
Ala Ala Ala Gly Arg Asp Ala Val Val Phe Val Trp Leu Leu Leu Ser
65 70 75 80
Thr Trp Cys Thr Ala Pro Ala Arg Ala Ile Gln Val Thr Val Ser Asn
85 90 95
Pro Tyr His Val Val Ile Leu Phe Gln Pro Val Thr Leu Pro Cys Thr
100 105 110
Tyr Gln Met Thr Ser Thr Pro Thr Gln Pro Ile Val Ile Trp Lys Tyr
115 120 125
Lys Ser Phe Cys Arg Asp Arg Ile Ala Asp Ala Phe Ser Pro Ala Ser

130 135 140
Val Asp Asn Gln Leu Asn Ala Gln Leu Ala Ala Gly Asn Pro Gly Tyr
145 150 155 160
Asn Pro Tyr Val Glu Cys Gln Asp Ser Val Arg Thr Val Arg Val Val
165 170 175
Ala Thr Lys Gln Gly Asn Ala Val Thr Leu Gly Asp Tyr Tyr Gln Gly
180 185 190
Arg Arg Ile Thr Ile Thr Gly Asn Ala Asp Leu Thr Phe Asp Gln Thr
195 200 205
Ala Trp Gly Asp Ser Gly Val Tyr Tyr Cys Ser Val Val Ser Ala Gln
210 215 220
Asp Leu Gln Gly Asn Asn Glu Ala Tyr Ala Glu Leu Ile Val Leu Asp
225 230 235 240
Trp Leu Phe Val Val Val Val Cys Leu Ala Ala Phe Leu Ile Phe Leu
245 250 255
Leu Leu Gly Ile Cys Trp Cys Gln Cys Cys Pro His Thr Cys Cys Cys
260 265 270
Tyr Val Arg Cys Pro Cys Cys Pro Asp Lys Cys Cys Cys Pro Glu Ala
275 280 285
Leu Tyr Ala Ala Gly Lys Ala Ala Thr Ser Gly Val Pro Ser Ile Tyr
290 295 300
Ala Pro Ser Thr Tyr Ala His Leu Ser Pro Ala Lys Thr Pro Pro Pro
305 310 315 320
Pro Ala Met Ile Pro Met Gly Pro Ala Tyr Asn Gly Tyr Pro Gly Gly
325 330 335
Tyr Pro Gly Asp Val Asp Arg Asn Ser Ser Ala Gly Gly Gln Gly Ser
340 345 350
Tyr Val Pro Leu Leu Arg Asp Thr Asp Ser Ser Val Ala Ser Val Arg
355 360 365

Ser Gly Tyr Arg Ile Gln Ala Ser Gln Gln Asp Asp Ser Met Arg Val
 370 375 380
 Leu Tyr Tyr Met Glu Lys Glu Leu Ala Asn Phe Asp Pro Ser Arg Pro
 385 390 395 400
 Gly Pro Pro Ser Gly Arg Val Glu Arg Ala Met Ser Glu Val Thr Ser
 405 410 415
 Leu His Glu Asp Asp Trp Arg Ser Arg Pro Ser Arg Gly Pro Ala Leu
 420 425 430
 Thr Pro Ile Arg Asp Glu Glu Trp Gly Gly His Ser Pro Arg Ser Pro
 435 440 445
 Arg Gly Trp Asp Gln Glu Pro Ala Arg Glu Gln Ala Gly Gly Gly Trp
 450 455 460
 Arg Ala Arg Arg Pro Arg Ala Arg Ser Val Asp Ala Leu Asp Asp Leu
 465 470 475 480
 Thr Pro Pro Ser Thr Ala Glu Ser Gly Ser Arg Ser Pro Thr Ser Asn
 485 490 495
 Gly Gly Arg Arg Ser Arg Ala Tyr Met Pro Pro Arg Ser Arg Ser Arg
 500 505 510
 Asp Asp Leu Tyr Asp Gln Asp Asp Ser Arg Asp Phe Pro Arg Ser Arg
 515 520 525
 Asp Pro His Tyr Asp Asp Phe Arg Ser Arg Glu Arg Pro Pro Ala Asp
 530 535 540
 Pro Arg Ser His His His Arg Thr Arg Asp Pro Arg Asp Asn Gly Ser
 545 550 555 560
 Arg Ser Gly Asp Leu Pro Tyr Asp Gly Arg Leu Leu Glu Glu Ala Val
 565 570 575
 Arg Lys Lys Gly Ser Glu Glu Arg Arg Arg Pro His Lys Glu Glu Glu
 580 585 590
 Glu Glu Ala Tyr Tyr Pro Pro Ala Pro Pro Pro Tyr Ser Glu Thr Asp

595 600 605
 Ser Gln Ala Ser Arg Glu Arg Arg Leu Lys Lys Asn Leu Ala Leu Ser
 610 615 620
 Arg Glu Ser Leu Val Val
 625 630

<210> 2210

<211> 575

<212> PRT

<213> Homo sapiens

<400> 2210

Met His Glu Thr Asn Gln Gly Glu Phe Ile Ala Ser Asp Ser Gln Glu
 1 5 10 15
 Ala Leu Phe Ser Lys Ser Ser Arg Gly Cys Leu Gln Asn Glu Lys Gln
 20 25 30
 Asp Glu Thr Leu Ser Ser Ser Glu Ile Thr Leu Trp Thr Glu Lys Gln
 35 40 45
 Ser Asn Gly Asp Lys Lys Ser Ile Glu Leu Asn Asp Gln Lys Phe Asn
 50 55 60
 Glu Leu Ile Lys Asn Cys Asn Lys His Asp Gly Arg Gly Ile Ile Val
 65 70 75 80
 Asp Ala Arg Gln Leu Pro Ser Pro Glu Pro Cys Glu Ile Gln Lys Asn
 85 90 95
 Leu Asn Asp Asn Glu Met Leu Phe His Ser Cys Gln Met Val Glu Glu
 100 105 110
 Ser His Glu Glu Glu Glu Leu Lys Pro Pro Glu Gln Glu Ile Glu Ile
 115 120 125

Asp Arg Asn Ile Ile Gln Glu Glu Glu Lys Gln Ala Ile Pro Glu Phe
 130 135 140
 Phe Glu Gly Arg Gln Ala Lys Thr Pro Glu Arg Tyr Leu Lys Ile Arg
 145 150 155 160
 Asn Tyr Ile Leu Asp Gln Trp Glu Ile Cys Lys Pro Lys Tyr Leu Asn
 165 170 175
 Lys Thr Ser Val Arg Pro Gly Leu Lys Asn Cys Gly Asp Val Asn Cys
 180 185 190
 Ile Gly Arg Ile His Thr Tyr Leu Glu Leu Ile Gly Ala Ile Asn Phe
 195 200 205
 Gly Cys Glu Gln Ala Val Tyr Asn Arg Pro Gln Thr Val Asp Lys Val
 210 215 220
 Arg Ile Arg Asp Arg Lys Asp Ala Val Glu Ala Tyr Gln Leu Ala Gln
 225 230 235 240
 Arg Leu Gln Ser Met Arg Thr Arg Arg Arg Arg Val Arg Asp Pro Trp
 245 250 255
 Gly Asn Trp Cys Asp Ala Lys Asp Leu Glu Gly Gln Thr Phe Glu His
 260 265 270
 Leu Ser Ala Glu Glu Leu Ala Lys Arg Arg Glu Glu Glu Lys Asp Arg
 275 280 285
 Pro Val Lys Ser Leu Lys Val Pro Arg Pro Thr Lys Ser Ser Phe Asp
 290 295 300
 Pro Phe Gln Leu Ile Pro Cys Asn Phe Phe Ser Glu Glu Lys Gln Glu
 305 310 315 320
 Pro Phe Gln Val Lys Val Ala Ser Glu Ala Leu Leu Ile Met Asp Leu
 325 330 335
 His Ala His Val Ser Met Ala Glu Val Ile Gly Leu Leu Gly Gly Arg
 340 345 350
 Tyr Ser Glu Val Asp Lys Val Val Glu Val Cys Ala Ala Glu Pro Cys

355 360 365
Asn Ser Leu Ser Thr Gly Leu Gln Cys Glu Met Asp Pro Val Ser Gln
370 375 380
Thr Gln Ala Ser Glu Thr Leu Ala Val Arg Gly Phe Ser Val Ile Gly
385 390 395 400
Trp Tyr His Ser His Pro Ala Phe Asp Pro Asn Pro Ser Leu Arg Asp
405 410 415
Ile Asp Thr Gln Ala Lys Tyr Gln Ser Tyr Phe Ser Arg Gly Gly Ala
420 425 430
Lys Phe Ile Gly Met Ile Val Ser Pro Tyr Asn Arg Asn Asn Pro Leu
435 440 445
Pro Tyr Ser Gln Ile Thr Cys Leu Val Ile Ser Glu Glu Ile Ser Pro
450 455 460
Asp Gly Ser Tyr Arg Leu Pro Tyr Lys Phe Glu Val Gln Gln Met Leu
465 470 475 480
Glu Glu Pro Gln Trp Gly Leu Val Phe Glu Lys Thr Arg Trp Ile Ile
485 490 495
Glu Lys Tyr Arg Leu Ser His Ser Ser Val Pro Met Asp Lys Ile Phe
500 505 510
Arg Arg Asp Ser Asp Leu Thr Cys Leu Gln Lys Leu Leu Glu Cys Met
515 520 525
Arg Lys Thr Leu Ser Lys Val Thr Asn Cys Phe Met Ala Glu Glu Phe
530 535 540
Leu Thr Glu Ile Glu Asn Leu Phe Leu Ser Asn Tyr Lys Ser Asn Gln
545 550 555 560
Glu Asn Gly Val Thr Glu Glu Asn Cys Thr Lys Glu Leu Leu Met
565 570 575

<210> 2211

<211> 509

<212> PRT

<213> Homo sapiens

<400> 2211

Met Leu Val Val Leu Leu Gln Gly Thr Arg Glu Glu Asp Asp Val Val

1 5 10 15

Ser Glu Asp Leu Val Gln Gln Asp Val Gln Asp Leu Tyr Glu Ala Gly

20 25 30

Glu Leu Lys Trp Gly Thr Asp Glu Ala Gln Phe Ile Tyr Ile Leu Gly

35 40 45

Asn Arg Ser Lys Gln His Leu Arg Leu Val Phe Asp Glu Tyr Leu Lys

50 55 60

Thr Thr Gly Lys Pro Ile Glu Ala Ser Ile Arg Gly Glu Leu Ser Gly

65 70 75 80

Asp Phe Glu Lys Leu Met Leu Ala Val Val Lys Arg Ile Arg Ser Thr

85 90 95

Pro Glu Tyr Phe Ala Glu Arg Leu Phe Lys Ala Met Lys Gly Leu Gly

100 105 110

Thr Arg Asp Asn Thr Leu Ile Arg Ile Met Val Ser Arg Ser Glu Leu

115 120 125

Asp Met Leu Asp Ile Arg Glu Ile Phe Arg Thr Lys Tyr Glu Lys Ser

130 135 140

Leu Tyr Ser Met Ile Lys Asn Asp Thr Ser Gly Glu Tyr Lys Lys Thr

145 150 155 160

Leu Leu Lys Leu Ser Gly Gly Asp Asp Asp Ala Ala Gly Gln Phe Phe

165 170 175

Pro Glu Ala Ala Gln Val Ala Tyr Gln Met Trp Glu Leu Ser Ala Val

180 185 190
Ala Arg Val Glu Leu Lys Gly Thr Val Arg Pro Ala Asn Asp Phe Asn
195 200 205
Pro Asp Ala Asp Ala Lys Ala Leu Arg Lys Ala Met Lys Gly Leu Gly
210 215 220
Thr Asp Glu Asp Thr Ile Ile Asp Ile Ile Thr His Arg Ser Asn Val
225 230 235 240
Gln Arg Gln Gln Ile Arg Gln Thr Phe Lys Ser His Phe Gly Arg Asp
245 250 255
Leu Met Thr Asp Leu Lys Ser Glu Ile Ser Gly Asp Leu Ala Arg Leu
260 265 270
Ile Leu Gly Leu Met Met Pro Pro Ala His Tyr Asp Ala Lys Gln Leu
275 280 285
Lys Lys Ala Met Glu Gly Ala Gly Thr Asp Glu Lys Ala Leu Ile Glu
290 295 300
Ile Leu Ala Thr Arg Thr Asn Ala Glu Ile Arg Ala Ile Asn Glu Ala
305 310 315 320
Tyr Lys Glu Asp Tyr His Lys Ser Leu Glu Asp Ala Leu Ser Ser Asp
325 330 335
Thr Ser Gly His Phe Arg Arg Ile Leu Ile Ser Leu Ala Thr Gly His
340 345 350
Arg Glu Glu Gly Gly Glu Asn Leu Asp Gln Ala Arg Glu Asp Ala Gln
355 360 365
Val Ala Ala Glu Ile Leu Glu Ile Ala Asp Thr Pro Ser Gly Asp Lys
370 375 380
Thr Ser Leu Glu Thr Arg Phe Met Thr Ile Leu Cys Thr Arg Ser Tyr
385 390 395 400
Pro His Leu Arg Arg Val Phe Gln Glu Phe Ile Lys Met Thr Asn Tyr
405 410 415

Asp Val Glu His Thr Ile Lys Lys Glu Met Ser Gly Asp Val Arg Asp

420

425

430

Ala Phe Val Ala Ile Val Gln Ser Val Lys Asn Lys Pro Leu Phe Phe

435

440

445

Ala Asp Lys Leu Tyr Lys Ser Met Lys Gly Ala Gly Thr Asp Glu Lys

450

455

460

Thr Leu Thr Arg Ile Met Val Ser Arg Ser Glu Ile Asp Leu Leu Asn

465

470

475

480

Ile Arg Arg Gly Trp Val Gly Leu Leu Ser Ser Val Glu Leu Arg Lys

485

490

495

Arg Ser His Ser His Gly Pro Ser Arg Ala Gln His Gly

500

505

<210> 2212

<211> 232

<212> PRT

<213> Homo sapiens

<400> 2212

Met Ala Ser Pro Pro Gly Leu Glu Leu Lys Thr Leu Ser Asn Gly Pro

1

5

10

15

Gln Ala Pro Arg Arg Ser Ala Pro Leu Gly Pro Val Ala Pro Thr Arg

20

25

30

Glu Gly Val Glu Asn Ala Cys Phe Ser Ser Glu Glu His Glu Thr His

35

40

45

Phe Gln Asn Pro Gly Asn Thr Arg Leu Gly Ser Ser Pro Ser Pro Pro

50

55

60

Gly Gly Val Ser Ser Leu Pro Arg Ser Gln Arg Asp Asp Leu Ser Leu

65 70 75 80
His Ser Glu Glu Gly Pro Ala Leu Glu Pro Val Ser Arg Pro Val Asp
 85 90 95
Tyr Gly Phe Val Ser Ala Leu Val Phe Leu Val Ser Gly Ile Leu Leu
 100 105 110
Val Val Thr Ala Tyr Ala Ile Pro Arg Glu Ala Arg Val Asn Pro Asp
 115 120 125
Thr Val Thr Ala Arg Glu Met Glu Arg Leu Glu Met Tyr Tyr Ala Arg
 130 135 140
Leu Gly Ser His Leu Asp Arg Cys Ile Ile Ala Gly Leu Gly Leu Leu
145 150 155 160
Thr Val Gly Gly Met Leu Leu Ser Val Leu Leu Met Val Ser Leu Cys
 165 170 175
Lys Gly Glu Leu Tyr Arg Arg Arg Thr Phe Val Pro Gly Lys Gly Ser
 180 185 190
Arg Lys Thr Tyr Gly Ser Ile Asn Leu Arg Met Arg Gln Leu Asn Gly
 195 200 205
Asp Gly Gly Gln Ala Leu Val Glu Asn Glu Val Val Gln Val Ser Glu
 210 215 220
Thr Ser His Thr Leu Gln Arg Ser
225 230

<210> 2213

<211> 190

<212> PRT

<213> Homo sapiens

<400> 2213

Met	Ser	Val	Gly	Pro	Ser	Pro	Phe	Ser	Arg	Gly	Pro	Gly	Arg	Gly	Leu
1				5						10				15	
Gly	Trp	Gly	Pro	Ser	Phe	Ala	Asp	Ala	Cys	Leu	Ser	Val	Leu	Pro	Cys
			20					25					30		
Leu	Pro	Cys	Pro	His	Leu	Leu	Phe	His	Cys	His	Phe	Cys	Val	Cys	Leu
		35					40					45			
Arg	Met	Leu	Ser	Gly	Tyr	His	Pro	Ile	His	Leu	Cys	Leu	Leu	Pro	Gly
	50					55					60				
Pro	Leu	Ser	Leu	Ala	Leu	Ile	Leu	Leu	Cys	Leu	Leu	Gly	Cys	Leu	Ser
65				70						75				80	
Leu	His	Ser	Pro	Val	Leu	Ala	Phe	Arg	Ser	Pro	Phe	Leu	Ser	Ser	Gly
				85					90					95	
Leu	Leu	Cys	Val	Thr	Ser	Val	Ser	Thr	Ser	Gly	Pro	Trp	Leu	Pro	Ser
			100					105					110		
Trp	Ser	His	Leu	Phe	Ser	Pro	Tyr	Pro	Cys	Phe	Ser	Leu	Pro	Val	Ile
		115					120					125			
Ser	Gly	Ala	Gly	Leu	Cys	Pro	Ser	Ile	Pro	Val	Ser	Ile	Ser	Val	Leu
		130					135					140			
Gly	Pro	Ala	Cys	Ser	His	Phe	Pro	Leu	Ile	Leu	Ala	Pro	Leu	Pro	Ala
145					150					155				160	
Pro	Pro	Thr	Ser	Pro	Leu	Ala	Pro	Leu	Pro	Phe	Phe	Leu	Ala	Gly	Ser
					165					170				175	
Ala	Arg	Gly	Pro	Asn	Cys	Gly	Asp	Thr	Met	Ala	His	Gly	Phe		
			180						185				190		

<210> 2214

<211> 107

<212> PRT

<213> Homo sapiens

<400> 2214

Met Phe Ser Ala His Cys Asn Leu Arg Leu Pro Gly Ser Gly Asp Ser
1 5 10 15
Pro Ala Leu Ala Ser Gln Val Ala Gly Ile Ala Gly Val Arg His His
20 25 30
Ala Trp Leu Ile Phe Val Phe Leu Val Glu Thr Gly Phe His Arg Val
35 40 45
Gly Arg Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro Ala Ser
50 55 60
Ala Ser Arg Gly Ala Gly Val Thr Gly Val Ser His Cys Ala Gln Pro
65 70 75 80
Leu Asn Ala Leu Gln Tyr Arg Asp Ala Ile Leu Asp Cys Leu Leu Leu
85 90 95
Gly Gly Arg Ala Gly Glu Gly Glu Ile Leu Leu
100 105

<210> 2215

<211> 219

<212> PRT

<213> Homo sapiens

<400> 2215

Met Val Lys Met Leu Pro Ala Gln Glu Ala Ala Lys Ile Tyr His Thr
1 5 10 15
Asn Tyr Val Arg Asn Ser Arg Ala Val Gly Val Met Trp Gly Thr Leu
20 25 30

Thr Ile Cys Phe Ser Val Leu Val Met Ala Leu Phe Ile Gln Pro Tyr
35 40 45
Trp Ile Gly Asp Ser Val Asn Thr Pro Gln Ala Gly Tyr Phe Gly Leu
50 55 60
Phe Ser Tyr Cys Val Gly Asn Val Leu Ser Ser Glu Leu Ile Cys Lys
65 70 75 80
Gly Gly Pro Leu Asp Phe Ser Ser Ile Pro Ser Arg Ala Phe Lys Thr
85 90 95
Ala Met Phe Phe Val Ala Leu Gly Met Phe Leu Ile Ile Gly Ser Ile
100 105 110
Ile Cys Phe Ser Leu Phe Phe Ile Cys Asn Thr Ala Thr Val Tyr Lys
115 120 125
Ile Cys Ala Trp Met Gln Leu Ala Ala Ala Thr Gly Leu Met Ile Gly
130 135 140
Cys Leu Val Tyr Pro Asp Gly Trp Asp Ser Ser Glu Val Arg Arg Met
145 150 155 160
Cys Gly Glu Gln Thr Gly Lys Tyr Thr Leu Gly His Cys Thr Ile Arg
165 170 175
Trp Ala Phe Met Leu Ala Ile Leu Ser Ile Gly Asp Ala Leu Ile Leu
180 185 190
Ser Phe Leu Ala Phe Val Leu Gly Tyr Arg Gln Asp Lys Leu Leu Pro
195 200 205
Asp Asp Tyr Lys Ala Asp Gly Thr Glu Glu Val
210 215

<210> 2216

<211> 177

<212> PRT

<213> Homo sapiens

<400> 2216

Met Arg Arg Phe Ile Leu Glu Arg Asn Pro Thr Asn Val Lys Asn Met

1 5 10 15

Ala Lys Leu Ser Pro Ile Pro His Thr Leu Leu Gly Ile Arg Lys Phe

20 25 30

Met Leu Glu Arg Asn His Thr Ser Val Ile Asn Val Ala Gln Pro Leu

35 40 45

Phe Tyr Pro Gln Pro Leu Val Asn Met Arg Arg Phe Ile Leu Glu Arg

50 55 60

Asn Ser Thr Asn Val Lys Asn Val Ala Lys Pro Ser Thr Ile Phe His

65 70 75 80

Thr Leu Leu Tyr Ile Arg Gln Phe Ile Leu Glu Arg Asn Ala Ile Asn

85 90 95

Gly Ile Lys Thr Phe Thr Trp Ser Ser Ser Pro His Lys His Arg Arg

100 105 110

Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala

115 120 125

Phe Thr Ala Ser Ser Thr Leu Ser Glu Tyr Lys Thr Ile His Thr Gly

130 135 140

Glu Lys Pro Tyr Lys Cys Glu Glu Cys Gly Lys Ala Phe Asn Trp Ser

145 150 155 160

Ser Asp Phe Asn Lys His Lys Arg Ile His Ser Gly Gln Lys Pro Ile

165 170 175

Leu

<210> 2217

<211> 158

<212> PRT

<213> Homo sapiens

<400> 2217

Met	Gln	Gln	Met	Met	Glu	Pro	Cys	Ser	Thr	Gln	Lys	Arg	Lys	Ser	Arg
1				5					10					15	
Arg	Ala	Leu	Val	Asp	Glu	Ser	Asn	Pro	Asp	Val	Pro	Gly	Pro	Leu	Ala
			20					25						30	
Thr	Ser	Thr	Thr	Gln	Arg	Gly	His	Val	His	Thr	Glu	Gly	Pro	Arg	Pro
			35				40						45		
Pro	His	Arg	Gly	Ala	Thr	Ser	Thr	Thr	Gln	Gly	Pro	Leu	Gly	Leu	Arg
			50				55						60		
Ile	Ser	Pro	Trp	Pro	Ala	Arg	Val	Ser	Ser	Phe	Pro	Asp	Leu	Trp	Asn
			65			70				75				80	
Lys	Ser	Leu	Ser	Gln	Glu	Gly	Leu	Glu	Leu	Glu	Pro	Leu	Lys	Arg	Pro
				85					90					95	
Pro	Leu	Leu	Ala	Arg	Met	Val	Asp	Arg	Lys	Gln	Cys	His	Val	Leu	Lys
			100						105					110	
Glu	Leu	His	Gln	Pro	Met	Leu	Leu	Trp	Lys	Thr	Gln	Gly	Arg	Gln	Arg
			115					120					125		
Arg	Trp	Leu	Gln	Met	Ala	Ala	Pro	Ile	Gly	Thr	Leu	Leu	Thr	Ser	Pro
			130				135						140		
Thr	Gly	Pro	Gly	Lys	Pro	Gly	Trp	Ala	Trp	Ala	Gly	Glu	Pro		
			145				150						155		

<210> 2218

<211> 172

<212> PRT

<213> Homo sapiens

<400> 2218

Met Pro Arg Ala Ser Cys Cys His Cys Leu Cys Gly Pro Glu Ser Trp

1 5 10 15

Thr Cys Pro Ser Asp Ser Gly Val Ala Ala Trp Ala Gly Ser Val Thr

20 25 30

Leu Gly Cys Tyr Thr Phe Trp Glu Leu Asp Arg Ser Gly Cys Leu Gly

35 40 45

Gly Leu Trp His Pro Gly Met Leu Tyr Ile Leu Gly Thr Gly Gln Glu

50 55 60

Trp Leu Leu Gly Trp Ala Leu Ala Pro Trp Asp Val Ile His Ser Gly

65 70 75 80

Asn Cys Asn Gln Pro Leu Glu Lys Ser Glu Leu Gln Glu Val Thr Leu

85 90 95

Gly Trp Asp Leu Gly Thr Trp Pro Gly Gln His Gly Asp Thr Arg Leu

100 105 110

Gln Gln Glu Leu Trp Ser Val Leu Gly Ser Leu Gly Ala Gly Leu Arg

115 120 125

Pro Trp Ala Gly Phe Leu Gln Ala Glu Val Leu Gly Lys Trp Gly Ser

130 135 140

Gln Ala Ser Cys Arg Leu Pro His Tyr Val Ala Ser Asp Ser Ser Ser

145 150 155 160

Leu Met Lys Ala Ile Trp Phe Ile Thr Leu Lys Leu

165 170

<210> 2219

<211> 141

<212> PRT

<213> Homo sapiens

<400> 2219

Met Ala Arg Gly Thr Pro Phe Ser Pro Thr Pro Ser Ser Gly Ser Ala

1 5 10 15

Pro Glu Leu Arg Ser Met His Arg Asn Ala Ala Gly Ser Glu Leu Ser

20 25 30

Glu Arg Gly Leu Arg Glu Thr Glu Ala Thr Arg Glu Cys Arg Gly Glu

35 40 45

Glu Ala Gly Gly Leu Ala Ser Gln Phe Arg Ala Leu Arg Ala Ser Arg

50 55 60

Gly Arg Ser Gly Gly Cys Arg Pro Ser Pro Ala Leu Gly Ser Gly Arg

65 70 75 80

Gly Ser Gln Thr Ser Leu Pro Ser Gly Pro Gly Met Pro Ala Pro Gln

85 90 95

Ser Ser Gln Arg Asn Pro Ala Asn Arg Gly Ala Gln Gln Ser Arg Gly

100 105 110

Gly Arg His Gln Gln Pro Thr Cys Ser Val Glu Gly Thr Leu Pro Ser

115 120 125

Ile Ala Ala Thr Ala Asp Ala Arg Arg Ser Ser Ser Arg

130 135 140

<210> 2220

<211> 707

<212> PRT

<213> Homo sapiens

<400> 2220

Met	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly	Arg	Leu	Gly	Trp	Leu	Phe	Ala
1				5				10					15		
Ala	Leu	Cys	Leu	Gly	Asn	Ala	Ala	Gly	Glu	Ala	Ala	Pro	Gly	Pro	Arg
			20					25					30		
Val	Leu	Gly	Phe	Cys	Leu	Glu	Glu	Asp	Gly	Ala	Ala	Gly	Ala	Gly	Trp
			35					40					45		
Val	Arg	Gly	Gly	Ala	Ala	Arg	Asp	Thr	Pro	Asp	Ala	Thr	Phe	Leu	Leu
			50					55					60		
Arg	Leu	Phe	Gly	Pro	Gly	Phe	Ala	Asn	Ser	Ser	Trp	Ser	Trp	Val	Ala
			65					70					75		80
Pro	Glu	Gly	Ala	Gly	Cys	Arg	Glu	Glu	Ala	Ala	Ser	Pro	Ala	Gly	Glu
								85					90		95
Trp	Arg	Ala	Leu	Leu	Arg	Leu	Arg	Leu	Arg	Ala	Glu	Ala	Val	Arg	Pro
			100					105					110		
His	Ser	Ala	Leu	Leu	Ala	Val	Arg	Val	Glu	Pro	Gly	Gly	Gly	Ala	Ala
			115					120					125		
Glu	Glu	Ala	Ala	Pro	Pro	Trp	Ala	Leu	Gly	Leu	Gly	Ala	Ala	Gly	Leu
			130					135					140		
Leu	Ala	Leu	Ala	Ala	Leu	Ala	Arg	Gly	Leu	Gln	Leu	Ser	Ala	Leu	Ala
			145					150					155		160
Leu	Ala	Pro	Ala	Glu	Val	Gln	Val	Leu	Arg	Glu	Ser	Gly	Ser	Glu	Ala
								165					170		175
Glu	Arg	Ala	Ala	Ala	Arg	Arg	Leu	Glu	Pro	Ala	Arg	Arg	Trp	Ala	Gly
			180					185					190		
Cys	Ala	Leu	Gly	Ala	Leu	Leu	Leu	Leu	Ala	Ser	Leu	Ala	Gln	Ala	Ala
								195					200		205

Leu Ala Val Leu Leu Tyr Arg Ala Ala Gly Gln Arg Ala Val Pro Ala
210 215 220
Val Leu Gly Ser Ala Gly Leu Val Phe Leu Val Gly Glu Val Val Pro
225 230 235 240
Ala Ala Val Ser Gly Arg Trp Thr Leu Ala Leu Ala Pro Arg Ala Leu
245 250 255
Gly Leu Ser Arg Leu Ala Val Leu Leu Thr Leu Pro Val Ala Leu Pro
260 265 270
Val Gly Gln Leu Leu Glu Leu Ala Ala Arg Pro Gly Arg Leu Arg Glu
275 280 285
Arg Val Leu Glu Leu Ala Arg Gly Gly Gly Asp Pro Tyr Ser Asp Leu
290 295 300
Ser Lys Gly Val Leu Arg Cys Arg Thr Val Glu Asp Val Leu Thr Pro
305 310 315 320
Leu Glu Asp Cys Phe Met Leu Asp Ala Ser Thr Val Leu Asp Phe Gly
325 330 335
Val Leu Ala Ser Ile Met Gln Ser Gly His Thr Arg Ile Pro Val Tyr
340 345 350
Glu Glu Glu Arg Ser Asn Ile Val Asp Met Leu Tyr Leu Lys Asp Leu
355 360 365
Ala Phe Val Asp Pro Glu Asp Cys Thr Pro Leu Ser Thr Ile Thr Arg
370 375 380
Phe Tyr Asn His Pro Leu His Phe Val Phe Asn Asp Thr Lys Leu Asp
385 390 395 400
Ala Val Leu Glu Glu Phe Lys Arg Gly Lys Ser His Leu Ala Ile Val
405 410 415
Gln Lys Val Asn Asn Glu Gly Glu Gly Asp Pro Phe Tyr Glu Val Leu
420 425 430
Gly Leu Val Thr Leu Glu Asp Val Ile Glu Glu Ile Ile Arg Ser Glu

435 440 445
Ile Leu Asp Glu Ser Glu Asp Tyr Arg Asp Thr Val Val Lys Arg Lys
450 455 460
Pro Ala Ser Leu Met Ala Pro Leu Lys Arg Lys Glu Glu Phe Ser Leu
465 470 475 480
Phe Lys Val Ser Asp Asp Glu Tyr Lys Val Thr Ile Ser Pro Gln Leu
485 490 495
Leu Leu Ala Thr Gln Arg Phe Leu Ser Arg Glu Val Asp Val Phe Ser
500 505 510
Pro Leu Arg Ile Ser Glu Lys Val Leu Leu His Leu Leu Lys His Pro
515 520 525
Ser Val Asn Gln Glu Val Arg Phe Asp Glu Ser Asn Arg Leu Ala Thr
530 535 540
His His Tyr Leu Tyr Gln Arg Ser Gln Pro Val Asp Tyr Phe Ile Leu
545 550 555 560
Ile Leu Gln Gly Arg Val Glu Val Glu Ile Gly Lys Glu Gly Leu Lys
565 570 575
Phe Glu Asn Gly Ala Phe Thr Tyr Tyr Gly Val Ser Ala Leu Thr Val
580 585 590
Pro Ser Ser Val His Gln Ser Pro Val Ser Ser Leu Gln Pro Ile Arg
595 600 605
His Asp Leu Gln Pro Asp Pro Gly Asp Gly Thr His Ser Ser Ala Tyr
610 615 620
Cys Pro Asp Tyr Thr Val Arg Ala Leu Ser Asp Leu Gln Leu Ile Lys
625 630 635 640
Val Thr Arg Leu Gln Tyr Leu Asn Ala Leu Leu Ala Thr Arg Ala Gln
645 650 655
Asn Leu Pro Gln Ser Pro Glu Asn Thr Asp Leu Gln Val Ile Pro Gly
660 665 670

Ser Gln Thr Arg Leu Leu Gly Glu Lys Thr Thr Thr Ala Ala Gly Ser

675

680

685

Ser His Ser Arg Pro Gly Val Pro Val Glu Gly Ser Pro Gly Arg Asn

690

695

700

Pro Gly Val

705

<210> 2221

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2221

Met Asn Gly Leu Glu Val Ala Pro Pro Gly Leu Ile Thr Asn Phe Ser

1

5

10

15

Leu Ala Thr Ala Glu Gln Cys Gly Gln Glu Thr Pro Leu Glu Asn Met

20

25

30

Leu Phe Ala Ser Phe Tyr Leu Leu Asp Phe Ile Pro Ala Leu Val Gly

35

40

45

Asn Thr Leu Ala Leu Trp Leu Phe Ile Arg Asp His Lys Ser Gly Thr

50

55

60

Pro Ala Asn Val Phe Leu Met His Leu Ala Val Ala Asp Leu Ser Cys

65

70

75

80

Val Leu Val Leu Pro Thr Arg Leu Val Tyr His Phe Ser Gly Asn His

85

90

95

Trp Pro Phe Gly Glu Ile Ala Cys Arg Leu Thr Gly Phe Leu Phe Tyr

100

105

110

Leu Asn Met Tyr Ala Ser Ile Tyr Phe Leu Thr Cys Ile Ser Ala Asp

115	120	125
Arg Phe Leu Ala Ile Val His Pro Val Lys Ser Leu Lys Leu Arg Arg		
130	135	140
Pro Leu Tyr Ala His Leu Ala Cys Ala Phe Leu Trp Val Val Val Ala		
145	150	155
Val Ala Met Ala Pro Leu Leu Val Ser Pro Gln Thr Val Gln Thr Asn		
165	170	175
His Thr Val Val Cys Leu Gln Leu Tyr Arg Glu Lys Ala Ser His His		
180	185	190
Ala Leu Val Ser Leu Ala Val Ala Phe Thr Phe Pro Phe Ile Thr Thr		
195	200	205
Val Thr Cys Tyr Leu Leu Ile Ile Arg Ser Leu Arg Gln Gly Leu Arg		
210	215	220
Ala Glu Lys Arg Leu Lys Thr Lys Ala Val Arg Met Ile Ala Ile Val		
225	230	235
Leu Ala Ile Phe Leu Val Cys Phe Val Pro Tyr His Val Asn Arg Ser		
245	250	255
Val Tyr Val Leu His Tyr Arg Ser His Gly Ala Ser Cys Ala Thr Gln		
260	265	270
Arg Ile Leu Ala Leu Ala Asn Arg Ile Thr Ser Cys Leu Thr Arg Leu		
275	280	285
Asn Gly Ala Leu Asp Pro Ile Met Tyr Phe Phe Val Ala Glu Lys Phe		
290	295	300
Arg His Ala Leu Cys Asn Leu Leu Cys Gly Lys Arg Leu Lys Gly Pro		
305	310	315
Pro Pro Ser Phe Glu Gly Lys Thr Asn Glu Ser Ser Leu Ser Ala Lys		
325	330	335
Ser Glu Leu		

<210> 2222

<211> 136

<212> PRT

<213> Homo sapiens

<400> 2222

Met Val Arg Gly Trp Pro Gly Ser Ile Ser His Gly Cys Ser Leu Asn

1 5 10 15

Cys Ile Gln Leu Leu Ile Val Thr His Met Ser Thr Gly Leu Thr His

20 25 30

Phe Ser Ser Val Ser His Ser Thr Thr Lys Glu His His Thr Gln Asp

35 40 45

Ser Gly Glu Ser His Arg Leu Glu Glu Pro Gly Ala Trp Pro His Leu

50 55 60

Gly Leu Ile Ser Ser Val Gly Cys Arg Ser Cys Ala Arg Ser Ser Trp

65 70 75 80

Val Leu Ala Ser Cys Cys Met Arg Arg Lys Trp Arg Ala Ala Pro Ile

85 90 95

Ser Ser Thr Val Thr Met Ala Gly Trp Val Ser Ser Arg Arg Val Thr

100 105 110

Cys Glu Gln Ser Pro Gly Leu Arg Val Ile Glu Val Pro Asn Val Arg

115 120 125

Gly Leu Ala Gly Ser Tyr Gln Gly

130 135

<210> 2223

<211> 1101

<212> PRT

<213> Homo sapiens

<400> 2223

Met Ser Glu Glu Pro Lys Glu Lys Asn Ala Lys Pro Ala His Arg Lys

1 5 10 15

Arg Lys Gly Lys Lys Ser Asp Ala Asn Ala Ser Tyr Leu Arg Ala Ala

20 25 30

Arg Ala Gly His Leu Glu Lys Ala Leu Gly Tyr Ile Ser Val Val Asp

35 40 45

Thr Leu Lys Ile Val Thr Glu Glu Thr Met Thr Thr Thr Thr Val Thr

50 55 60

Glu Lys His Lys Met Asn Val Pro Glu Thr Met Asn Glu Val Leu Asp

65 70 75 80

Met Ser Asp Asp Glu Val Arg Lys Ala Asn Ala Pro Glu Met Leu Ser

85 90 95

Asp Gly Glu Tyr Ile Ser Asp Val Glu Glu Gly Glu Asp Ala Met Thr

100 105 110

Gly Asp Thr Asp Lys Tyr Leu Gly Pro Gln Asp Leu Lys Glu Leu Gly

115 120 125

Asp Asp Ser Leu Pro Ala Glu Gly Tyr Met Gly Phe Ser Leu Gly Ala

130 135 140

Arg Ser Ala Ser Leu Arg Ser Phe Ser Ser Asp Arg Ser Tyr Thr Leu

145 150 155 160

Asn Arg Ser Ser Tyr Ala Arg Asp Ser Met Met Ile Glu Glu Leu Leu

165 170 175

Val Pro Ser Lys Glu Gln His Leu Thr Phe Thr Arg Glu Phe Asp Ser

180 185 190

Asp Ser Leu Arg His Tyr Ser Trp Ala Ala Asp Thr Leu Asp Asn Val			
195	200	205	
Asn Leu Val Ser Ser Pro Ile His Ser Gly Phe Leu Val Ser Phe Met			
210	215	220	
Val Asp Ala Arg Gly Gly Ser Met Arg Gly Ser Arg His His Gly Met			
225	230	235	240
Arg Ile Ile Ile Pro Pro Arg Lys Cys Thr Ala Pro Thr Arg Ile Thr			
245	250	255	
Cys Arg Leu Val Lys Arg His Lys Leu Ala Asn Pro Pro Pro Met Val			
260	265	270	
Glu Gly Glu Gly Leu Ala Ser Arg Leu Val Glu Met Gly Pro Ala Gly			
275	280	285	
Ala Gln Phe Leu Gly Pro Val Ile Val Glu Ile Pro His Phe Gly Ser			
290	295	300	
Met Arg Gly Lys Glu Arg Glu Leu Ile Val Leu Arg Ser Glu Asn Gly			
305	310	315	320
Glu Thr Trp Lys Glu His Gln Phe Asp Ser Lys Asn Glu Asp Leu Thr			
325	330	335	
Glu Leu Leu Asn Gly Met Asp Glu Glu Leu Asp Ser Pro Glu Glu Leu			
340	345	350	
Gly Lys Lys Arg Ile Cys Arg Ile Ile Thr Lys Asp Phe Pro Gln Tyr			
355	360	365	
Phe Ala Val Val Ser Arg Ile Lys Gln Glu Ser Asn Gln Ile Gly Pro			
370	375	380	
Glu Gly Gly Ile Leu Ser Ser Thr Thr Val Pro Leu Val Gln Ala Ser			
385	390	395	400
Phe Pro Glu Gly Ala Leu Thr Lys Arg Ile Arg Val Gly Leu Gln Ala			
405	410	415	
Gln Pro Val Pro Asp Glu Ile Val Lys Lys Ile Leu Gly Asn Lys Ala			

420 425 430
Thr Phe Ser Pro Ile Val Thr Val Glu Pro Arg Arg Arg Lys Phe His
435 440 445
Lys Pro Ile Thr Met Thr Ile Pro Val Pro Pro Pro Ser Gly Glu Gly
450 455 460
Val Ser Asn Gly Tyr Lys Gly Asp Thr Thr Pro Asn Leu Arg Leu Leu
465 470 475 480
Cys Ser Ile Thr Gly Gly Thr Ser Pro Ala Gln Trp Glu Asp Ile Thr
485 490 495
Gly Thr Thr Pro Leu Thr Phe Ile Lys Asp Cys Val Ser Phe Thr Thr
500 505 510
Asn Val Ser Ala Arg Phe Trp Leu Ala Asp Cys His Gln Val Leu Glu
515 520 525
Thr Val Gly Leu Ala Thr Gln Leu Tyr Arg Glu Leu Ile Cys Val Pro
530 535 540
Tyr Met Ala Lys Phe Val Val Phe Ala Lys Met Asn Asp Pro Val Glu
545 550 555 560
Ser Ser Leu Arg Cys Phe Cys Met Thr Asp Asp Lys Val Asp Lys Thr
565 570 575
Leu Glu Gln Gln Glu Asn Phe Glu Glu Val Ala Arg Ser Lys Asp Ile
580 585 590
Glu Val Leu Glu Gly Lys Pro Ile Tyr Val Asp Cys Tyr Gly Asn Leu
595 600 605
Ala Pro Leu Thr Lys Gly Gly Gln Gln Leu Val Phe Asn Phe Tyr Ser
610 615 620
Phe Lys Glu Asn Arg Leu Pro Phe Ser Ile Lys Ile Arg Asp Thr Ser
625 630 635 640
Gln Glu Pro Cys Gly Arg Leu Ser Ser Leu Lys Glu Pro Lys Thr Thr
645 650 655

Lys Gly Leu Pro Gln Thr Ala Val Cys Asn Leu Asn Ile Thr Leu Pro
660 665 670
Ala His Lys Lys Ile Glu Lys Thr Asp Arg Arg Gln Ser Phe Ala Ser
675 680 685
Leu Ala Leu Arg Lys Arg Tyr Ser Tyr Leu Thr Glu Pro Gly Met Ser
690 695 700
Pro Gln Ser Pro Cys Glu Arg Thr Asp Ile Arg Met Ala Ile Val Ala
705 710 715 720
Asp His Leu Gly Leu Ser Trp Thr Glu Leu Ala Arg Glu Leu Asn Phe
725 730 735
Ser Val Asp Glu Ile Asn Gln Ile Arg Val Glu Asn Pro Asn Ser Leu
740 745 750
Ile Ser Gln Ser Phe Met Leu Leu Lys Lys Trp Val Thr Arg Asp Gly
755 760 765
Lys Asn Ala Thr Thr Asp Ala Leu Thr Ser Val Leu Thr Lys Ile Asn
770 775 780
Arg Ile Asp Ile Val Thr Leu Leu Glu Gly Pro Ile Phe Asp Tyr Gly
785 790 795 800
Asn Ile Ser Gly Thr Arg Ser Phe Ala Asp Glu Asn Asn Val Phe His
805 810 815
Asp Pro Val Asp Gly Tyr Pro Ser Leu Gln Val Glu Leu Glu Thr Pro
820 825 830
Thr Gly Leu His Tyr Thr Pro Pro Thr Pro Phe Gln Gln Asp Asp Tyr
835 840 845
Phe Ser Asp Ile Ser Ser Ile Glu Ser Pro Leu Arg Thr Pro Ser Arg
850 855 860
Leu Ser Asp Gly Leu Val Pro Ser Gln Gly Asn Ile Glu His Ser Ala
865 870 875 880
Asp Gly Pro Pro Val Val Thr Ala Glu Asp Ala Ser Leu Glu Asp Ser

885 890 895
Lys Leu Glu Asp Ser Val Pro Leu Thr Glu Met Pro Glu Ala Val Asp
900 905 910
Val Asp Glu Ser Gln Leu Glu Asn Val Cys Leu Ser Trp Gln Asn Glu
915 920 925
Thr Ser Ser Gly Asn Leu Glu Ser Cys Ala Gln Ala Arg Arg Val Thr
930 935 940
Gly Gly Leu Leu Asp Arg Leu Asp Asp Ser Pro Asp Gln Cys Arg Asp
945 950 955 960
Ser Ile Thr Ser Tyr Leu Lys Gly Glu Ala Gly Lys Phe Glu Ala Asn
965 970 975
Gly Ser His Thr Glu Ile Thr Pro Glu Ala Lys Thr Lys Ser Tyr Phe
980 985 990
Pro Glu Ser Gln Asn Asp Val Gly Lys Gln Ser Thr Lys Glu Thr Leu
995 1000 1005
Lys Pro Lys Ile His Gly Ser Gly His Val Glu Glu Pro Ala Ser Pro
1010 1015 1020
Leu Ala Ala Tyr Gln Lys Ser Leu Glu Glu Thr Ser Lys Leu Ile Ile
1025 1030 1035 1040
Glu Glu Thr Lys Pro Cys Val Pro Val Ser Met Lys Lys Met Ser Arg
1045 1050 1055
Thr Ser Pro Ala Asp Gly Lys Pro Arg Leu Ser Leu His Glu Glu Glu
1060 1065 1070
Gly Ser Ser Gly Ser Glu Gln Lys Gly Glu Gly Phe Lys Val Lys Thr
1075 1080 1085
Lys Lys Glu Ile Arg His Val Glu Lys Lys Ser His Ser
1090 1095 1100

<210> 2224

<211> 237

<212> PRT

<213> Homo sapiens

<400> 2224

Met Pro Val His Pro Ala Trp Leu Gly Ser Ala Cys Leu Pro His Ala

1 5 10 15

Ser His Gly Pro Ala Pro Gln Ser Ser Val Gly Gly Leu Leu Val Ser

20 25 30

Val Lys Ser Pro Pro Gly Asp Val His Ala Ala Arg Ala Cys Ala Pro

35 40 45

Gly Arg His Ser Gly Glu Gly Pro Pro Gln Gly Asn Leu Ser Pro Ser

50 55 60

Cys Pro Ala Glu Ala Gly His Gly Cys Ala Ser Thr Gly Arg Gln Val

65 70 75 80

Gly Val Ser Gly Ala Gly Ser Ser Pro Ser Gly Pro Ala Pro Cys Val

85 90 95

Lys Cys Ser Ala Trp Val Gly Thr Cys Phe Pro Leu Ser Leu Leu Gln

100 105 110

Ala Ala Gly Gly Pro Ala Gly Ser Pro Asn Gly Phe Cys Pro Glu Pro

115 120 125

Trp Ala Pro Asp His Ala Pro Thr Leu His Gly Leu Asn Lys Ser Leu

130 135 140

Cys Gln Gly Pro Arg Ser Gly Gly Ala Gln Arg Lys Pro Arg Ala His

145 150 155 160

Thr Gly Glu Gly Val Ser Val Leu Gly Leu Thr Gln Pro Arg Leu Ser

165 170 175

Ser Ser Leu Arg Ile Ser Trp His Leu Leu Ala Cys Val Ala Thr Gln

180 185 190
 Val Gly Cys Ala Cys Arg Leu Thr Glu Lys Thr Leu Gly Glu Asp Tyr
 195 200 205
 Val Ser Ala Phe Leu Pro Ser Thr Gly Pro Ser Trp Ala His Cys Asp
 210 215 220
 Gln Thr Met Cys Lys Ser Thr Arg Glu Ser Gly Arg Ser
 225 230 235

<210> 2225

<211> 216

<212> PRT

<213> Homo sapiens

<400> 2225

Met Leu Ile Ala Lys Thr Met Gly Lys Met Ser Pro Arg Ala Cys Gln
 1 5 10 15
 Arg Ser Ser Trp Leu Pro Leu Gln Tyr Arg Pro Gly Gly Leu Arg Gly
 20 25 30
 Lys Asn Gly Phe Met Gly Gln Ser Gln Ser Pro Ala Ala Asn Cys Ile
 35 40 45
 Leu Gly Thr Trp Cys Pro Ala Ser Gln Pro Leu Gln Leu Gln Leu Trp
 50 55 60
 Leu Trp Leu Lys Gly Ala Asn Val Gln Leu Gly Pro Trp Leu Gln Arg
 65 70 75 80
 Val Gln Ala Thr Ser Leu Gly Gly Phe His Met Val Leu Gly Leu Trp
 85 90 95
 Val His Lys Arg Gln Glu Lys Arg Phe Gly Ser Leu His Leu Asp Phe
 100 105 110

Arg Gly Cys Met Glu Met Pro Gly Cys Pro Gly Arg Thr Pro Leu Gln

115

120

125

Gly Gln Ser Pro His Gly Asp Pro Leu Leu Gly Gln Cys Arg Gly Gly

130

135

140

Asn Val Gly Leu Glu Pro Ser Gln Arg Val Ser Thr Arg Ala Leu Pro

145

150

155

160

Asn Gly Ala Val Gly Arg Gly Pro Ser Ser Ser Arg Pro His Lys Gly

165

170

175

Gly Ser Thr Asp Ser Leu His Cys Val Pro Ala Lys Val Ala Gly Thr

180

185

190

Gln Cys Gln Pro Ile Lys Ala Ala Val Gly Ala Val Ser Cys Arg Ala

195

200

205

Met Gly Gln Ser Cys Gln Arg Pro

210

215

<210> 2226

<211> 854

<212> PRT

<213> Homo sapiens

<400> 2226

Met Thr Leu Ile Ser Pro Ile Ile Leu Lys Lys Tyr Gly Ile Pro Phe

1

5

10

15

Ser Arg Ile Thr Gln Glu Ala Gly Glu Phe Met Ile Thr Phe Pro Tyr

20

25

30

Gly Tyr His Ala Gly Phe Asn His Gly Phe Asn Cys Ala Glu Ser Thr

35

40

45

Asn Phe Ala Thr Leu Arg Trp Ile Asp Tyr Gly Lys Val Ala Thr Gln

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Val Val Pro Arg Pro Gly Lys Ala Ala Phe Asn Gln Glu His Val Ser
290 295 300
Cys Gln Gln Ala Phe Glu His Phe Ala Gln Lys Gly Pro Thr Trp Lys
305 310 315 320
Glu Pro Val Ser Pro Met Glu Leu Thr Gly Pro Glu Asp Gly Ala Ala
325 330 335
Ser Ser Gly Ala Gly Arg Met Glu Thr Lys Ala Arg Ala Gly Glu Gly
340 345 350
Gln Ala Pro Ser Thr Phe Ser Lys Leu Lys Met Glu Ile Lys Lys Ser
355 360 365
Arg Arg His Pro Leu Gly Arg Pro Pro Thr Arg Ser Pro Leu Ser Val
370 375 380
Val Lys Gln Glu Ala Ser Ser Asp Glu Glu Ala Ser Pro Phe Ser Gly
385 390 395 400
Glu Glu Asp Val Ser Asp Pro Asp Ala Leu Arg Pro Leu Leu Ser Leu
405 410 415
Gln Trp Lys Asn Arg Ala Ala Ser Phe Gln Ala Glu Arg Lys Phe Asn
420 425 430
Ala Ala Ala Ala Arg Thr Glu Pro Tyr Cys Ala Ile Cys Thr Leu Phe
435 440 445
Tyr Pro Tyr Cys Gln Ala Leu Gln Thr Glu Lys Glu Ala Pro Ile Ala
450 455 460
Ser Leu Gly Glu Gly Cys Pro Ala Thr Leu Pro Ser Lys Ser Arg Gln
465 470 475 480
Lys Thr Arg Pro Leu Ile Pro Glu Met Cys Phe Thr Ser Gly Gly Glu
485 490 495
Asn Thr Glu Pro Leu Pro Ala Asn Ser Tyr Ile Gly Asp Asp Gly Thr
500 505 510
Ser Pro Leu Ile Ala Cys Gly Lys Cys Cys Leu Gln Val His Ala Ser

515	520	525
Cys Tyr Gly Ile Arg Pro Glu Leu Val Asn Glu Gly Trp Thr Cys Ser		
530	535	540
Arg Cys Ala Ala His Ala Trp Thr Ala Glu Cys Cys Leu Cys Asn Leu		
545	550	555
Arg Gly Gly Ala Leu Gln Met Thr Thr Asp Arg Arg Trp Ile His Val		
565	570	575
Ile Cys Ala Ile Ala Val Pro Glu Ala Arg Phe Leu Asn Val Ile Glu		
580	585	590
Arg His Pro Val Asp Ile Ser Ala Ile Pro Glu Gln Arg Trp Lys Leu		
595	600	605
Lys Cys Val Tyr Cys Arg Lys Arg Met Lys Lys Val Ser Gly Ala Cys		
610	615	620
Ile Gln Cys Ser Tyr Glu His Cys Ser Thr Ser Phe His Val Thr Cys		
625	630	635
Ala His Ala Ala Gly Val Leu Met Glu Pro Asp Asp Trp Pro Tyr Val		
645	650	655
Val Ser Ile Thr Cys Leu Lys His Lys Ser Gly Gly His Ala Val Gln		
660	665	670
Leu Leu Arg Ala Val Ser Leu Gly Gln Val Val Ile Thr Lys Asn Arg		
675	680	685
Asn Gly Leu Tyr Tyr Arg Cys Arg Val Ile Gly Ala Ala Ser Gln Thr		
690	695	700
Cys Tyr Glu Val Asn Phe Asp Asp Gly Ser Tyr Ser Asp Asn Leu Tyr		
705	710	715
Pro Glu Ser Ile Thr Ser Arg Asp Cys Val Gln Leu Gly Pro Pro Ser		
725	730	735
Glu Gly Glu Leu Val Glu Leu Arg Trp Thr Asp Gly Asn Leu Tyr Lys		
740	745	750

Ala Lys Phe Ile Ser Ser Val Thr Ser His Ile Tyr Gln Val Glu Phe
 755 760 765
 Glu Asp Gly Ser Gln Leu Thr Val Lys Arg Gly Asp Ile Phe Thr Leu
 770 775 780
 Glu Glu Glu Leu Pro Lys Arg Val Arg Ser Arg Leu Ser Leu Ser Thr
 785 790 795 800
 Gly Ala Pro Gln Glu Pro Ala Phe Ser Gly Glu Glu Ala Lys Ala Ala
 805 810 815
 Lys Arg Pro Arg Val Gly Thr Pro Leu Ala Thr Glu Asp Ser Gly Arg
 820 825 830
 Ser Gln Asp Tyr Val Ala Phe Val Glu Ser Leu Leu Gln Val Gln Gly
 835 840 845
 Arg Pro Gly Ala Pro Phe
 850

<210> 2227

<211> 165

<212> PRT

<213> Homo sapiens

<400> 2227

Met Glu Ile Cys His Phe Gly Gln Val Leu Leu Thr Val Pro Val Thr
 1 5 10 15
 Ser Pro Arg Arg Arg Ala Thr Thr Ser Arg Pro His Asp Pro Ser Asp
 20 25 30
 Cys His His Thr Gly Ser Arg Arg Arg Ile Ser Met Ala Phe Leu Thr
 35 40 45
 Leu Cys Leu Gln Arg Ile Ser Phe Phe Ile Val Phe Phe Phe Phe

50 55 60
Tyr Phe Leu Phe Ser Phe Phe Phe Glu Thr Glu Ser Leu Ser Val Ala
65 70 75 80
Gln Ala Gly Val Gln Trp His Asp Leu Gly Ser Leu Gln Pro Arg Pro
85 90 95
Pro Gly Phe Lys Gln Phe Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp
100 105 110
Tyr Gly His Thr Pro Gln Arg Ser Ala Asn Phe Cys Ile Phe Arg Lys
115 120 125
Asp Arg Val Leu Pro Cys Trp Pro Gly Trp Ser Arg Ser Ser Glu Leu
130 135 140
Val Ile His Leu Pro Arg Pro Pro Lys Cys Trp Asp Tyr Arg Arg Glu
145 150 155 160
Pro Pro His Pro Ala
165

<210> 2228

<211> 113

<212> PRT

<213> Homo sapiens

<400> 2228

Met Ala His Ser Ala Ala Ala Val Pro Leu Gly Ala Leu Glu Gln Gly
1 5 10 15
Cys Pro Ile Arg Val Glu His Asp Arg Arg Arg Arg Gln Phe Thr Val
20 25 30
Arg Leu Asn Gly Cys His Asp Arg Ala Val Leu Leu Tyr Glu Tyr Val
35 40 45

Gly Lys Arg Ile Val Asp Leu Gln His Thr Glu Val Pro Asp Ala Tyr
 50 55 60
 Arg Gly Arg Gly Ile Ala Lys His Leu Ala Lys Ala Ala Leu Asp Phe
 65 70 75 80
 Val Val Glu Glu Asp Leu Lys Ala His Leu Thr Cys Trp Tyr Ile Gln
 85 90 95
 Lys Tyr Val Lys Glu Asn Pro Leu Pro Gln Tyr Leu Glu Arg Leu Gln
 100 105 110
 Pro

<210> 2229

<211> 154

<212> PRT

<213> Homo sapiens

<400> 2229

Met His Gly Phe Lys Thr Pro Ser Ser Gln Ser Leu Gln Thr Lys Leu
 1 5 10 15
 Ser Val His Leu Ile Cys Leu Val Trp Gln Met Arg Trp His Ile Gly
 20 25 30
 Gly Thr Ser Pro Gly Met Asp Thr Trp Leu Cys Ser Leu Leu Ala Arg
 35 40 45
 Val Ala Arg Gly Val Leu Gly Ser Arg Arg Lys Arg Ser Cys Ser Cys
 50 55 60
 Cys Arg Trp Gln Phe Pro Ser Ala Ala Leu Ala Pro Leu Ala Asp Glu
 65 70 75 80
 Lys Lys Cys Ser Phe Lys Ala Lys Gln Trp Ser Gly Cys Thr Phe Thr

	85		90		95
His Arg Ser Ala Ala Leu Phe Cys Arg Ala Val Val Met Pro Gly Thr					
	100		105		110
Thr Pro Trp Gly Leu Gly Ile Arg Phe Gln Phe Ser Leu Thr Glu Leu					
	115		120		125
Glu Ile Gln Leu Ala Phe Ala Glu Gly Gly Arg Glu Lys Trp Asn Glu					
	130		135		140
Lys Thr Ser Ser Pro Gly Cys His Phe Tyr					
	145		150		

<210> 2230

<211> 131

<212> PRT

<213> Homo sapiens

<400> 2230

Met Pro Gly Glu His Ile Glu Gly His Pro Gln Glu Gly Asp Asp Pro			
1	5	10	15
Ala Pro Thr Gly Leu Ala Ala Ser Ser Asp His Glu Ala Gln Gly Val			
	20	25	30
Ser Pro Gly Pro His Leu Ser Ala Gly Lys Val His Leu Gly Gln Leu			
	35	40	45
Pro Leu His Ser Ser Pro Ala Pro Leu Cys Val Gly Pro Ala Thr Pro			
	50	55	60
Ala Lys Glu Gln Arg Pro His Leu Pro Gln Ala His Leu Ala Pro Thr			
	65	70	75
Ser Ser Pro Ala Ala Thr Gly Ala Gly Arg Trp Trp Ala Phe Leu Phe			
	85	90	95

Arg Gln Gly Ala Cys Gly Pro Gly Arg Trp Leu Asp Leu His Trp Cys
 100 105 110
 Leu Val Gly Arg Ser Val Gly Trp Asn His Ala Pro Val Phe Pro Gln
 115 120 125
 Thr Arg Gly
 130

<210> 2231

<211> 439

<212> PRT

<213> Homo sapiens

<400> 2231

Met Thr Val Glu Gln Lys Phe Gly Leu Phe Ser Ala Glu Ile Lys Glu
 1 5 10 15
 Ala Asp Pro Leu Ala Ala Ser Glu Ala Ser Gln Pro Lys Pro Cys Pro
 20 25 30
 Pro Glu Val Thr Pro His Tyr Ile Trp Ile Asp Phe Leu Val Gln Arg
 35 40 45
 Phe Glu Ile Ala Lys Tyr Cys Ser Ser Asp Gln Val Glu Ile Phe Ser
 50 55 60
 Ser Leu Leu Gln Arg Ser Met Ser Leu Asn Ile Gly Arg Ala Lys Gly
 65 70 75 80
 Ser Met Asn Arg His Val Ala Ala Ile Gly Pro Arg Phe Lys Leu Leu
 85 90 95
 Thr Leu Gly Leu Ser Leu Leu His Ala Asp Val Val Pro Asn Ala Thr
 100 105 110
 Ile Arg Asn Val Leu Arg Glu Lys Ile Tyr Ser Thr Ala Phe Asp Tyr

115	120	125
Phe Ser Cys Pro Pro Lys Phe Pro Thr Gln Gly Glu Lys Arg Leu Arg		
130	135	140
Glu Asp Ile Ser Ile Met Ile Lys Phe Trp Thr Ala Met Phe Ser Asp		
145	150	155
Lys Lys Tyr Leu Thr Ala Ser Gln Leu Val Pro Pro Ala Asp Ile Gly		
165	170	175
Asp Leu Leu Glu Gln Leu Val Glu Glu Asn Thr Gly Ser Leu Ser Gly		
180	185	190
Pro Ala Lys Asp Phe Tyr Gln Arg Glu Phe Asp Phe Phe Asn Lys Ile		
195	200	205
Thr Asn Val Ser Ala Ile Ile Lys Pro Tyr Pro Lys Gly Asp Glu Arg		
210	215	220
Lys Lys Ala Cys Leu Ser Ala Leu Ser Glu Val Thr Val Gln Pro Gly		
225	230	235
Cys Ser Leu Pro Ser Asn Pro Glu Ala Ile Val Leu Asp Val Asp Tyr		
245	250	255
Lys Ser Gly Thr Pro Met Gln Ser Ala Ala Lys Ala Pro Tyr Leu Ala		
260	265	270
Lys Phe Lys Val Lys Arg Cys Gly Val Ser Glu Leu Glu Lys Glu Gly		
275	280	285
Leu Arg Cys Arg Ser Asp Ser Glu Asp Glu Cys Ser Thr Gln Glu Ala		
290	295	300
Asp Gly Gln Lys Ile Ser Trp Gln Ala Ala Ile Phe Lys Leu Gly Asp		
305	310	315
Asp Cys Arg Gln Asp Met Leu Ala Leu Gln Ile Ile Asp Leu Phe Lys		
325	330	335
Asn Ile Phe Gln Leu Val Gly Leu Asp Leu Phe Val Phe Pro Tyr Arg		
340	345	350

Val Val Ala Thr Ala Pro Gly Cys Gly Val Ile Glu Cys Ile Pro Asp
 355 360 365
 Cys Thr Ser Arg Asp Gln Leu Gly Arg Gln Thr Asp Phe Gly Met Tyr
 370 375 380
 Asp Tyr Phe Thr Arg Gln Tyr Gly Asp Glu Ser Thr Leu Ala Phe Gln
 385 390 395 400
 Gln Val Ala Arg Val Ala Thr Gly Arg Gly Lys Ser Cys Val Leu His
 405 410 415
 Pro Thr Pro Ala Thr His Thr Gln Pro Leu Pro Thr Pro Cys Ser Pro
 420 425 430
 Gln Ser Ser Phe Val Lys Gly
 435

<210> 2232

<211> 115

<212> PRT

<213> Homo sapiens

<400> 2232

Met Ser Ser Pro Ser Ser Pro Phe Arg Glu Gln Ser Phe Leu Cys Ala
 1 5 10 15
 Ala Gly Asp Ala Gly Glu Glu Ser Arg Val Gln Val Leu Lys Asn Glu
 20 25 30
 Val Arg Arg Gly Ser Pro Val Leu Leu Gly Trp Val Glu Gln Ala Tyr
 35 40 45
 Ala Asp Lys Cys Val Cys Gly Pro Ser Ala Pro Pro Ala Pro Thr Pro
 50 55 60
 Pro Ser Leu Ser Gln Arg Val Met Cys Asn Asp Leu Phe Lys Val Asn

65 70 75 80
 Pro Phe Gln Leu Gln Gln Phe Arg Ala Asp Pro Ser Thr Ala Ser Leu
 85 90 95
 Leu Leu Cys Pro Gly Gly Leu Asp His Lys Leu Asn Leu Arg Gly Lys
 100 105 110
 Ala Trp Gly
 115

<210> 2233

<211> 139

<212> PRT

<213> Homo sapiens

<400> 2233

Met Ala Ala Gly Ser Ser Gly Ala Ser Met Gly Trp Arg Gly Ser Pro
 1 5 10 15
 Gly Arg Pro Ser Gly Arg Ser Gln His Arg Pro Arg Thr Ser Ser Ala
 20 25 30
 Cys Ala Arg Trp Ala Arg Tyr Gly Gly Ser Phe Gln Gly Phe Tyr Pro
 35 40 45
 Asn Ser Thr Tyr Phe Tyr Leu Phe Ser Leu Glu Leu Phe Cys Leu Tyr
 50 55 60
 Leu Ser Phe Ile Cys Lys Asn Ser Ile Arg Lys Ile His Arg Val Asn
 65 70 75 80
 Ala His Gln Ala Tyr Arg Arg Ser Gly Arg Asn Met Phe Ser Pro Ala
 85 90 95
 His Phe Gln Ser Val Phe Glu His Arg Gly Phe His Gly Phe Asp Ser
 100 105 110

Phe His Lys Arg Leu Val Leu Ser Val Phe Thr Ile Tyr Val Ser Glu
 115 120 125

Thr Ile Asn Tyr Ile Ile Phe Met Phe Thr His
 130 135

<210> 2234

<211> 817

<212> PRT

<213> Homo sapiens

<400> 2234

Met Ser Ser Val Ser Glu Val Asn Val Asp Ile Lys Asp Phe Leu Met
 1 5 10 15

Ser Ile Asn Leu Glu Gln Tyr Leu Leu His Phe His Glu Ser Gly Phe
 20 25 30

Thr Thr Val Lys Asp Cys Ala Ala Ile Asn Asp Ser Leu Leu Gln Lys
 35 40 45

Ile Gly Ile Ser Pro Thr Gly His Arg Arg Arg Ile Leu Lys Gln Leu
 50 55 60

Gln Ile Ile Leu Ser Lys Met Gln Asp Ile Pro Ile Tyr Ala Asn Val
 65 70 75 80

His Lys Thr Lys Lys Asn Asp Asp Pro Ser Lys Asp Tyr His Val Pro
 85 90 95

Ser Ser Asp Gln Asn Ile Cys Ile Glu Leu Ser Asn Ser Gly Ser Val
 100 105 110

Gln Thr Ser Ser Pro Pro Gln Leu Glu Thr Val Arg Lys Asn Leu Glu
 115 120 125

Asp Ser Asp Ala Ser Val Glu Arg Ser Gln Tyr Pro Gln Ser Asp Asp

130 135 140
Lys Leu Ser Pro Pro Lys Arg Asp Phe Pro Thr Ala Glu Glu Pro His
145 150 155 160
Leu Asn Leu Gly Ser Leu Asn Asp Ser Leu Phe Gly Ser Asp Asn Ile
165 170 175
Lys Ile Glu Ser Leu Ile Thr Lys Lys Thr Val Asp His Thr Val Glu
180 185 190
Glu Gln Gln Thr Glu Lys Val Lys Leu Ile Thr Glu Asn Leu Ser Lys
195 200 205
Leu Pro Asn Ala Asp Ser Glu Cys Leu Ser Phe Val Gly Cys Ser Thr
210 215 220
Ser Gly Thr Asn Ser Gly Asn Gly Thr Asn Gly Leu Leu Glu Gly Ser
225 230 235 240
Pro Pro Ser Pro Phe Phe Lys Phe Gln Gly Glu Met Ile Val Asn Asp
245 250 255
Leu Tyr Val Pro Ser Ser Pro Ile Leu Ala Pro Val Arg Ser Arg Ser
260 265 270
Lys Leu Val Ser Arg Pro Ser Arg Ser Phe Leu Leu Arg His Arg Pro
275 280 285
Val Pro Glu Ile Pro Gly Ser Thr Lys Gly Val Ser Gly Ser Tyr Phe
290 295 300
Arg Glu Arg Arg Asn Val Ala Thr Ser Thr Glu Lys Ser Val Ala Trp
305 310 315 320
Gln Asn Ser Asn Glu Glu Asn Ser Ser Ser Ile Phe Pro Tyr Gly Glu
325 330 335
Thr Phe Leu Phe Gln Arg Leu Glu Asn Ser Lys Lys Arg Ser Ile Lys
340 345 350
Asn Glu Phe Leu Thr Gln Gly Glu Ala Leu Lys Gly Glu Ala Ala Thr
355 360 365

Ala Thr Asn Ser Phe Ile Ile Lys Ser Ser Ile Tyr Asp Asn Arg Lys
370 375 380
Glu Lys Ile Ser Glu Asp Lys Val Glu Asp Ile Trp Ile Pro Arg Glu
385 390 395 400
Asp Lys Asn Asn Phe Leu Ile Asp Thr Ala Ser Glu Ser Glu Tyr Ser
405 410 415
Thr Val Glu Glu Cys Phe Gln Ser Leu Arg Arg Lys Asn Ser Lys Ala
420 425 430
Ser Lys Ser Arg Thr Gln Lys Ala Leu Ile Leu Asp Ser Val Asn Arg
435 440 445
His Ser Tyr Pro Leu Ser Ser Thr Ser Gly Asn Ala Asp Ser Ser Ala
450 455 460
Val Ser Ser Gln Ala Ile Ser Pro Tyr Ala Cys Phe Tyr Gly Ala Ser
465 470 475 480
Ala Lys Lys Val Lys Ser Gly Trp Leu Asp Lys Leu Ser Pro Gln Gly
485 490 495
Lys Arg Met Phe Gln Lys Arg Trp Val Lys Phe Asp Gly Leu Ser Ile
500 505 510
Ser Tyr Tyr Asn Asn Glu Lys Glu Met Tyr Ser Lys Gly Ile Ile Pro
515 520 525
Leu Ser Ala Ile Ser Thr Val Arg Val Gln Gly Asp Asn Lys Phe Glu
530 535 540
Val Val Thr Thr Gln Arg Thr Phe Val Phe Arg Val Glu Lys Glu Glu
545 550 555 560
Glu Arg Asn Asp Trp Ile Ser Ile Leu Leu Asn Ala Leu Lys Ser Gln
565 570 575
Ser Leu Thr Ser Gln Ser Gln Ala Val Val Thr Pro Glu Lys Cys Gly
580 585 590
Tyr Leu Glu Leu Arg Gly Tyr Lys Ala Lys Ile Phe Thr Val Leu Ser

595	600	605
Gly Asn Ser Val Trp Leu Cys Lys Asn Glu Gln Asp Phe Lys Ser Gly		
610	615	620
Leu Gly Ile Thr Ile Ile Pro Met Asn Val Ala Asn Val Lys Gln Val		
625	630	635
Asp Arg Thr Val Lys Gln Ser Phe Glu Ile Ile Thr Pro Tyr Arg Ser		
645	650	655
Phe Ser Phe Thr Ala Glu Thr Glu Lys Glu Lys Gln Asp Trp Ile Glu		
660	665	670
Ala Val Gln Gln Ser Ile Ala Glu Thr Leu Ser Asp Tyr Glu Val Ala		
675	680	685
Glu Lys Ile Trp Phe Asn Glu Ser Asn Arg Ser Cys Ala Asp Cys Lys		
690	695	700
Ala Pro Asp Pro Asp Trp Ala Ser Ile Asn Leu Cys Val Val Ile Cys		
705	710	715
Lys Lys Cys Ala Gly Gln His Arg Ser Leu Gly Pro Lys Asp Ser Lys		
725	730	735
Val Arg Ser Leu Lys Met Asp Ala Ser Ile Trp Ser Asn Glu Leu Ile		
740	745	750
Glu Leu Phe Ile Val Ile Gly Ser Lys Arg Ala Asn Asp Phe Trp Ala		
755	760	765
Gly Asn Leu Gln Lys Asp Glu Glu Leu His Met Asp Ser Pro Val Glu		
770	775	780
Lys Arg Lys Asn Phe Ile Thr Gln Lys Tyr Lys Glu Gly Lys Phe Arg		
785	790	795
Lys Thr Leu Leu Ala Ser Leu Thr Lys Glu Glu Leu Asn Lys Val Phe		
805	810	815
Asn		

<210> 2235

<211> 131

<212> PRT

<213> Homo sapiens

<400> 2235

Met Glu Gln Gln Asp Lys Glu Asp Asp Thr Ala Phe Asn Leu Arg Ser

1 5 10 15

Arg Ser Leu Pro Arg Pro Cys Asp Gly Val Leu Gly Arg Lys Arg Gln

20 25 30

Gly Gln Ser Ala Trp Gly Leu His Pro Gly Pro Ala Pro Ser Thr Cys

35 40 45

Val Cys Arg Pro Leu Pro Ala Pro Pro Thr Pro Gln Arg Arg Cys Ser

50 55 60

Gln Gly Glu Gly Arg Arg Val Leu Glu Leu Gln Leu Pro Arg Val Pro

65 70 75 80

Glu Asp Pro Gly Leu Gly Pro Ala Pro Gln Pro Glu Val Pro Arg Ala

85 90 95

Ser Lys Asp Pro Glu Asn His His Leu Thr Gly Pro Gln Ser Ser Pro

100 105 110

Lys Ile Pro Arg Val Pro Glu Asp Ser Glu Pro Pro Leu Ile Gly Ser

115 120 125

Gln Ser Pro

130

<210> 2236

<211> 196

<212> PRT

<213> Homo sapiens

<400> 2236

Met Val Ile Pro Gly Leu Thr Thr Leu Leu Ile Lys Thr Thr Phe Trp
1 5 10 15
Gly Phe Arg Phe Gly Glu Leu Gly Met Gly Arg Gly Ser Ala Ser Ser
20 25 30
Arg Cys Leu Val Ser Pro Ser Phe Ser Leu Leu His Val Gly Gly Arg
35 40 45
Leu Asp Gln Leu Ala Cys Thr Leu Pro Lys Glu Leu Arg Gly Lys Asp
50 55 60
Met Arg Met Val Pro Met Glu Met Phe Asn Tyr Cys Ser Gln Leu Glu
65 70 75 80
Asp Glu Asn Ser Ser Ala Gly Leu Asp Ile Pro Gly Pro Pro Cys Thr
85 90 95
Lys Ala Ser Pro Glu Pro Ala Lys Pro Lys Pro Gly Ala Glu Pro Glu
100 105 110
Pro Glu Pro Ser Thr Ala Cys Pro Gln Lys Gln Arg His Arg Pro Ala
115 120 125
Ser Val Arg Arg Ala Met Gly Thr Val Ile Ile Ala Gly Val Val Cys
130 135 140
Gly Val Val Cys Ile Met Met Val Val Ala Ala Ala Tyr Gly Cys Ile
145 150 155 160
Tyr Ala Ser Leu Met Ala Lys Tyr His Arg Glu Leu Lys Lys Arg Gln
165 170 175
Pro Leu Met Gly Asp Pro Glu Gly Glu His Glu Asp Gln Lys Gln Ile
180 185 190

Ser Ser Val Ala

195

<210> 2237

<211> 101

<212> PRT

<213> Homo sapiens

<400> 2237

Met Val Asn Phe Ile Arg Leu Ile Glu Val Lys Ala Ile Phe Pro Lys

1 5 10 15

Thr Asn Lys Ile Pro Tyr Ile Val Phe Trp Val Trp Phe Val Asp Val

20 25 30

Met Pro Ile Ser Lys His Gln Leu Val Thr Thr Asn Met Gly Ile Phe

35 40 45

Ser Asp Ile Phe Val Val Ile Val Lys Ile Pro Gly Lys Lys Arg Lys

50 55 60

Ser Leu Arg Gln Arg Lys Ile His Leu Pro Gln Gly Lys Ser Glu Met

65 70 75 80

Phe Ile Leu Thr Phe Ala Phe Leu Ile Ile Cys Gly His Phe Phe Ile

85 90 95

Val Thr Val Gly Ser

100

<210> 2238

<211> 750

<212> PRT

<213> Homo sapiens

<400> 2238

Met Ser Ser Ser Pro Val Asn Val Lys Lys Leu Lys Val Ser Glu Leu
 1 5 10 15
 Lys Glu Glu Leu Lys Lys Arg Arg Leu Ser Asp Lys Gly Leu Lys Ala
 20 25 30
 Glu Leu Met Glu Arg Leu Gln Ala Ala Leu Asp Asp Glu Glu Ala Gly
 35 40 45
 Gly Arg Pro Ala Met Glu Pro Gly Asn Gly Asp Asp Gln Gly Phe Gln
 50 55 60
 Glu Gly Glu Asp Glu Leu Gly Asp Glu Glu Glu Gly Ala Gly Asp Glu
 65 70 75 80
 Asn Gly His Gly Glu Gln Gln Pro Gln Pro Pro Ala Thr Gln Gln Gln
 85 90 95
 Gln Pro Gln Gln Gln Arg Gly Ala Ala Lys Glu Ala Ala Gly Lys Ser
 100 105 110
 Ser Gly Pro Thr Ser Leu Phe Ala Val Thr Val Ala Pro Pro Gly Ala
 115 120 125
 Arg Gln Gly Gln Gln Gln Ala Gly Gly Lys Lys Lys Ala Glu Gly Gly
 130 135 140
 Gly Gly Gly Gly Arg Pro Gly Ala Pro Ala Ala Gly Asp Gly Lys Thr
 145 150 155 160
 Glu Gln Lys Gly Gly Asp Lys Lys Arg Gly Val Lys Arg Pro Arg Glu
 165 170 175
 Asp His Gly Arg Gly Tyr Phe Glu Tyr Ile Glu Glu Asn Lys Tyr Ser
 180 185 190
 Arg Ala Lys Ser Pro Gln Pro Pro Val Glu Glu Glu Asp Glu His Phe
 195 200 205

Asp Asp Thr Val Val Cys Leu Asp Thr Tyr Asn Cys Asp Leu His Phe
 210 215 220
 Lys Ile Ser Arg Asp Arg Leu Ser Ala Ser Ser Leu Thr Met Glu Ser
 225 230 235 240
 Phe Ala Phe Leu Trp Ala Gly Gly Arg Ala Ser Tyr Gly Val Ser Lys
 245 250 255
 Gly Lys Val Cys Phe Glu Met Lys Val Thr Glu Lys Ile Pro Val Arg
 260 265 270
 His Leu Tyr Thr Lys Asp Ile Asp Ile His Glu Val Arg Ile Gly Trp
 275 280 285
 Ser Leu Thr Thr Ser Gly Met Leu Leu Gly Glu Glu Glu Phe Ser Tyr
 290 295 300
 Gly Tyr Ser Leu Lys Gly Ile Lys Thr Cys Asn Cys Glu Thr Glu Asp
 305 310 315 320
 Tyr Gly Glu Lys Phe Asp Glu Asn Asp Val Ile Thr Cys Phe Ala Asn
 325 330 335
 Phe Glu Ser Asp Glu Val Glu Leu Ser Tyr Ala Lys Asn Gly Gln Asp
 340 345 350
 Leu Gly Val Ala Phe Lys Ile Ser Lys Glu Val Leu Ala Gly Arg Pro
 355 360 365
 Leu Phe Pro His Val Leu Cys His Asn Cys Ala Val Glu Phe Asn Phe
 370 375 380
 Gly Gln Lys Glu Lys Pro Tyr Phe Pro Ile Pro Glu Glu Tyr Thr Phe
 385 390 395 400
 Ile Gln Asn Val Pro Leu Glu Asp Arg Val Arg Gly Pro Lys Gly Pro
 405 410 415
 Glu Glu Lys Lys Asp Cys Glu Val Val Met Met Ile Gly Leu Pro Gly
 420 425 430
 Ala Gly Lys Thr Thr Trp Val Thr Lys His Ala Ala Glu Asn Pro Gly

435	440	445
Lys Tyr Asn Ile Leu Gly Thr Asn Thr Ile Met Asp Lys Met Met Val		
450	455	460
Ala Gly Phe Lys Lys Gln Met Ala Asp Thr Gly Lys Leu Asn Thr Leu		
465	470	475
Leu Gln Arg Ala Pro Gln Cys Leu Gly Lys Phe Ile Glu Ile Ala Ala		
485	490	495
Arg Lys Lys Arg Asn Phe Ile Leu Asp Gln Thr Asn Val Ser Ala Ala		
500	505	510
Ala Gln Arg Arg Lys Met Cys Leu Phe Ala Gly Phe Gln Arg Lys Ala		
515	520	525
Val Val Val Cys Pro Lys Asp Glu Asp Tyr Lys Gln Arg Thr Gln Lys		
530	535	540
Lys Ala Glu Val Glu Gly Lys Asp Leu Pro Glu His Ala Val Leu Lys		
545	550	555
Met Lys Gly Asn Phe Thr Leu Pro Glu Val Ala Glu Cys Phe Asp Glu		
565	570	575
Ile Thr Tyr Val Glu Leu Gln Lys Glu Glu Ala Gln Lys Leu Leu Glu		
580	585	590
Gln Tyr Lys Glu Glu Ser Lys Lys Ala Leu Pro Pro Glu Lys Lys Gln		
595	600	605
Asn Thr Gly Ser Lys Lys Ser Asn Lys Asn Lys Ser Gly Lys Asn Gln		
610	615	620
Phe Asn Arg Gly Gly Gly His Arg Gly Arg Gly Gly Phe Asn Met Arg		
625	630	635
Gly Gly Asn Phe Arg Gly Gly Ala Pro Gly Asn Arg Gly Gly Tyr Asn		
645	650	655
Arg Arg Gly Asn Met Pro Gln Arg Gly Gly Gly Gly Gly Gly Ser Gly		
660	665	670

Gly Ile Gly Tyr Pro Tyr Pro Arg Ala Pro Val Phe Pro Gly Arg Gly
 675 680 685
 Ser Tyr Ser Asn Arg Gly Asn Tyr Asn Arg Gly Gly Met Pro Asn Arg
 690 695 700
 Gly Asn Tyr Asn Gln Asn Phe Arg Gly Arg Gly Asn Asn Arg Gly Tyr
 705 710 715 720
 Lys Asn Gln Ser Gln Gly Tyr Asn Gln Trp Gln Gln Gly Gln Phe Trp
 725 730 735
 Gly Gln Lys Pro Trp Ser Gln His Tyr His Gln Gly Tyr Tyr
 740 745 750

<210> 2239

<211> 453

<212> PRT

<213> Homo sapiens

<400> 2239

Met Tyr Val Gly Leu Thr Pro Asp Lys Arg Phe Leu Pro Gly His Leu
 1 5 10 15
 Gly Met Gly Leu Val Glu Gly Tyr Asp Ser Met Gly Tyr Glu Met Ser
 20 25 30
 Lys Pro Asp Leu Arg Ala Glu Leu Glu Ala Asp Leu Lys Leu Ile Cys
 35 40 45
 Asp Gly Lys Lys Asp Lys Phe Val Val Leu Arg Gln Gln Val Gln Lys
 50 55 60
 Tyr Lys Gln Val Phe Ile Glu Ala Val Ala Lys Ala Lys Lys Leu Asp
 65 70 75 80
 Glu Ala Leu Ala Gln Tyr Phe Gly Asn Gly Thr Glu Leu Ala Gln Gln

	85	90	95
Glu Asp Ile Tyr Pro Ala Met Pro Glu Pro Ile Arg Lys Cys Pro Gln			
100	105	110	
Cys Asn Lys Asp Met Val Leu Lys Thr Lys Lys Asn Gly Gly Phe Tyr			
115	120	125	
Leu Ser Cys Met Gly Phe Pro Glu Cys Arg Ser Ala Val Trp Leu Pro			
130	135	140	
Asp Ser Val Leu Glu Ala Ser Arg Asp Ser Ser Val Cys Pro Val Cys			
145	150	155	160
Gln Pro His Pro Val Tyr Arg Leu Lys Leu Lys Phe Lys Arg Gly Ser			
165	170	175	
Leu Pro Pro Thr Met Pro Leu Glu Phe Val Cys Cys Ile Gly Gly Cys			
180	185	190	
Asp Asp Thr Leu Arg Glu Ile Leu Asp Leu Arg Phe Ser Gly Gly Pro			
195	200	205	
Pro Arg Ala Ser Gln Pro Ser Gly Arg Leu Gln Ala Asn Gln Ser Leu			
210	215	220	
Asn Arg Met Asp Asn Ser Gln His Pro Gln Pro Ala Asp Ser Arg Gln			
225	230	235	240
Thr Gly Ser Ser Lys Ala Leu Ala Gln Thr Leu Pro Pro Pro Thr Ala			
245	250	255	
Ala Gly Glu Ser Asn Ser Val Thr Cys Asn Cys Gly Gln Glu Ala Val			
260	265	270	
Leu Leu Thr Val Arg Lys Glu Gly Pro Asn Arg Gly Arg Gln Phe Phe			
275	280	285	
Lys Cys Asn Gly Gly Ser Cys Asn Phe Phe Leu Trp Ala Asp Ser Pro			
290	295	300	
Asn Pro Gly Ala Gly Gly Pro Pro Ala Leu Ala Tyr Arg Pro Leu Gly			
305	310	315	320

<210> 2240

<211> 283

<212> PRT

<213> Homo sapiens

<400> 2240

出証特 2 0 0 4 - 3 0 5 9 6 6 1

20	25	30	
Ser His Lys Cys His His Ile Trp Leu Trp Val Gly Val Pro Ala Trp			
35	40	45	
His Pro Arg Ala Ser Arg Cys Gly Gly Ala Gln Pro Ser Ser Trp Leu			
50	55	60	
His Gln Lys Ala Ala Arg Ala Phe Trp Leu Ser Leu Pro Ala Ala Lys			
65	70	75	80
Leu Arg His His Ser Ser Arg Trp Leu Arg Arg Ser Gly Ala Phe Ser			
85	90	95	
Ser Gly Ser Thr Leu Lys Pro Pro Pro Ser Pro Ser Pro Ala Pro Leu			
100	105	110	
Cys His Ala Asp Asn Leu Arg Thr Gly Arg Thr Arg Pro Ser Gly Gly			
115	120	125	
Arg Pro Trp Phe Leu Leu Gly Gly Asp Glu Arg Glu Arg Leu Trp Ala			
130	135	140	
Glu Leu Leu Arg Thr Val Ser Pro Glu Leu Ile Leu Asp His Glu Val			
145	150	155	160
Pro Ser Leu Pro Ala Phe Pro Gly Gln Glu Pro Arg Cys Gly Pro Glu			
165	170	175	
Pro Thr Glu Val Phe Thr Val Gly Pro Lys Thr Phe Ser Trp Thr Pro			
180	185	190	
Phe Pro Pro Asp Leu Trp Gly Pro Gly Arg Ser Tyr Arg Leu Leu His			
195	200	205	
Gly Ala Gly Gly His Leu Glu Ser Pro Ala Arg Ser Leu Pro Gln Arg			
210	215	220	
Pro Ala Pro Asp Pro Cys Arg Ala Pro Arg Val Glu Gln Gln Pro Ser			
225	230	235	240
Val Glu Gly Ala Ala Ala Leu Arg Ser Cys Pro Met Cys Gln Lys Glu			
245	250	255	

Phe Ala Pro Arg Leu Thr Gln Leu Asp Val Asp Ser His Leu Ala Gln

260

265

270

Cys Leu Ala Glu Ser Thr Glu Asp Val Thr Trp

275

280

<210> 2241

<211> 743

<212> PRT

<213> Homo sapiens

<400> 2241

Met Glu Ser Arg Pro Pro Val Leu Ser Leu Ser Pro Ile Phe Leu Tyr

1

5

10

15

Thr Cys Glu Met Phe Gln Asp Pro Val Ala Phe Glu Asp Val Ala Val

20

25

30

Asn Phe Thr Gln Glu Glu Trp Thr Leu Leu Asp Ile Ser Gln Lys Asn

35

40

45

Leu Phe Arg Glu Val Met Leu Glu Thr Phe Arg Asn Leu Thr Ser Ile

50

55

60

Gly Lys Lys Trp Ser Asp Gln Asn Ile Glu Tyr Glu Tyr Gln Asn Pro

65

70

75

80

Arg Arg Ser Phe Arg Ser Leu Ile Glu Glu Lys Val Asn Glu Ile Lys

85

90

95

Glu Asp Ser His Cys Gly Glu Thr Phe Thr Gln Val Pro Asp Asp Arg

100

105

110

Leu Asn Phe Gln Glu Lys Lys Ala Ser Pro Glu Val Lys Ser Cys Asp

115

120

125

Ser Phe Val Cys Ala Glu Val Gly Ile Gly Asn Ser Ser Phe Asn Met

130 135 140
Ser Ile Arg Gly Asp Thr Gly His Lys Ala Tyr Glu Tyr Gln Glu Tyr
145 150 155 160
Gly Pro Lys Pro Tyr Lys Cys Gln Gln Pro Lys Asn Lys Lys Ala Phe
165 170 175
Arg Tyr Arg Pro Ser Ile Arg Thr Gln Glu Arg Asp His Thr Gly Glu
180 185 190
Lys Pro Tyr Ala Cys Lys Val Cys Gly Lys Thr Phe Ile Phe His Ser
195 200 205
Ser Ile Arg Arg His Met Val Met His Ser Gly Asp Gly Thr Tyr Lys
210 215 220
Cys Lys Phe Cys Gly Lys Ala Phe His Ser Phe Ser Leu Tyr Leu Ile
225 230 235 240
His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys
245 250 255
Gly Lys Ser Phe Thr Tyr Ser Ala Thr Leu Gln Ile His Glu Arg Thr
260 265 270
His Thr Gly Glu Lys Pro Tyr Glu Cys Ser Lys Cys Asp Lys Ala Phe
275 280 285
His Ser Ser Ser Ser Tyr His Arg His Glu Arg Ser His Met Gly Glu
290 295 300
Lys Pro Tyr Gln Cys Lys Glu Cys Gly Lys Ala Phe Ala Tyr Thr Ser
305 310 315 320
Ser Leu Arg Arg His Glu Arg Thr His Ser Gly Lys Lys Pro Tyr Glu
325 330 335
Cys Lys Gln Tyr Gly Glu Gly Leu Ser Tyr Leu Ile Ser Phe Gln Thr
340 345 350
His Ile Arg Met Asn Ser Gly Glu Arg Pro Tyr Lys Cys Lys Ile Cys
355 360 365

Gly Lys Gly Phe Tyr Ser Ala Lys Ser Phe Gln Thr His Glu Lys Thr

370

375

380

His Thr Gly Glu Lys Arg Tyr Lys Cys Lys Gln Cys Gly Lys Ala Phe

385

390

395

400

Asn Leu Ser Ser Ser Phe Arg Tyr His Glu Arg Ile His Thr Gly Glu

405

410

415

Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Arg Ser Ala Ser

420

425

430

Gln Leu Arg Val His Gly Gly Thr His Thr Gly Glu Lys Pro Tyr Glu

435

440

445

Cys Lys Glu Cys Gly Lys Ala Phe Arg Ser Thr Ser His Leu Arg Val

450

455

460

His Gly Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys

465

470

475

480

Gly Lys Ala Phe Arg Tyr Val Lys His Leu Gln Ile His Glu Arg Thr

485

490

495

Glu Lys His Ile Arg Met Pro Ser Gly Glu Arg Pro Tyr Lys Cys Ser

500

505

510

Ile Cys Glu Lys Gly Phe Tyr Ser Ala Lys Ser Phe Gln Thr His Glu

515

520

525

Lys Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys

530

535

540

Ala Phe Arg Cys Cys Asn Ser Leu Arg Tyr His Glu Arg Thr His Thr

545

550

555

560

Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Arg Ser

565

570

575

Ala Ser His Leu Arg Met His Glu Arg Thr His Thr Gly Glu Lys Pro

580

585

590

Tyr Glu Cys Lys Gln Cys Gly Lys Ala Phe Ser Cys Ala Ser Asn Leu

出証特 2 0 0 4 - 3 0 5 9 6 6 1

Pro Pro Val Glu Pro Glu Leu Ser Pro Ser Glu Gln Glu Gln Pro Ala
 20 25 30
 Gln Pro Ser Gly Glu Val Glu Ser Ser Pro Ala Gln Gln Glu Thr Pro
 35 40 45
 Ala Gln Pro Pro Glu His His Glu Val Thr Val Ser Pro Pro Gly His
 50 55 60
 His Gln Thr Gln His Ser Asp Leu Pro Asn Val Ser Val Lys Pro Pro
 65 70 75 80
 Asp Met Gln Leu Thr Ile Ala Thr Glu Pro Ser Ala Glu Val Gly Thr
 85 90 95
 Ser Pro Val His Gln Glu Ala Thr Ala Gln Leu Ser Gly Pro Gly Asn
 100 105 110
 Asp Val Glu Pro Pro Thr Ile Gln His Gly Gly Pro Pro Leu Pro Pro
 115 120 125
 Glu Ser Pro Glu Asp Ala Gly Pro Leu Ala Ile Gln Gln Glu Thr Ser
 130 135 140
 Val Gln Ser Pro Glu Pro Ile Asn Asn Glu Asn Pro Ser Pro Thr Gln
 145 150 155 160
 Gln Glu Ala Ala Ala Glu His Pro Gln Thr Ala Glu Lys Gly Lys Ser
 165 170 175
 Ser Leu Thr Gln Gln Glu Ala Pro Ala Glu Thr Pro Glu Leu Pro Asn
 180 185 190
 Val Val Val Ala Gln Ser Pro Glu His Ser Asn Leu Thr Gln Ala Thr
 195 200 205
 Val Gln Pro Leu Asp Leu Gly Leu Thr Ile Thr Pro Glu Ser Thr Thr
 210 215 220
 Glu Val Glu Leu Ser Pro Thr Met Gln Glu Thr Pro Thr His Pro Pro
 225 230 235 240
 Lys Lys Val Val Pro Gln Leu Pro Val Tyr Gln Glu Val Thr Ile Pro

	245		250		255
Thr	Pro	Gly	Gln	Asp	Gln
Ala	Gln	His	Pro	Met	Ser
Pro	Ser	Ile	Thr		
	260		265		270
Val	Gln	Pro	Leu	Asp	Leu
Gly	Leu	Thr	Ile	Thr	Pro
Glu	Pro	Thr	Thr		
	275		280		285
Glu	Val	Gly	His	Ser	Thr
Pro	Leu	Lys	Lys	Asn	Val
Val	Pro	Pro	Lys		
	290		295		300
His	Pro	Lys	Val	Thr	Leu
Pro	His	Pro	Asp	Gln	Val
Gln	Thr	Gln	His		
	305		310		315
					320
Ser	Asn	Leu	Thr	Gln	Ala
Thr	Val	Gln	Pro	Leu	Asp
Leu	Gly	Leu	Thr		
	325		330		335
Thr	Thr	Pro	Glu	Ser	Thr
Thr	Glu	Ile	Glu	Pro	Ser
Ala	Ala	Leu	Thr		
	340		345		350
Thr	Thr	Ala	Pro	Pro	Pro
Glu	His	Pro	Glu	Val	Thr
Leu	Pro	Pro	Ser		
	355		360		365
Asp	Lys	Gly	Arg	Ala	Gln
His	Ser	Asn	Leu	Thr	Gln
Val	Thr	Leu	Pro		
	370		375		380
Pro	Leu	Asp	Leu	Glu	Leu
Thr	Ile	Thr	Thr	Glu	Pro
Thr	Thr	Glu	Val		
	385		390		395
					400
Lys	Pro	Ser	Pro	Thr	Thr
Glu	Glu	Thr	Ser	Thr	Gln
Pro	Pro	Asp	Leu		
	405		410		415
Gly	Leu	Ala	Ile	Thr	Pro
Glu	Pro	Thr	Thr	Glu	Thr
Gly	His	Ser	Thr		
	420		425		430
Ala	Leu	Glu	Lys	Thr	Thr
Ala	Pro	His	Pro	Asp	Gln
Val	Gln	Thr	Leu		
	435		440		445
His	Arg	Lys	Leu	Thr	Glu
Val	Thr	Gly	Pro	Pro	Thr
Glu	Leu	Glu	Pro		
	450		455		460
Thr	Gln	Asp	Ser	Leu	Val
Gln	Ser	Glu	Ser	Tyr	Ala
Gln	Asn	Lys	Ala		
	465		470		475
					480

Leu Thr Ala Pro Glu Glu Gln

485

<210> 2243

<211> 605

<212> PRT

<213> Homo sapiens

<400> 2243

Met	Asp	Lys	Arg	Val	Lys	Lys	Leu	Pro	Leu	Met	Ala	Leu	Ser	Thr	Thr
1				5					10					15	
Met	Ala	Glu	Ser	Phe	Lys	Glu	Leu	Asp	Pro	Asp	Ser	Ser	Met	Gly	Lys
				20				25					30		
Ala	Leu	Glu	Met	Ser	Cys	Ala	Ile	Gln	Asn	Gln	Leu	Ala	Arg	Ile	Leu
			35				40				45				
Ala	Glu	Phe	Glu	Met	Thr	Leu	Glu	Arg	Asp	Val	Leu	Gln	Pro	Leu	Ser
	50					55					60				
Arg	Leu	Ser	Glu	Glu	Glu	Leu	Pro	Ala	Ile	Leu	Lys	His	Lys	Lys	Ser
65					70					75				80	
Leu	Gln	Lys	Leu	Val	Ser	Asp	Trp	Asn	Thr	Leu	Lys	Ser	Arg	Leu	Ser
				85				90					95		
Gln	Ala	Thr	Lys	Asn	Ser	Gly	Ser	Ser	Gln	Gly	Leu	Gly	Gly	Ser	Pro
			100					105					110		
Gly	Ser	His	Ser	His	Thr	Thr	Met	Ala	Asn	Lys	Val	Glu	Thr	Leu	Lys
		115					120					125			
Glu	Glu	Glu	Glu	Glu	Leu	Lys	Arg	Lys	Val	Glu	Gln	Cys	Arg	Asp	Glu
	130					135						140			
Tyr	Leu	Ala	Asp	Leu	Tyr	His	Phe	Val	Thr	Lys	Glu	Asp	Ser	Tyr	Ala

145 150 155 160
Asn Tyr Phe Ile Arg Leu Leu Glu Ile Gln Ala Asp Tyr His Arg Arg
 165 170 175
Ser Leu Ser Ser Leu Asp Thr Ala Leu Ala Glu Leu Arg Glu Asn His
 180 185 190
Gly Gln Ala Asp His Ser Pro Ser Met Thr Ala Thr His Phe Pro Arg
 195 200 205
Val Tyr Gly Val Ser Leu Ala Thr His Leu Gln Glu Leu Gly Arg Glu
 210 215 220
Ile Ala Leu Pro Ile Glu Ala Cys Val Met Met Leu Leu Ser Glu Gly
225 230 235 240
Met Lys Glu Glu Gly Leu Phe Arg Leu Ala Ala Gly Ala Ser Val Leu
 245 250 255
Lys Arg Leu Lys Gln Thr Met Ala Ser Asp Pro His Ser Leu Glu Glu
 260 265 270
Phe Cys Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu
 275 280 285
Arg Glu Leu Pro Glu Pro Leu Met Thr Phe Asp Leu Tyr Asp Asp Trp
 290 295 300
Met Arg Ala Ala Ser Leu Lys Glu Pro Gly Ala Arg Leu Gln Ala Leu
305 310 315 320
Gln Glu Val Cys Ser Arg Leu Pro Pro Glu Asn Leu Ser Asn Leu Arg
 325 330 335
Tyr Leu Met Lys Phe Leu Ala Arg Leu Ala Glu Glu Gln Glu Val Asn
 340 345 350
Lys Met Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu
 355 360 365
Trp Pro Pro Glu Lys Glu Gly Asp Gln Ala Gln Leu Asp Ala Ala Ser
 370 375 380

Val Ser Ser Ile Gln Val Val Gly Val Val Glu Ala Leu Ile Gln Ser
385 390 395 400
Ala Asp Thr Leu Phe Pro Gly Asp Ile Asn Phe Asn Val Ser Gly Leu
405 410 415
Phe Ser Ala Val Thr Leu Gln Asp Thr Val Ser Asp Arg Leu Ala Ser
420 425 430
Glu Glu Leu Pro Ser Thr Ala Val Pro Thr Pro Ala Thr Thr Pro Ala
435 440 445
Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Pro Ala Leu Ala Ser Ala
450 455 460
Ala Thr Lys Glu Arg Thr Glu Ser Glu Val Pro Pro Arg Pro Ala Ser
465 470 475 480
Pro Lys Val Thr Arg Ser Pro Pro Glu Thr Ala Ala Pro Val Glu Asp
485 490 495
Met Ala Arg Arg Ser Thr Gly Ser Leu Ala Ala Ala Val Glu Thr Ala
500 505 510
Ser Gly Arg Gln Ala Leu Val Val Gly Lys Pro Ser Pro Tyr Met Phe
515 520 525
Glu Cys Ile Thr Glu Asn Phe Ser Ile Asp Pro Ala Arg Thr Leu Met
530 535 540
Val Gly Asp Arg Leu Glu Thr Asp Ile Leu Phe Gly His Arg Cys Gly
545 550 555 560
Met Thr Thr Val Leu Thr Leu Thr Gly Val Ser Arg Leu Glu Glu Ala
565 570 575
Gln Ala Tyr Leu Ala Ala Gly Gln His Asp Leu Val Pro His Tyr Tyr
580 585 590
Val Glu Ser Ile Ala Asp Leu Thr Glu Gly Leu Glu Asp
595 600 605

<210> 2244

<211> 701

<212> PRT

<213> Homo sapiens

<400> 2244

Met	Val	Phe	Leu	Gly	Arg	Ile	Asn	Glu	Val	Glu	Pro	Ala	Lys	Gly	Leu
1				5				10					15		
Ala	Glu	Ser	Leu	Ala	Pro	Thr	Glu	Arg	Ser	Val	Lys	Ser	Leu	Asp	Met
			20					25					30		
Glu	Glu	Lys	Asp	Tyr	Ser	Glu	Ala	Asp	Gly	Leu	Ser	Glu	Arg	Thr	Thr
		35					40					45			
Pro	Ser	Lys	Ala	Gln	Lys	Ser	Pro	Gln	Lys	Ile	Ala	Lys	Lys	Tyr	Lys
	50					55					60				
Ser	Ala	Ile	Cys	Arg	Val	Thr	Leu	Leu	Asp	Ala	Ser	Glu	Tyr	Glu	Cys
65				70					75					80	
Glu	Val	Glu	Lys	His	Gly	Arg	Gly	Gln	Val	Leu	Phe	Asp	Leu	Val	Cys
				85					90					95	
Glu	His	Leu	Asn	Leu	Leu	Glu	Lys	Asp	Tyr	Phe	Gly	Leu	Thr	Phe	Cys
		100						105					110		
Asp	Ala	Asp	Ser	Gln	Lys	Asn	Trp	Leu	Asp	Pro	Ser	Lys	Glu	Ile	Lys
		115						120					125		
Lys	Gln	Ile	Arg	Ser	Ser	Pro	Trp	Asn	Phe	Ala	Phe	Thr	Val	Lys	Phe
	130					135					140				
Tyr	Pro	Pro	Asp	Pro	Ala	Gln	Leu	Thr	Glu	Asp	Ile	Thr	Arg	Tyr	Tyr
145				150						155				160	
Leu	Cys	Leu	Gln	Leu	Arg	Ala	Asp	Ile	Ile	Thr	Gly	Arg	Leu	Pro	Cys
				165						170				175	